

FILE 'REGISTRY' ENTERED AT 14:23:21 ON 01 MAR 2004  
L1 18 SEA ABB=ON PLU=ON AGACAATCACAGTCTCTGCGGA | ATCCTTGTCCTC  
CACGGGTT | CTCATTTGGAATTTTGCC | CGAGTGAAGATCCCCTT/SQSN  
AND SQL=<60

L1 ANSWER 1 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 644078-30-8 REGISTRY  
CN DNA, d(C-C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T-T-T-A) (9CI) (CA INDEX  
NAME)

OTHER NAMES:

CN 143: PN: WO2004003140 SEQID: 144 unclaimed DNA  
CI MAN  
SQL 22

SEQ 1 ccgagtgaag atccccctttt ta  
=====

HITS AT: 2-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 140:92602

L1 ANSWER 2 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 644078-29-5 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C-G-A-T-T) (9CI) (CA INDEX  
NAME)

OTHER NAMES:

CN 142: PN: WO2004003140 SEQID: 143 unclaimed DNA  
CI MAN  
SQL 22

SEQ 1 ctcatttgga attttgccga tt  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 140:92602

L1 ANSWER 3 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 566959-46-4 REGISTRY  
CN DNA, d(C-C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T-T-T-A) (9CI) (CA INDEX  
NAME)

OTHER NAMES:

CN 127: PN: WO03060090 SEQID: 129 claimed DNA  
CI MAN  
SQL 22

SEQ 1 ccgagtgaag atccccctttt ta  
=====

HITS AT: 2-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 139:132464

L1 ANSWER 4 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 566959-45-3 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-G-C-C-G-A-T-T) (9CI) (CA INDEX  
NAME)

OTHER NAMES:

CN 126: PN: WO03060090 SEQID: 128 claimed DNA  
CI MAN  
SQL 22

SEQ 1 ctcatTTgga attttgccga tt  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 139:132464

L1 ANSWER 5 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 515226-13-8 REGISTRY  
CN DNA, d(C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T-T-T-A) (9CI) (CA INDEX  
NAME)  
CI MAN  
SQL 21

SEQ 1 cgagtgaaga tccccttttt a  
=====

HITS AT: 1-17

REFERENCE 1: 138:332416

L1 ANSWER 6 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 515226-12-7 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C-G-A-T-T) (9CI) (CA INDEX  
NAME)  
CI MAN  
SQL 22

SEQ 1 ctcatTTgga attttgccga tt  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 138:332416

L1 ANSWER 7 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 479323-55-2 REGISTRY  
CN DNA, d(C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 17

SEQ 1 cgagtgaaga tcccctt  
=====

HITS AT: 1-17

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*



REFERENCE 1: 137:380556

L1 ANSWER 8 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 479323-54-1 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 18

SEQ 1 ctcatttgga attttgcc  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 9 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 479323-53-0 REGISTRY  
CN DNA, d(C-C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T-T-T-A) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 22

SEQ 1 ccgagtgaag atcccctttt ta  
=====

HITS AT: 2-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 10 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 479323-52-9 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C-G-A-T-T) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 22

SEQ 1 ctcatttgga attttgccga tt  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 11 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 475604-53-6 REGISTRY  
CN DNA, d(A-T-C-C-T-T-G-T-C-C-T-C-C-A-C-G-G-G-T-T) (9CI) (CA INDEX NAME)  
CI MAN  
SQL 20

SEQ 1 atccttgtcc tccacgggtt  
=====

HITS AT: 1-20

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 12 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 475604-52-5 REGISTRY  
CN DNA, d(A-G-A-C-A-A-T-C-A-C-A-G-T-C-T-C-T-G-C-G-G-A) (9CI) (CA INDEX  
NAME)  
CI MAN  
SQL 22

SEQ 1 agacaatcac agtctctgcg ga  
=====

HITS AT: 1-22

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:380556

L1 ANSWER 13 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-56-0 REGISTRY  
CN DNA, d(C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 17: PN: WO02070751 SEQID: 17 claimed DNA  
CI MAN  
SQL 17

SEQ 1 cgagtgaaga tcccctt  
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HITS AT: 1-17

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

L1 ANSWER 14 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-55-9 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 16: PN: WO02070751 SEQID: 16 claimed DNA  
CI MAN  
SQL 18

SEQ 1 ctcatTTTgga attttgcc  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

L1 ANSWER 15 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-50-4 REGISTRY  
CN DNA, d(A-T-C-C-T-T-G-T-C-C-T-C-C-A-C-G-G-G-T-T) (9CI) (CA INDEX

NAME)  
OTHER NAMES:  
CN 7: PN: WO02070751 SEQID: 7 claimed DNA  
CI MAN  
SQL 20

SEQ 1 atccttggtc tccacgggtt  
=====

HITS AT: 1-20

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

L1 ANSWER 16 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-49-1 REGISTRY  
CN DNA, d(A-G-A-C-A-A-T-C-A-C-A-G-T-C-T-C-T-G-C-G-G-A) (9CI) (CA INDEX  
NAME)

OTHER NAMES:  
CN 6: PN: WO02070751 SEQID: 6 claimed DNA  
CI MAN  
SQL 22

SEQ 1 agacaatcac agtctctgcg ga  
=====

HITS AT: 1-22

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

L1 ANSWER 17 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-48-0 REGISTRY  
CN DNA, d(C-C-G-A-G-T-G-A-A-G-A-T-C-C-C-C-T-T-T-T-T-A) (9CI) (CA INDEX  
NAME)

OTHER NAMES:  
CN 4: PN: WO02070751 SEQID: 4 claimed DNA  
CI MAN  
SQL 22

SEQ 1 ccgagtgaag atccccctttt ta  
=====

HITS AT: 2-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

L1 ANSWER 18 OF 18 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 458572-47-9 REGISTRY  
CN DNA, d(C-T-C-A-T-T-T-G-G-A-A-T-T-T-T-G-C-C-G-A-T-T) (9CI) (CA INDEX  
NAME)

OTHER NAMES:  
CN 3: PN: WO02070751 SEQID: 3 claimed DNA  
CI MAN  
SQL 22

SEQ 1 ctcatttgga attttgccga tt  
=====

HITS AT: 1-18

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

REFERENCE 1: 137:227595

FILE 'HCAPLUS' ENTERED AT 14:27:10 ON 01 MAR 2004  
L2 5 S L1

L2 ANSWER 1 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN  
ED Entered STN: 11 Jan 2004

ACCESSION NUMBER: 2004:20803 HCAPLUS

DOCUMENT NUMBER: 140:92602

TITLE: Cytokine receptor zcytor17 multimers, encoding  
polynucleotides and antibodies for diagnosis and  
treatment of inflammatory diseases

INVENTOR(S): Sprecher, Cindy A.; Gao, Zeren; Kuijper, Joseph  
L.; Dasovich, Maria M.; Grant, Francis J.;  
Presnell, Scott R.; Whitmore, Theodore E.;  
Hammond, Angela K.; Novak, Julia E.; Gross, Jane  
A.; Dillon, Stacey R.

PATENT ASSIGNEE(S): Zymogenetics, Inc., USA

SOURCE: PCT Int. Appl., 372 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004003140	A2	20040108	WO 2003-US1983	20030121
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2003215838	A1	20031120	US 2003-351157	20030121
PRIORITY APPLN. INFO.:			US 2002-350325P	P 20020118
			US 2002-389108P	P 20020614
			US 2002-435361P	P 20021219

AB Novel polypeptide combinations, polynucleotides encoding the polypeptides, and related compns. and methods are disclosed for zcytor17-containing multimeric or heterodimer cytokine receptors that may be used as novel cytokine antagonists, and within methods for detecting ligands that stimulate the proliferation and/or development of hematopoietic, lymphoid and myeloid cells in vitro

and in vivo. The present invention also includes methods for producing the multimeric or heterodimeric cytokine receptor, uses therefor and antibodies thereto.

IT 644078-29-5 644078-30-8

RL: PRP (Properties)

(unclaimed nucleotide sequence; cytokine receptor zcytor17 multimers, encoding polynucleotides and antibodies for diagnosis and treatment of inflammatory diseases)

L2 ANSWER 2 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN

ED Entered STN: 25 Jul 2003

ACCESSION NUMBER: 2003:571117 HCAPLUS

DOCUMENT NUMBER: 139:132464

TITLE: Cytokine zcytor17 ligand, polynucleotides and antibodies for diagnosis and treatment of acute inflammatory diseases

INVENTOR(S): Sprecher, Cindy A.; Kuijper, Joseph L.; Dasovich, Maria M.; Grant, Francis J.; Hammond, Angela K.; Novak, Julia E.; Gross, Jane A.; Dillon, Stacey R.

PATENT ASSIGNEE(S): Zymogenetics, Inc., USA

SOURCE: PCT Int. Appl., 372 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003060090	A2	20030724	WO 2003-US1984	20030121
W:				
AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW:				
GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003224487	A1	20031204	US 2003-352554	20030121
PRIORITY APPLN. INFO.:			US 2002-350325P	P 20020118
			US 2002-375323P	P 20020425
			US 2002-435315P	P 20021219

AB The present invention relates to zcytor17lig polynucleotide, polypeptide and anti-zcytor17 antibody mols. The zcytor17lig is a novel cytokine. The polypeptides may be used within methods for stimulating the immune system, and proliferation and/or development of hematopoietic cells or hematopoietic cell progenitors in vitro and in vivo. The present invention also includes methods for producing the protein, polynucleotides and antibodies for diagnosis and treatment of acute inflammatory diseases such as inflammatory bowel disease, ulcerative colitis, Crohn's disease, atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia, toxic shock

syndrome, and infectious disease.

IT 566959-45-3 566959-46-4  
RL: ARU (Analytical role, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
(cytokine zcytor17 ligand for hematopoietic cell expansion and for diagnosis and treatment of acute inflammatory diseases)

L2 ANSWER 3 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN  
ED Entered STN: 04 Mar 2003

ACCESSION NUMBER: 2003:161443 HCAPLUS

DOCUMENT NUMBER: 138:332416

TITLE: Quantitative intra-individual monitoring of BCR-ABL transcript levels in archival bone marrow trephines of patients with chronic myeloid leukemia

AUTHOR(S): Bock, Oliver; Lehmann, Ulrich; Kreipe, Hans  
CORPORATE SOURCE: Institute of Pathology, Medizinische Hochschule Hannover, Hannover, Germany

SOURCE: Journal of Molecular Diagnostics (2003), 5(1), 54-60

CODEN: JMDIFP; ISSN: 1525-1578

PUBLISHER: Association for Molecular Pathology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We established a quant. real-time RT-PCR assay for the detection of chimeric BCR-ABL transcripts in archival formalin-fixed bone marrow trephines, both acrylate-embedded and paraffin-embedded. This new methodol. enables determination of transcript levels in direct comparison to histopathol. findings and therapeutic interventions during the time course of the disease in a retrospective and a prospective manner. We found an excellent correlation between the quant. mol. data and the morphol. evaluation as well as the clin. outcome for a cohort of chronic myeloid leukemia patients (n = 10). To the best of our knowledge, this is the first study demonstrating the feasibility of large-scale quant. expression anal. in archival bone marrow trephines for monitoring mol. markers over several years or even decades.

IT 515226-12-7 515226-13-8  
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(PCR primer for BCR-ABL transcript in chronic myeloid leukemia; quant. intra-individual monitoring of BCR-ABL transcript levels in archival bone marrow trephines of patients with chronic myeloid leukemia)

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN  
ED Entered STN: 13 Sep 2002

ACCESSION NUMBER: 2002:696171 HCAPLUS

DOCUMENT NUMBER: 137:227595

TITLE: Methods for quantitative multiplex reverse transcriptase-polymerase chain reaction for

esophageal adenocarcinoma diagnosis by detection  
of carcinoembryonic antigen gene expression in  
sentinel lymph nodes

INVENTOR(S): Godfrey, Tony E.; Luketich, James D.; Raja,  
Siva; Kelly, Lori A.; Finkelstein, Sydney D.  
PATENT ASSIGNEE(S): University of Pittsburgh of the Commonwealth  
System of Higher Education, USA  
SOURCE: PCT Int. Appl., 141 pp.  
CODEN: PIXXD2  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

WO 2002070751 A1 20020912 WO 2002-US6504 20020304

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,  
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,  
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,  
LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,  
TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ,  
BY, KG, KZ, MD, RU, TJ, TM  
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,  
CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT,  
SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,  
SN, TD, TG

US 2003017482 A1 20030123 US 2002-90326 20020304  
EP 1373569 A1 20040102 EP 2002-715027 20020304

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,  
PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

PRIORITY APPLN. INFO.: US 2001-273277P P 20010302  
WO 2002-US6504 W 20020304

AB A method for balancing multiplexed PCR methods is provided. In the  
method, two or more sequential temporal PCR stages are used to  
effectively sep. two or more PCR reactions in a single tube as an  
alternative to primer limiting to modulate the relative rate of  
production of a first amplicon by a first primer set and a second  
amplicon by a second primer set during the first and second  
amplification stages. Also provided are rapid RT-PCR methods that  
find particular use in intraoperative diagnoses and prognoses, for  
instance in diagnosing malignant esophageal adenocarcinoma by determining  
expression levels of carcinoembryonic antigen (CEA) in sentinel  
lymph nodes.

IT 458572-47-9 458572-48-0 458572-49-1  
458572-50-4 458572-55-9 458572-56-0  
RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP  
(Properties); ANST (Analytical study); BIOL (Biological study); USES  
(Uses)  
(primer sequence; methods for multiplex quant. RT-PCR for  
esophageal adenocarcinoma diagnosis by detection of  
carcinoembryonic antigen gene expression in sentinel lymph nodes)

L2 ANSWER 5 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN  
RD Entered STN: 04 Aug 2002

ACCESSION NUMBER: 2002:576750 HCAPLUS  
DOCUMENT NUMBER: 137:380556  
TITLE: Temperature-controlled primer limit for  
multiplexing of rapid, quantitative reverse  
transcription-PCR assays: application to  
intraoperative cancer diagnostics  
AUTHOR(S): Raja, Siva; El-Hefnawy, Talal; Kelly, Lori A.;  
Chestney, Melissa L.; Luketich, James D.;  
Godfrey, Tony E.  
CORPORATE SOURCE: Division of Thoracic Surgery, University of  
Pittsburgh Medical Center, Pittsburgh, PA,  
15213, USA  
SOURCE: Clinical Chemistry (Washington, DC, United  
States) (2002), 48(8), 1329-1337  
CODEN: CLCHAU; ISSN: 0009-9147  
PUBLISHER: American Association for Clinical Chemistry  
DOCUMENT TYPE: Journal  
LANGUAGE: English

AB Rapid-cycling, real-time PCR instruments bring the opportunity for improved intraoperative detection of metastasis to sentinel lymph nodes. Rapid, standardized, and internally controlled assays need to be developed that are sensitive and accurate. The authors describe rapid, multiplexed, internally controlled, quant. reverse transcription-PCR (QRT-PCR) assays for tyrosinase and carcinoembryonic antigen mRNAs on the SmartCycler (Cepheid). A temperature-controlled primer-limiting approach was used to eliminate amplification of the endogenous control gene as soon as its signal had reached threshold. Pos.-control oligonucleotide mimics were incorporated into all reactions to differentiate failed reactions from true neg. samples. The optimized assays for rapid QRT-PCR yielded results with threshold cycle values that were only 1-2 cycles higher than slower, more conventional protocols. In rapid PCR, the temperature-controlled multiplex assay was quant. over a dynamic range of at least 15 cycles, compared with only 6 cycles for conventional multiplexing methods. All histol. pos. lymph nodes examined were also QRT-PCR pos. for the appropriate marker, and the exogenous, internal pos.-control mimics produced signals in all neg. samples. Internally controlled, rapid QRT-PCR assays can be performed in an intraoperative time frame and with sufficient sensitivity to detect histol. identified metastases to lymph nodes.

IT 475604-52-5 475604-53-6 479323-52-9  
479323-53-0 479323-54-1 479323-55-2

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
(primer; temperature-controlled primer limit for multiplexing of rapid, quant. reverse transcription-PCR assays and application to intraoperative cancer diagnostics)

REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE  
FOR THIS RECORD. ALL CITATIONS AVAILABLE  
IN THE RE FORMAT

=> fil hom  
FILE 'HOME' ENTERED AT 14:28:07 ON 01 MAR 2004

reprints' link

August 2002



09:38:24 2004

us-10-090-326-6.max.rge

GenCore version 5.1.6  
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eic search, using sw model  
February 29, 2004, 08:42:24 ; Search time 686.857 Seconds  
(without alignments)  
1388.275 Million cell updates/sec

S-10-090-326-6  
2  
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DENSITY\_NUC  
apop 10.0 , Gapext 1.0  
470272 seqs, 21671516995 residues  
its satisfying chosen parameters: 1685580

ngth: 0  
ngth: 60  
Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

GenEmbl: \*  
.: gb.ba.\*  
.: gb.htg.\*  
.: gb.in.\*  
.: gb.om.\*  
.: gb.ov.\*  
.: gb.pat.\*  
.: gb.ph.\*  
.: gb.pl.\*  
.: gb.pr.\*  
.: gb.ro.\*  
.: gb.sts.\*  
.: gb.sy.\*  
.: gb.un.\*  
.: gb.vi.\*  
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.: em.fun.\*  
.: em.hum.\*  
.: em.in.\*  
.: em.mu.\*  
.: em.om.\*  
.: em.or.\*  
.: em.ov.\*  
.: em.pat.\*  
.: em.ph.\*  
.: em.pl.\*  
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.: em.un.\*  
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.: em.htg.hum.\*  
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.: em.htg.other.\*  
.: em.htg.mus.\*  
.: em.htg.pln.\*  
.: em.htg.pln.\*  
.: em.htg.rod.\*  
.: em.htg.mam.\*  
.: em.htg.vrt.\*  
.: em.sv.\*  
.: em.htgo.hum.\*  
.: em.htgo.mus.\*  
.: em.htgo.other.\*

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being pr  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Descriptic
1	15.8	71.8	46	6	A39901	A39901 Seq
C 2	15.8	71.8	46	6	A39902	A39902 Seq
3	15.8	71.8	46	6	I67749	I67749 Seq
C 4	15.8	71.8	46	6	I67750	I67750 Seq
C 5	15.6	70.9	30	6	AR073249	AR073249 S
C 6	14.2	64.5	20	12	AB069564	AB069564
7	14	63.6	25	6	AX688871	AX688871 S
8	14	63.6	25	6	AX688872	AX688872 S
9	14	63.6	25	6	AX688873	AX688873 S
10	14	63.6	25	6	AX688874	AX688874 S
11	14	63.6	58	11	BX322287	BX322287
12	13.6	61.8	21	6	AX154379	AX154379 S
13	13.6	61.8	37	6	AR368993	AR368993 S
14	13.6	61.8	50	6	AX794202	AX794202 S
15	13.6	61.8	50	14	APHCNOV5E	MI0505 FC
16	13.6	61.8	53	6	AX794228	AX794228 S
C 17	13.2	60.0	22	6	AR252308	AR252308 S
C 18	13.2	60.0	22	6	BD133429	BD133429 S
C 19	13.2	60.0	35	6	I20757	I20757 Seq
C 20	13.2	60.0	35	6	AR381829	AR381829 S
C 21	13.2	60.0	35	6	BD107806	BD107806 C
22	13.2	60.0	47	6	AR289738	AR289738 S
23	13.2	60.0	51	6	AX199173	AX199173 S
24	13.2	60.0	51	6	AX199174	AX199174 S
C 25	13	59.1	22	6	AR072233	AR072233 S
C 26	13	59.1	22	6	I26344	I26344 Seq
C 27	13	59.1	25	6	AX688870	AX688870 S
28	13	59.1	25	6	AX688875	AX688875 S
29	13	59.1	28	6	AR090992	AR090992 S
30	13	59.1	28	6	AR198027	AR198027 S
31	13	59.1	28	6	AR260181	AR260181 S
32	13	59.1	28	6	AX794235	AX794235 S
33	13	59.1	34	6	I92361	I92361 Seq
34	13	59.1	40	6	AX538476	AX538476 S
C 35	13	59.1	47	6	AX195024	AX195024 S
36	13	59.1	50	6	AX234381	AX234381 S
37	13	59.1	51	6	AX158793	AX158793 S
38	13	59.1	51	6	AX158794	AX158794 S
39	13	59.1	51	6	AX158795	AX158795 S
C 40	13	59.1	60	6	AX234390	AX234390 S
C 41	12.8	58.2	20	6	AX285267	AX285267 S
C 42	12.8	58.2	20	6	AX302070	AX302070 S
C 43	12.8	58.2	24	6	AR289827	AR289827 S
C 44	12.8	58.2	47	6	AX117974	AX117974 S
C 45	12.8	58.2	51	6	AX190056	AX190056 S
C 46	12.8	58.2	53	6	A38622	A38622 Se
C 47	12.6	57.3	20	6	BD000414	BD000414
48	12.6	57.3	24	6	AX444764	AX444764 S
49	12.6	57.3	25	6	AX487737	AX487737 S
50	12.6	57.3	25	6	AX688876	AX688876 S
51	12.6	57.3	25	6	AX688877	AX688877 S
C 52	12.6	57.3	28	6	BD012173	BD012173 S
C 53	12.6	57.3	29	6	BD007101	BD007101 S
C 54	12.6	57.3	30	6	AX611183	AX611183 S
55	12.6	57.3	35	6	EL1201	EL1201 Pr
C 56	12.6	57.3	35	6	AR381830	AR381830 S
C 57	12.6	57.3	35	6	BD107807	BD107807 S
C 58	12.6	57.3	45	6	E41224	E41224 Me
59	12.6	57.3	47	6	AR291461	AR291461 S
C 60	12.6	57.3	48	6	AR038999	AR038999 S
61	12.6	57.3	48	6	AR107391	AR107391 S
62	12.6	57.3	48	6	AR179353	AR179353 S
63	12.6	57.3	48	6	BD191616	BD191616 S
C 64	12.6	57.3	49	6	I88612	I88612 Se
65	12.6	57.3	50	6	BD021860	BD021860 S

57.3	51	6	AX156752	Sequence	139	12.2	55.5	43	6	AR066433	AR066433
57.3	59	6	AR117938	Sequence	140	12.2	55.5	48	6	AR032396	AR032396
57.3	59	6	AX702420	Sequence	141	12.2	55.5	48	6	I29136	I29136 Se
57.3	60	6	AX601604	Sequence	142	12.2	55.5	48	6	I90810	I90810 Se
57.3	60	9	HUMSAU3A18	D49602 Homo sapien	143	12.2	55.5	49	6	AR209060	AR209060
57.3	60	14	POLDIPE	M30215 Poliovirus	144	12.2	55.5	49	6	AR032467	AR032467
56.4	17	6	AR264874	Sequence	145	12.2	55.5	49	6	I29207	I29207 Se
56.4	17	6	AX672976	Sequence	146	12.2	55.5	49	6	I90881	I90881 Se
56.4	21	6	AX096905	Sequence	147	12.2	55.5	49	6	AR209131	AR209131
56.4	23	6	AX609017	Sequence	148	12.2	55.5	50	6	AR282107	AR282107
56.4	24	6	BD123414	SREBP-2 g	149	12.2	55.5	50	6	AR282183	AR282183
56.4	27	6	AX115218	Sequence	150	12.2	55.5	51	6	AX155780	AX155780
56.4	29	6	AR275150	Sequence	151	12.2	55.5	51	6	AX203927	AX203927
56.4	29	6	AR275152	Sequence	152	12.2	55.5	52	6	AX358962	AX358962
56.4	29	6	AR275152	Sequence	153	12.2	55.5	52	6	AX823877	AX823877
56.4	29	6	AR275656	Sequence	154	12.2	54.5	20	6	BD142669	BD142669
56.4	29	6	AR275658	Sequence	155	12.2	54.5	21	6	AR092578	AR092578
56.4	29	6	AR302383	Sequence	156	12.2	54.5	21	6	AX546754	AX546754
56.4	29	6	AR302385	Sequence	157	12.2	54.5	21	6	BD076524	BD076524
56.4	30	6	AR201030	Sequence	158	12.2	54.5	22	6	AR173645	AR173645
56.4	30	6	AR202721	Sequence	159	12.2	54.5	22	6	BD057079	BD057079
56.4	30	6	BD009773	Humanized	160	12.2	54.5	23	6	AR252592	AR252592
56.4	30	6	BD103748	A method	161	12.2	54.5	23	6	AX055761	AX055761
56.4	33	6	AX166487	Sequence	162	12.2	54.5	23	6	AX403436	AX403436
56.4	34	6	AR073271	Sequence	163	12.2	54.5	23	6	AX742290	AX742290
56.4	34	6	AR073272	Sequence	164	12.2	54.5	23	6	AX742689	AX742689
56.4	35	6	AR261794	Sequence	165	12.2	54.5	23	6	BD184114	BD184114
56.4	40	6	A22794	NS3/NS4 HCV	166	12.2	54.5	23	6	BD184542	BD184542
56.4	40	6	AR031221	Sequence	167	12.2	54.5	24	6	AR124725	AR124725
56.4	40	6	AR145037	Sequence	168	12.2	54.5	24	6	E44013	E44013 NC
56.4	47	6	AR291053	Sequence	169	12.2	54.5	25	6	AX688869	AX688869
56.4	48	6	AX538900	Sequence	170	12.2	54.5	26	6	AX181875	AX181875
56.4	48	6	AX538901	Sequence	171	12.2	54.5	26	6	BD077275	BD077275
56.4	48	6	AX777222	Sequence	172	12.2	54.5	26	6	BD077275	BD077275
56.4	50	10	MMU41939	U41939 Mus musculi	173	12.2	54.5	29	6	E44009	E44009 NC
56.4	51	6	AX158733	Sequence	174	12.2	54.5	30	6	AX923503	AX923503
56.4	51	6	AX158734	Sequence	175	12.2	54.5	30	6	AR092575	AR092575
56.4	51	6	AX161895	Sequence	176	12.2	54.5	30	6	AR161734	AR161734
56.4	51	6	AX189854	Sequence	177	12.2	54.5	30	6	BD076521	BD076521
56.4	51	6	AX189855	Sequence	178	12.2	54.5	32	6	BD228400	BD228400
55.5	21	6	AX1613803	Sequence	179	12.2	54.5	32	6	AX021034	AX021034
55.5	22	6	AR164381	Sequence	180	12.2	54.5	32	6	AX742153	AX742153
55.5	22	6	AR205924	Sequence	181	12.2	54.5	33	6	AR216133	AR216133
55.5	22	6	AX613801	Sequence	182	12.2	54.5	34	6	BD091493	BD091493
55.5	22	6	BD204896	BD204896 Compositi	183	12.2	54.5	34	6	BD091522	BD091522
55.5	24	6	AR164359	Sequence	184	12.2	54.5	35	6	I86946	I86946 S
55.5	24	6	AR205902	Sequence	185	12.2	54.5	39	6	AR075226	AR075226
55.5	25	6	AX487081	Sequence	186	12.2	54.5	39	6	AR110756	AR110756
55.5	27	6	AX804126	Sequence	187	12.2	54.5	39	6	AR152638	AR152638
55.5	29	6	A94089	Sequence	188	12.2	54.5	39	6	I61250	I61250 S
55.5	29	6	BD234835	Sequence	189	12.2	54.5	39	6	AR238478	AR238478
55.5	29	6	AX011174	Sequence	190	12.2	54.5	39	6	AX323317	AX323317
55.5	29	6	AX115675	Sequence	191	12.2	54.5	39	6	AX453615	AX453615
55.5	30	6	E09320	Primer. 9/1	192	12.2	54.5	40	6	AR088238	AR088238
55.5	32	6	AX397876	Sequence	193	12.2	54.5	41	6	AR031370	AR031370
55.5	33	6	AX138388	Sequence	194	12.2	54.5	41	6	BD428932	BD428932
55.5	36	6	BD234834	FAP-alpha	195	12.2	54.5	41	6	AR009738	AR009738
55.5	36	6	AR232610	Sequence	196	12.2	54.5	41	6	BD134372	BD134372
55.5	37	6	AX011173	Sequence	197	12.2	54.5	42	6	AR087150	AR087150
55.5	38	6	AX351243	Sequence	198	12.2	54.5	42	6	AR087567	AR087567
55.5	38	6	AX351227	Sequence	199	12.2	54.5	42	6	I23964	I23964 S
55.5	38	6	AX351241	Sequence	200	12.2	54.5	42	6	AX538891	AX538891
55.5	38	6	AX351242	Sequence	201	12.2	54.5	48	6	AR239863	AR239863
55.5	38	6	AX351244	Sequence	202	12.2	54.5	48	6	AX279665	AX279665
55.5	38	6	AX351245	Sequence	203	12.2	54.5	49	6	AX098901	AX098901
55.5	38	6	AX351249	Sequence	204	12.2	54.5	49	6	AX099321	AX099321
55.5	42	6	A33012	Synthetic P	205	12.2	54.5	51	6	AX203930	AX203930
55.5	42	6	AX357182	Sequence	206	12.2	54.5	51	6	AX204088	AX204088
55.5	42	6	AX357182	Sequence	207	12.2	54.5	52	6	AX098924	AX098924
55.5	42	6	AX357182	Sequence	208	12.2	54.5	52	6	AX099344	AX099344
55.5	42	6	AX357182	Sequence	209	12.2	54.5	52	6	AX616677	AX616677
55.5	42	6	AX357182	Sequence	210	12.2	54.5	52	6	AF22410	AF22410
55.5	42	6	AX357182	Sequence	211	12.2	54.5	57	6	A20235	A20235 C
55.5	42	6	AX357182	Sequence	211	12.2	54.5	57	6	A21530	A21530 C

54.5	57	6	I43788	I43788 Sequence 6	C 285	11.8	53.6	36	6	E15602	E15602 PCF
54.5	60	6	AX365982	AX365982 Sequence	C 286	11.8	53.6	36	6	AX241669	AX241669 S
54.5	60	6	BD102027	BD102027 Agonist a	C 287	11.8	53.6	36	6	AR255385	AR255385 S
54.5	60	6	BD102181	BD102181 Apoptosis	C 288	11.8	53.6	36	6	BD131670	BD131670 V
54.5	60	6	BD169241	BD169241 Degraded	C 289	11.8	53.6	37	6	A73059	A73059 Sec
54.5	60	6	BD169352	BD169352 Small rem	C 290	11.8	53.6	37	6	A73151	A73151 Sec
54.5	17	6	AX731931	AX731931 Sequence	C 291	11.8	53.6	37	6	AR091834	AR091834 S
53.6	17	6	AX736472	AX736472 Sequence	C 292	11.8	53.6	37	6	AR093116	AR093116 S
53.6	20	6	AR015985	AR015985 Sequence	C 293	11.8	53.6	37	6	AR126955	AR126955 S
53.6	20	6	AR082026	AR082026 Sequence	C 294	11.8	53.6	37	6	AR157742	AR157742 S
53.6	20	6	AR082026	AR082026 Sequence	C 295	11.8	53.6	37	6	AX329127	AX329127 S
53.6	20	6	BD37290	BD37290 Sequence	C 296	11.8	53.6	37	6	AX351239	AX351239 S
53.6	20	6	BD231273	BD231273 Genes for	C 297	11.8	53.6	38	6	E17023	E17023 Pr
53.6	20	6	AR311725	AR311725 Sequence	C 298	11.8	53.6	38	6	AX351230	AX351230 S
53.6	20	6	AR311728	AR311728 Sequence	C 299	11.8	53.6	38	6	AX351240	AX351240 S
53.6	20	6	AR337230	AR337230 Sequence	C 300	11.8	53.6	39	6	BD101752	BD101752 C
53.6	20	6	AR337231	AR337231 Sequence	C 301	11.8	53.6	40	6	A62104	A62104 Sec
53.6	20	6	AX037412	AX037412 Sequence	C 302	11.8	53.6	40	6	AR077632	AR077632 S
53.6	20	6	BD075164	BD075164 Methods f	C 303	11.8	53.6	41	6	BD271465	BD271465 S
53.6	22	6	AX804127	AX804127 Sequence	C 304	11.8	53.6	41	6	AR265695	AR265695 S
53.6	23	6	BD130428	BD130428 DNAs and	C 305	11.8	53.6	41	6	BD092132	BD092132 I
53.6	24	6	A07553	A07553 Synthetic O	C 306	11.8	53.6	42	6	AX351180	AX351180 S
53.6	25	6	AX614257	AX614257 Sequence	C 307	11.8	53.6	43	6	E54984	E54984 Pei
53.6	27	6	AR085434	AR085434 Sequence	C 308	11.8	53.6	43	6	I08287	I08287 Sec
53.6	27	6	AR088840	AR088840 Sequence	C 309	11.8	53.6	43	6	AX601780	AX601780 S
53.6	27	6	AR167314	AR167314 Sequence 6	C 310	11.8	53.6	45	6	BD092131	BD092131 I
53.6	27	6	I36697	I36697 Sequence 6	C 311	11.8	53.6	46	6	A25742	A25742 Mo
53.6	27	6	AX467533	AX467533 Sequence	C 312	11.8	53.6	46	6	AR051359	AR051359 S
53.6	28	6	AR091064	AR091064 Sequence	C 313	11.8	53.6	47	6	AR362003	AR362003 S
53.6	28	6	AR158099	AR158099 Sequence	C 314	11.8	53.6	47	6	AX194953	AX194953 S
53.6	28	6	AR260253	AR260253 Sequence	C 315	11.8	53.6	48	6	AR078401	AR078401 S
53.6	28	6	AX006984	AX006984 Sequence	C 316	11.8	53.6	48	6	I05893	I05893 Sec
53.6	30	6	AR089389	AR089389 Sequence	C 317	11.8	53.6	48	6	I05937	I05937 Sec
53.6	30	6	AR093589	AR093589 Sequence	C 318	11.8	53.6	48	6	I09170	I09170 Sec
53.6	30	6	E23305	E23305 Antibody ag	C 319	11.8	53.6	48	6	AR431342	AR431342 S
53.6	30	6	E27074	E27074 Remedy for	C 320	11.8	53.6	50	6	A25699	A25699 MO
53.6	30	6	AX793129	AX793129 Sequence	C 321	11.8	53.6	50	6	AR051358	AR051358 S
53.6	30	6	BD011905	BD011905 Ameliorat	C 322	11.8	53.6	50	6	AX156824	AX156824 S
53.6	30	6	BD011961	BD011961 Therapeut	C 323	11.8	53.6	51	6	AR251898	AR251898 S
53.6	30	6	BD012022	BD012022 Therapeut	C 324	11.8	53.6	51	6	AR356682	AR356682 S
53.6	30	6	BD012909	BD012909 Inhibitin	C 325	11.8	53.6	51	6	AX118085	AX118085 S
53.6	30	6	BD095479	BD095479 Remedies	C 326	11.8	53.6	51	6	AX156823	AX156823 S
53.6	30	6	BD095640	BD095640 Stable an	C 327	11.8	53.6	51	6	AX160633	AX160633 S
53.6	30	6	BD140965	BD140965 An agent	C 328	11.8	53.6	53	6	BD057275	BD057275 S
53.6	30	6	BD182377	BD182377 An agent	C 329	11.8	53.6	53	6	BD174596	BD174596 S
53.6	31	6	A07573	A07573 p11197 DNA	C 330	11.8	53.6	56	6	E30639	E30639 An
53.6	31	6	A07575	A07575 p11197 DNA	C 331	11.8	53.6	56	6	E31248	E31248 De
53.6	31	6	AR7722	AR7722 Sequence 16	C 332	11.8	53.6	57	10	AY205874	AY205874
53.6	31	6	E07915	E07915 Synthetic D	C 333	11.8	53.6	57	10	AY205896	AY205896
53.6	31	6	E30637	E30637 Antibody an	C 334	11.8	53.6	57	10	AY205907	AY205907
53.6	31	6	E31246	E31246 Device for	C 335	11.8	53.6	60	5	AF416916	AF416916
53.6	31	6	BD219869	BD219869 Sequence	C 336	11.8	53.6	60	6	AX100156	AX100156
53.6	31	6	BD195818	BD195818 Method fo	C 337	11.8	53.6	60	10	AY205721	AY205721
53.6	31	6	BD195839	BD195839 Method fo	C 338	11.8	53.6	60	10	AY205734	AY205734
53.6	31	6	BD195851	BD195851 Method fo	C 339	11.8	53.6	60	10	AY205894	AY205894
53.6	31	6	BD195868	BD195868 Method fo	C 340	11.8	53.6	60	10	AY205924	AY205924
53.6	32	6	AR022569	AR022569 Sequence	C 341	11.8	53.6	60	10	AY205945	AY205945
53.6	32	6	AR037584	AR037584 Sequence	C 342	11.8	53.6	60	10	AR292947	AR292947
53.6	32	6	AR084675	AR084675 Sequence	C 343	11.6	52.7	18	6	AR136354	AR136354
53.6	32	6	AR096198	AR096198 Sequence	C 344	11.6	52.7	20	6	AR144293	AR144293
53.6	32	6	AR178042	AR178042 Sequence	C 345	11.6	52.7	20	6	BD247809	BD247809
53.6	32	6	E15598	E15598 PCR primer.	C 346	11.6	52.7	20	6	AR298926	AR298926
53.6	32	6	AR210597	AR210597 Sequence	C 347	11.6	52.7	22	6	AR037111	AR037111
53.6	32	6	AR255381	AR255381 Sequence	C 348	11.6	52.7	22	6	AR070349	AR070349
53.6	32	6	BD131666	BD131666 Variable	C 349	11.6	52.7	22	6	AR349320	AR349320
53.6	33	6	AR152555	AR152555 Sequence	C 350	11.6	52.7	23	6	E10558	E10558 PC
53.6	33	6	AX351179	AX351179 Sequence	C 351	11.6	52.7	23	6	AX445988	AX445988
53.6	35	6	AG2593	AG2593 Sequence 12	C 352	11.6	52.7	25	6	E17210	E17210 PC
53.6	35	6	AR381831	AR381831 Sequence	C 353	11.6	52.7	25	6	AX610204	AX610204
53.6	35	6	BD107808	BD107808 Opsonic a	C 354	11.6	52.7	25	6	AX688878	AX688878
53.6	36	6	A62102	A62102 Sequence 2	C 355	11.6	52.7	28	6	BD012169	BD012169
53.6	36	6	A62105	A62105 Sequence 5	C 356	11.6	52.7	30	6	I71916	I71916 Se
53.6	36	6	AR084679	AR084679 Sequence	C 357	11.6	52.7				
53.6	36	6	AR174687	AR174687 Sequence	C 357	11.6	52.7				

52.7	30	6	AX611107	AX611107 Sequence	431	11.4	51.8	27	6	AR344251	AR344251
52.7	30	6	AX710177	AX710177 Sequence	432	11.4	51.8	27	6	AR363454	AR363454
52.7	30	6	AX710183	AX710183 Sequence	433	11.4	51.8	27	6	AX019224	AX019224
52.7	30	6	BD009722	BD009722 A small v	434	11.4	51.8	27	6	AX380913	AX380913
52.7	30	10	MMJ4BMAR	MMJ4BMAR	435	11.4	51.8	27	6	BD130451	BD130451
52.7	31	6	E26048	E26048 M.musculus	436	11.4	51.8	28	6	AR090417	AR090417
52.7	31	6	BD175925	BD175925 Adenoviru	437	11.4	51.8	28	6	AR197452	AR197452
52.7	31	6	BD175926	BD175926 Adenoviru	438	11.4	51.8	28	6	AR259606	AR259606
52.7	36	6	I57363	I57363 Sequence 6	439	11.4	51.8	28	6	AX546587	AX546587
52.7	38	6	AR286994	AR286994 Sequence	440	11.4	51.8	28	6	BD062367	BD062367
52.7	38	6	AR398984	AR398984 Sequence	441	11.4	51.8	28	6	BD062528	BD062528
52.7	40	6	AR026948	AR026948 Sequence	442	11.4	51.8	28	6	BD123404	BD123404
52.7	40	6	E04719	E04719 Probe for d	443	11.4	51.8	30	6	A23417	A23417
52.7	40	6	E05927	E05927 DNA sequenc	444	11.4	51.8	30	6	AR162670	AR162670
52.7	40	6	AX538479	AX538479 Sequence	445	11.4	51.8	30	6	I32364	I32364
52.7	42	6	AR072943	AR072943 Sequence	446	11.4	51.8	30	6	I32366	I32366
52.7	42	6	AR072947	AR072947 Sequence	447	11.4	51.8	30	6	AX467155	AX467155
52.7	42	6	AR220076	AR220076 Sequence	448	11.4	51.8	30	6	AX8211	AX8211
52.7	42	6	AR220080	AR220080 Sequence	449	11.4	51.8	30	6	AX765911	AX765911
52.7	42	6	BD002269	BD002269 Cellulase	450	11.4	51.8	32	6	AR242441	AR242441
52.7	42	6	BD002273	BD002273 Cellulase	451	11.4	51.8	32	6	AR280209	AR280209
52.7	42	6	BD010873	BD010873 Cellulase	452	11.4	51.8	32	6	AR322424	AR322424
52.7	42	6	BD010877	BD010877 Cellulase	453	11.4	51.8	32	6	AX298092	AX298092
52.7	43	6	AR018916	AR018916 Sequence	454	11.4	51.8	32	6	BD000519	BD000519
52.7	43	6	AR061564	AR061564 Sequence	455	11.4	51.8	33	6	AR041116	AR041116
52.7	43	6	AR066544	AR066544 Sequence	456	11.4	51.8	33	6	AR041116	AR041116
52.7	43	6	AR108463	AR108463 Sequence	457	11.4	51.8	33	6	AR066010	AR066010
52.7	43	6	AR112082	AR112082 Sequence	458	11.4	51.8	33	6	AR072752	AR072752
52.7	43	6	I16420	I16420 Sequence 24	459	11.4	51.8	34	6	A05385	A05385
52.7	43	6	I66906	I66906 Sequence 24	460	11.4	51.8	34	6	A09592	A09592
52.7	43	6	I72261	I72261 Sequence 38	461	11.4	51.8	34	6	AR052830	AR052830
52.7	43	6	I76828	I76828 Sequence 38	462	11.4	51.8	34	6	AR288142	AR288142
52.7	43	6	I85000	I85000 Sequence 24	463	11.4	51.8	34	6	AX027687	AX027687
52.7	43	6	AR263424	AR263424 Sequence	464	11.4	51.8	37	6	AX219934	AX219934
52.7	45	6	AR042820	AR042820 Sequence	465	11.4	51.8	38	6	AR365398	AR365398
52.7	46	6	AX705163	AX705163 Sequence	466	11.4	51.8	39	6	AR084390	AR084390
52.7	47	6	AR212399	AR212399 Sequence	467	11.4	51.8	39	6	AR083790	AR083790
52.7	47	6	AR289748	AR289748 Sequence	468	11.4	51.8	40	6	AR089791	AR089791
52.7	47	6	AX194957	AX194957 Sequence	469	11.4	51.8	40	6	BD232084	BD232084
52.7	47	6	AX513771	AX513771 Sequence	470	11.4	51.8	40	6	AX431429	AX431429
52.7	50	6	AX697124	AX697124 Sequence	471	11.4	51.8	41	6	A26543	A26543
52.7	50	6	A25124	A25124 Synthetic F	472	11.4	51.8	41	6	A26544	A26544
52.7	51	6	AX115581	AX115581 Sequence	473	11.4	51.8	41	6	A26545	A26545
52.7	51	6	AX204427	AX204427 Sequence	474	11.4	51.8	41	6	AR077633	AR077633
52.7	51	10	MM086736	MM086736	475	11.4	51.8	41	6	BD271466	BD271466
52.7	51	10	MM086740	MM086740	476	11.4	51.8	41	6	AR265696	AR265696
51.8	16	6	A39006	A39006 Sequence 93	477	11.4	51.8	41	6	AX365219	AX365219
51.8	16	6	AR054397	AR054397 Sequence	478	11.4	51.8	41	6	AX514816	AX514816
51.8	16	6	AR265147	AR265147 Sequence	479	11.4	51.8	41	6	AX517174	AX517174
51.8	17	6	BD241733	BD241733 Methods a	480	11.4	51.8	42	6	AR7720	AR7720
51.8	17	6	AX760444	AX760444 Sequence	481	11.4	51.8	42	6	AR086060	AR086060
51.8	17	6	BD200699	BD200699 Method an	482	11.4	51.8	42	6	AR140414	AR140414
51.8	17	6	BD203129	BD203129 Method an	483	11.4	51.8	42	6	AR146895	AR146895
51.8	17	6	BD203130	BD203130 Method an	484	11.4	51.8	42	6	AX179394	AX179394
51.8	19	6	A65726	A65726 Sequence 7	485	11.4	51.8	42	6	AX259868	AX259868
51.8	19	6	AR7715	AR7715 Sequence 9	486	11.4	51.8	42	6	BD195803	BD195803
51.8	19	6	BD195812	BD195812 Method fo	487	11.4	51.8	43	6	AX601639	AX601639
51.8	19	6	BD195862	BD195862 Method fo	488	11.4	51.8	45	6	A33049	A33049
51.8	20	6	AR310983	AR310983 Sequence	489	11.4	51.8	45	6	AR062253	AR062253
51.8	20	6	AR310988	AR310988 Sequence	490	11.4	51.8	45	6	AX304972	AX304972
51.8	21	6	BD168673	BD168673 Novel G p	491	11.4	51.8	45	6	AX306501	AX306501
51.8	21	6	BD183781	BD183781 Novel G p	492	11.4	51.8	45	6	BD015548	BD015548
51.8	22	6	AR077182	AR077182 Sequence	493	11.4	51.8	45	6	BD094926	BD094926
51.8	22	6	AX642816	AX642816 Sequence	494	11.4	51.8	46	12	BD131219	BD131219
51.8	22	6	AX298966	AX298966 Sequence	495	11.4	51.8	46	12	SYNPRWF	SYNPRWF
51.8	23	6	I63118	I63118 Sequence 1	496	11.4	51.8	47	6	I05912	I05912
51.8	24	6	I85497	I85497 Sequence 3	497	11.4	51.8	47	6	I05957	I05957
51.8	24	6	AR157582	AR157582 Sequence	498	11.4	51.8	47	6	I09192	I09192
51.8	25	6	AR212631	AR212631 Sequence	499	11.4	51.8	47	6	AR284836	AR284836
51.8	25	6	AR430029	AR430029 Sequence	500	11.4	51.8	47	6	AR290374	AR290374
51.8	25	6	AX115456	AX115456 Sequence	501	11.4	51.8	47	6	AR292006	AR292006
51.8	25	6	AX201530	AX201530 Sequence	502	11.4	51.8	47	6	AR292117	AR292117
51.8	25	6	AX675234	AX675234 Sequence	503	11.4	51.8	47	6	AR431365	AR431365
51.8	25	6			504	11.4	51.8	47	6	AX214331	AX214331

51.8	48	6	BD135852	BD135852 Selective	c	577	11.2	50.9	23	6	AR345232	AR345232
51.8	50	6	AR040811	AR040811 Sequence	578	11.2	50.9	24	6	E37252	E37252 No	
51.8	50	9	S59168	S59168 TCR delta {	579	11.2	50.9	24	6	AR266294	AR266294	
51.8	51	6	AX115457	AX115457 Sequence	c	580	11.2	50.9	24	6	AX446937	AX446937
51.8	51	6	AX156991	AX156991 Sequence	c	581	11.2	50.9	24	6	AX447316	AX447316
51.8	51	6	AX156992	AX156992 Sequence	c	582	11.2	50.9	24	6	AX493448	AX493448
51.8	51	6	AX158796	AX158796 Sequence	583	11.2	50.9	24	6	AX776557	AX776557	
51.8	51	6	AX161602	AX161602 Sequence	584	11.2	50.9	24	6	ASE011719	ASE011719	
51.8	51	6	AX165013	AX165013 Sequence	585	11.2	50.9	24	12	ASE011719	ASE011719	
51.8	51	6	MUSMABBS	K00122 Mouse MHC c	586	11.2	50.9	25	6	AX688865	AX688865	
51.8	51	10	MUSMABBS	K00113 Mouse MHC c	587	11.2	50.9	25	6	AX688866	AX688866	
51.8	51	10	MUSMABBS	Al0854 Oligonucleo	588	11.2	50.9	25	6	AX688867	AX688867	
51.8	52	6	Al0854	Al0855 Oligonucleo	589	11.2	50.9	25	6	AX688868	AX688868	
51.8	54	6	Al0855	AX913960 Sequence	590	11.2	50.9	25	6	AX688879	AX688879	
51.8	54	6	AX913960	BD049493 Sequence	c	591	11.2	50.9	25	6	AX688880	AX688880
51.8	54	6	BD049493	AX594012 Sequence	c	592	11.2	50.9	25	6	AX691206	AX691206
51.8	57	6	AX594012	BD135845 Selective	c	593	11.2	50.9	25	6	AX691207	AX691207
51.8	57	6	BD135845	BD237364 Improve	c	594	11.2	50.9	25	6	AX691208	AX691208
51.8	58	6	BD237364	AX027031 Sequence	c	595	11.2	50.9	25	6	AX691209	AX691209
51.8	58	6	AX027031	BD135846 Selective	c	596	11.2	50.9	25	6	AX691210	AX691210
51.8	59	6	AX011439	BD225730 Screening	c	597	11.2	50.9	25	6	AX691211	AX691211
51.8	59	6	BD225730	BD225730 Screening	c	598	11.2	50.9	25	6	AX691212	AX691212
51.8	59	9	AX152457	AX152457 Homo sapi	c	599	11.2	50.9	25	6	AX691213	AX691213
51.8	60	6	A27400	A27400 cloning sit	c	600	11.2	50.9	25	6	AX691214	AX691214
51.8	60	6	A33042	A33042 Synthetic f	c	601	11.2	50.9	26	6	AX691215	AX691215
51.8	60	6	A93057	B65256 Mutant of E	c	602	11.2	50.9	26	6	AR3750	AR3750 Se
51.8	60	6	B65256	AR227925 Sequence	c	603	11.2	50.9	26	6	AR054696	AR054696
51.8	60	6	AR227925	AR436222 Sequence	c	604	11.2	50.9	26	6	AX300568	AX300568
51.8	16	6	AR436222	BD241336 Methods a	c	605	11.2	50.9	27	6	AX105555	AX105555
50.9	17	6	BD241336	AX266671 Sequence	c	606	11.2	50.9	27	6	AX350069	AX350069
50.9	17	6	AX266671	AX266672 Sequence	c	607	11.2	50.9	28	6	AX456997	AX456997
50.9	17	6	AX266672	AX687368 Sequence	c	608	11.2	50.9	28	6	AR083272	AR083272
50.9	17	6	AX687368	AX687369 Sequence	c	609	11.2	50.9	29	6	AR105934	AR105934
50.9	17	6	AX687369	AX687374 Sequence	c	610	11.2	50.9	29	6	AX002800	AX002800
50.9	17	6	AX687374	AX687375 Sequence	c	611	11.2	50.9	29	6	AX078805	AX078805
50.9	17	6	AX687375	AX690745 Sequence	c	612	11.2	50.9	29	6	AX149568	AX149568
50.9	17	6	AX690745	AX690746 Sequence	c	613	11.2	50.9	29	6	BD092214	BD092214
50.9	17	6	AX690746	AX732199 Sequence	c	614	11.2	50.9	29	6	BD136170	BD136170
50.9	17	6	AX732199	AX734876 Sequence	c	615	11.2	50.9	30	6	AR090106	AR090106
50.9	17	6	AX734876	AX738428 Sequence	c	616	11.2	50.9	30	6	AR141393	AR141393
50.9	17	6	AX738428	AX760170 Sequence	c	617	11.2	50.9	30	6	E32127	E32127 Se
50.9	17	6	AX760170	AX302181 Sequence	c	618	11.2	50.9	30	6	AR197141	AR197141
50.9	17	6	AX302181	AX112174 Sequence	c	619	11.2	50.9	30	6	AR259295	AR259295
50.9	18	6	AX112174	AX358732 Sequence	c	620	11.2	50.9	30	6	AR203796	AR203796
50.9	18	6	AX358732	AX684999 Sequence	c	621	11.2	50.9	31	6	A59857	A59857 Se
50.9	18	6	AX684999	AX815724 Sequence	c	622	11.2	50.9	31	6	A84815	A84815 Se
50.9	18	6	AX815724	AR067175 Sequence	c	623	11.2	50.9	31	6	AR075169	AR075169
50.9	20	6	AR067175	AR100386 Sequence	c	624	11.2	50.9	31	6	AR154131	AR154131
50.9	20	6	AR100386	AR150041 Sequence	c	625	11.2	50.9	31	6	AR339674	AR339674
50.9	20	6	AR150041	BD227914 Antisense	c	626	11.2	50.9	31	6	AX089633	AX089633
50.9	20	6	BD227914	EO8943 PCR primer	c	627	11.2	50.9	31	6	AX248977	AX248977
50.9	20	6	EO8943	E15115 Primer. 7/1	c	628	11.2	50.9	31	6	AX477522	AX477522
50.9	20	6	E15115	AR228974 Sequence	c	629	11.2	50.9	31	6	BD002360	BD002360
50.9	20	6	AR228974	AR311783 Sequence	c	630	11.2	50.9	32	6	BD082263	BD082263
50.9	20	6	AR311783	AR313956 Sequence	c	631	11.2	50.9	32	6	AR090305	AR090305
50.9	20	6	AR313956	AX080381 Sequence	c	632	11.2	50.9	32	6	AR197340	AR197340
50.9	20	6	AX080381	AX119655 Sequence	c	633	11.2	50.9	32	6	AR259494	AR259494
50.9	20	6	AX119655	AX348129 Sequence	c	634	11.2	50.9	33	6	AX203794	AX203794
50.9	20	6	AX348129	AX418249 Sequence	c	635	11.2	50.9	34	6	BD263615	BD263615
50.9	20	6	AX418249	AX662849 Sequence	c	636	11.2	50.9	34	6	E59675	E59675 Me
50.9	20	6	AX662849	AX785499 Sequence	c	637	11.2	50.9	34	6	AX168006	AX168006
50.9	20	6	AX785499	AX785501 Sequence	c	638	11.2	50.9	34	6	AX343116	AX343116
50.9	20	6	AX785501	BD266155 Universal	c	639	11.2	50.9	35	6	I15205	I15205 Se
50.9	21	6	BD266155	E58784 Novel human	c	640	11.2	50.9	35	6	AR430578	AR430578
50.9	21	6	E58784	AX203448 Sequence	c	641	11.2	50.9	36	6	AR106146	AR106146
50.9	21	6	AX203448	AX804691 Sequence	c	642	11.2	50.9	36	6	E15059	E15059 Pi
50.9	21	6	AX804691	BD056670 Method to	c	643	11.2	50.9	36	6	E15097	E15097 Pi
50.9	21	6	BD056670	AX040624 Sequence	c	644	11.2	50.9	36	6	AR436526	AR436526
50.9	22	6	AX040624	BD133433 Method fo	c	645	11.2	50.9	37	6	AR034257	AR034257
50.9	22	6	BD133433	AR112639 Sequence	c	646	11.2	50.9	37	6	BD235638	BD235638
50.9	23	6	AR112639	BD272795 Detection	c	647	11.2	50.9	38	6	AR287723	AR287723
50.9	23	6	BD272795	AR279424 Sequence	c	648	11.2	50.9	38	6	A84837	A84837 Se
50.9	23	6	AR279424		649	11.2	50.9	38	6	AR063769	AR063769	
50.9	23	6						38	6	I30132	I30132 Se	

50.9	38	6	AR339696	AR339696 Sequence	723	11	50.0	20	6	AX643826	AX643826
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50.9	38	6	AX425451	AX425451 Sequence	c 725	11	50.0	20	11	HUMPEX5B	DS0194
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50.9	39	6	AR366555	AR366555 Sequence	c 728	11	50.0	21	6	BD177808	BD177808
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50.9	39	6	BD008468	BD008468 Targeting	c 731	11	50.0	22	6	I46723	I46723
50.9	40	6	AX496368	AX496368 Sequence	c 732	11	50.0	22	6	I46725	I46725
50.9	40	6	AX538299	AX538299 Sequence	c 733	11	50.0	23	6	AR084413	AR084413
50.9	40	6	BD013117	BD013117 Peptide 1	734	11	50.0	23	6	AR403813	AR403813
50.9	40	6	BD188770	BD188770 Peptide 1	735	11	50.0	23	6	AX612644	AX612644
50.9	41	6	BD260010	BD260010 Polynucle	c 736	11	50.0	23	6	BD140220	BD140220
50.9	41	6	I32610	I32610 Sequence 1	737	11	50.0	23	6	BD142818	BD142818
50.9	41	6	I32614	I32614 Sequence 5	c 738	11	50.0	24	6	AX3153	AX3153
50.9	41	6	AX045496	AX045496 Sequence	739	11	50.0	24	6	A43154	A43154
50.9	41	6	AX298062	AX298062 Sequence	c 740	11	50.0	24	6	AR079543	AR079543
50.9	41	6	AX411701	AX411701 Sequence	c 741	11	50.0	24	6	AR079544	AR079544
50.9	41	6	AX411705	AX411705 Sequence	c 742	11	50.0	24	6	AR097511	AR097511
50.9	41	6	AX516593	AX516593 Sequence	c 743	11	50.0	24	6	ARI03738	ARI03738
50.9	41	6	AX518766	AX518766 Sequence	c 744	11	50.0	24	6	ARI039825	ARI039825
50.9	41	6	AX520397	AX520397 Sequence	c 745	11	50.0	24	6	ARI40132	ARI40132
50.9	42	6	AR200741	AR200741 Sequence	c 746	11	50.0	24	6	ARI42849	ARI42849
50.9	42	6	AX776725	AX776725 Sequence	c 747	11	50.0	24	6	I05926	I05926
50.9	42	6	AR238604	AR238604 Sequence	748	11	50.0	24	6	AR374664	AR374664
50.9	43	6	AX484449	AX484449 Sequence	749	11	50.0	24	6	AR431378	AR431378
50.9	44	6	E63267	E63267 Collagen-bi	751	11	50.0	24	6	AX289899	AX289899
50.9	44	6	BD142781	BD142781 Collagen-	c 752	11	50.0	24	6	AX292167	AX292167
50.9	45	6	AR064068	AR064068 Sequence	c 753	11	50.0	24	6	AX446993	AX446993
50.9	45	6	AR366554	AR366554 Sequence	c 754	11	50.0	24	6	AX487427	AX487427
50.9	45	6	AR430708	AR430708 Sequence	755	11	50.0	24	6	BD129968	BD129968
50.9	45	6	BD008467	BD008467 Targeting	756	11	50.0	24	6	BD183607	BD183607
50.9	46	6	AX225236	AX225236 Sequence	c 757	11	50.0	25	6	A00437	A00437
50.9	47	6	AR284696	AR284696 Sequence	c 758	11	50.0	25	6	AR090383	AR090383
50.9	47	6	AR289080	AR289080 Sequence	c 759	11	50.0	25	6	AR197418	AR197418
50.9	47	6	AX195009	AX195009 Sequence	c 760	11	50.0	25	6	AR259572	AR259572
50.9	48	6	AR009864	AR009864 Sequence	761	11	50.0	25	6	AX118148	AX118148
50.9	50	6	AX159152	AX159152 Sequence	c 762	11	50.0	26	6	AX378885	AX378885
50.9	50	6	AX159154	AX159154 Sequence	c 763	11	50.0	26	6	AX181783	AX181783
50.9	50	6	AX159155	AX159155 Sequence	c 764	11	50.0	26	6	BD077186	BD077186
50.9	51	6	AX118229	AX118229 Sequence	c 765	11	50.0	26	6	BD170718	BD170718
50.9	51	6	AX159153	AX159153 Sequence	c 766	11	50.0	27	6	A94073	A94073
50.9	51	6	AX165288	AX165288 Sequence	c 767	11	50.0	27	6	BD234826	BD234826
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50.9	53	14	S65447	S65447 {5, region,	c 769	11	50.0	27	6	AX011158	AX011158
50.9	55	14	S65449	S65449 {5, region,	c 770	11	50.0	27	6	BD102001	BD102001
50.9	60	6	A47881	A47881 Sequence 1	c 771	11	50.0	27	6	BD169215	BD169215
50.9	60	6	A59312	A59312 Sequence 1	772	11	50.0	27	6	BD169326	BD169326
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901 3 from Patent EP0618292.
901 1 GI:2296119
901.1 sapiens (human)
to sapiens
to sapiens

ALIGNMENTS
46 bp
DNA
linear
PAT 05-MAR-1997

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AR244397 Sequence
AR367326 Sequence
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AR355543 Sequence
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VERSION A39902.1 GI:2296120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 46)
Tersikh,A., Pelegriin,A. and Mach,J.
CEA derivatives lacking the Hydrophobic C-terminal doma
Patent: EP 0618292-A 4 05-OCT-1994;
HOFFMANN LA ROCHE (CH)
Other publication CA 2116640 940926
Other publication JP 6321992 941122.
Location/Qualifiers
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 46)
Tersikh,A., Pelegriin,A. and Mach,J.
CEA derivatives lacking the Hydrophobic C-terminal doma
Patent: EP 0618292-A 4 05-OCT-1994;
HOFFMANN LA ROCHE (CH)
Other publication CA 2116640 940926
Other publication JP 6321992 941122.
Location/Qualifiers
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Matches 17; Conservative 0; Mismatches 2; Indels 0;

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DEFINITION I67749
ACCESSION I67749
VERSION I67745.1 GI:2731284
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
1 (bases 1 to 46)
Tersikh,A., Pelegriin,A. and Mach,J.-P.
Carcano-embryonic antigen derivatives lacking the carbo
end

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us-10-090-326-6.max.rge

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      ssified.
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ACCESSION
  AB069564
  GI:15130368
VERSION
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KEYWORDS
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SOURCE
  synthetic construct
  artificial sequences.
ORGANISM
  1
REFERENCE
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  Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
  Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H
  Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M.,
  and Soeda,E.
  A BAC-based STS-content map spanning a 35-Mb region of h
  chromosome lp35-p36
  Genomics 74 (1), 55-70 (2001)
JOURNAL
  MEDLINE
  PUBMED
  11374902
REFERENCE
  2 (bases 1 to 20)
  Horii,A.
  Direct Submission
  Submitted (04-AUG-2001) Akira Horii, Tohoku University S
  Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku,
  Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.j
  Tel:81-22-717-8042, Fax:81-22-717-8047)
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  Shannon,M., Gu,Y. and Nguyen,C.T.
  Four human zinc-finger-containing proteins : mdz3, mdz4,
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mon.M., Gu.Y. and Nguyen,C.T.
r human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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nt: EP 1281758-A 1604 05-FEB-2003;
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38873.1 GI:29411577
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mon.M., Gu.Y. and Nguyen,C.T.
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12
nt: EP 1281758-A 1605 05-FEB-2003;
nica, Inc. (US)
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Db 2 AGTCATTCTCAGTCTCTCGGA 23

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ACCESSION AX688874.1 GI:29411578
VERSION
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4,
TITLE mdz12
JOURNAL Patent: EP 1281758-A 1606 05-FEB-2003;
Aeonica, Inc. (US)
FEATURES Location/Qualifiers
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Db 1 AGTCATTCTCAGTCTCTCGGA 22

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DEFINITION tagged site.
ACCESSION BX322287.1 GI:29465926
VERSION STS; STS, sequence tagged site.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
rosids; eurosids II; Brassicales; Brassicaceae; Arabido
1
REFERENCE Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B
AUTHORS Murphy,G., Langham,S., LeGrys,C., Jones,J.D.G. and Beva
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 58)
AUTHORS Clarke,J.H.
JOURNAL Direct Submission
TITLE Submitted (01-APR-2003) Clarke J.H., John Innes Centre,
COMMENT Lane, Norwich, NR4 7UJ, UK
AT denotes an activation tag dissociation transposon wi
single line, ET an enhancer trap dissociation transposo
trap dissociation transposon, MT a mis-expression enhan
dissociation transposon, SM a defective suppressor muta
transposon. 3 denotes a sequence derived from the 3' en
transposon, 5 denotes a sequence derived from the 5' en
transposon BBSRC GARNET, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NA
code: NI21894.
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63.6%; Score 14; DB 11; Length 58;
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Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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1379.1 GI:14535993
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ill.M., Ireland, J.S. and Lander, E.S.
a single nucleotide polymorphisms
it: WO 0138576-A 477 31-MAY-2001;
HEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
Location/Qualifiers
1. .21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

61.8%; Score 13.6; DB 6; Length 21;
ilarity 92.9%; Pred. No. 2.7e+04;
Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ACAATCACAGTC 14
|||||
ACAATCAVAGTC 15

8993 37 bp DNA linear PAT 10-APR-2003
ence 41 from patent US 6500646.
8993
8993.1 GI:29699809
OWN.
own.
assified.
bases 1 to 37)
yama, S. and Hasegawa, T.
membrane-directed drugs
nt: US 6500646-A 41 31-DEC-2002;
Location/Qualifiers
1. .37
/organism="unknown"
/mol_type="genomic DNA"

61.8%; Score 13.6; DB 6; Length 37;
ilarity 80.0%; Pred. No. 2.8e+04;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CAATCACAGTCTCTGCGG 21
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Db 9 GATCTTCAGAGTCTCTGCGG 28

RESULT 14
AX794202
LOCUS 50 bp DNA linear PAT
DEFINITION Sequence 33 from Patent WO02092827.
ACCESSION AX794202
VERSION AX794202.1 GI:32959626
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Rottier, P.J., de Haan, C.A., Haijema, B.J. and Bosch, B.J.
Corona-virus-like particles comprising functionally dele
Patent: WO 02092827-A 33 21-NOV-2002;
Universiteit Utrecht (NL); STICHTING VOOR DE TECHNISCHE
WETENSCHAPPEN (NL)
FEATURES
Location/Qualifiers
source 1. .50
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="sequence of new junction created in reco
MHV-virus"
ORIGIN
Query Match 61.8%; Score 13.6; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0;

Qy 2 GACAATCACAGTCTCTGCGG 21
|||||
8 GACTATCACAGCCCTGCAG 27
Db

RESULT 15
APHCNOV5E 50 bp ss-RNA linear VRL
DEFINITION Foot and mouth disease virus (serotype C Nov) RNA, 5' en
ACCESSION M10505
VERSION M10505.1 GI:210404
KEYWORDS Foot-and-mouth disease virus
SOURCE Foot-and-mouth disease virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Aphthovirus.
REFERENCE
1 (bases 1 to 50)
Harris, T.J.
AUTHORS Comparison of the nucleotide sequence at the 5' end of R
TITLE nine aphthoviruses, including representatives of the Sev
serotypes
J. Virol. 36 (3), 659-664 (1980)
JOURNAL
MEDLINE 81119945
PUBMED 6257918
COMMENT source text: Foot and mouth disease virus RNA.
FEATURES
Location/Qualifiers
source 1. .50
/organism="Foot-and-mouth disease virus"
/mol_type="genomic RNA"
/db_xref="taxon:12110"
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Query Match 61.8%; Score 13.6; DB 14; Length 50;
Best Local Similarity 80.0%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0;

Qy 1 AGACAATCACAGTCTCTGCGG 20
|||||
31 AGCCAACGACAGTCCCTGCGG 50
Db
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1228 53 bp DNA linear PAT 17-JUL-2003  
 since 59 from Patent WO02092827.  
 1228  
 1228.1 GI:32959634  
 netic construct  
 netic construct  
 ficial sequences.  
 ier,P.J., de Haan,C.A., Haijema,B.J. and Bosch,B.J.  
 na-virus-like particles comprising functionally deleted genomes  
 nt: WO 02092827-A 59 21-NOV-2002;  
 ersiteit Utrecht (NL) ; STICHTING VOOR DE TECHNISCHE  
 NSCHAPPEN (NL)  
 Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="sequence of junction generated in recombinant  
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 61.8%; Score 13.6; DB 6; Length 53;  
 ilarity 80.0%; Pred. No. 2.8e+04;  
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 CAATCAGTCTCTGCGG 21  
 CTATCAGCCCTGCGAG 27  
 32308 22 bp DNA linear PAT 20-DEC-2002  
 hence 8 from patent US 6476296.  
 32308  
 32308.1 GI:27300203  
 nown.  
 nown.  
 lassified.  
 (bases 1 to 22)  
 cher,R.I., Choi,Y. and Hannon,M.  
 leic acids that control seed and fruit development in plants  
 ent: US 6476296-A 8 05-NOV-2002;  
 Location/Qualifiers  
 1..22  
 /organism="unknown"  
 /mol\_type="genomic DNA"  
 60.0%; Score 13.2; DB 6; Length 22;  
 ilarity 83.3%; Pred. No. 4.6e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 ACAATCAGTCTCTGCG 19  
 ACAATAACCGTCTCTCC 1  
 33429 22 bp DNA linear PAT 18-SEP-2002  
 hod for assaying glutathione S-transferase, and probe and kit  
 refer.  
 33429  
 33429.1 GI:23228374  
 2002058483-A/27.  
 identified  
 identified

unclassified.  
 1 (bases 1 to 22)  
 Nishimura,M., Yaguchi,H., Naito,S. and Hiraoka,I.  
 Method for assaying glutathione S-transferase, and probe  
 therefor  
 Patent: JP 2002058483-A 27 26-FEB-2002;  
 OTSUKA PHARMACEUTICAL FACTORY INC  
 human GSTM2 gene  
 OS  
 PN JP 2002058483-A/27  
 PD 26-FEB-2002  
 PF 14-AUG-2000 JP 2000245951  
 PI MASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,I  
 PC C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G0  
 PC C12N15/00  
 CC Method for assaying glutathione S-transferase, and  
 CC kit therefor  
 FH Key  
 FT Location/Qualifiers  
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 1..22  
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 /db\_xref="taxon:32644"  
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 Best Local Similarity 83.3%; Pred. No. 4.6e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;  
 QY 5 AATCAGTCTCTGCGGA 22  
 DB 22 ACTCAGTTTCTGCGGA 5  
 RESULT 19  
 I20757/C  
 LOCUS 35 bp DNA linear PAT  
 DEFINITION Sequence 10 from patent US 5516637.  
 I20757  
 ACCESSION I20757  
 VERSION I20757.1 GI:1601112  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 35)  
 Huang,G.P., Rhode,P.R., Stinson,J.R. and Wong,H.C.  
 Method involving display of protein binding pairs on th  
 bacterial pili and bacteriophage  
 Patent: US 5516637-A 10 14-MAY-1996;  
 JOURNAL Location/Qualifiers  
 FEATURES  
 1..35  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match 60.0%; Score 13.2; DB 6; Length 35;  
 Best Local Similarity 72.2%; Pred. No. 4.7e+04;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0;  
 QY 4 CAATCAGTCTCTGCGG 21  
 DB 32 CASTCAGTCTCTCKAG 15  
 RESULT 20  
 AR381829/C  
 LOCUS 35 bp DNA linear PAT  
 DEFINITION Sequence 73 from patent US 6610293.  
 AR381829  
 ACCESSION AR381829  
 VERSION AR381829.1 GI:40090090  
 KEYWORDS  
 SOURCE Unknown.

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wn.
ssified.
ases 1 to 35)
er.G.W., Schuman,R.F., Wong,H. and Stinson,J.R.
tic and protective monoclonal and chimeric antibodies specific
ipoteichoic acid of gram positive bacteria
it: US 6610293-A 73 26-AUG-2003;
Location/Qualifiers
1. .35
/organism="unknown"
/mol_type="unassigned DNA"

60.0%; Score 13.2; DB 6; Length 35;
larity 72.2%; Pred. No. 4.7e+04;
Conservative 3; Mismatches 2; Indels 0; Gaps 0;
ATCAGTCTCTGCGG 21
|||||:||||:|
|TCACHGTCTCYKAG 15

'806 35 bp. DNA linear PAT 18-SEP-2002
tic and protective monoclonal and chimeric antibodies specific
ipoteichoic acid of gram positive bacteria.
'806
'806.1 GI:23202624
102503966-A/39.
ntified
ntified
ssified.
ases 1 to 35)
er.G.W., Schuman,R.F., Wong,H. and Stinson,J.L.
tic and protective monoclonal and chimeric antibodies specific
ipoteichoic acid of gram positive bacteria
it: JP 2002503966-A 39 05-FEB-2002;
' M JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY MEDICINE
Unidentified
JP 2002503966-A/39
05-FEB-2002
16-JUN-1998 JP 1999504633
16-JUN-1997 US 60/049871
GERALD W FISCHER, RICHARD F SCHUMAN, HING WONG, JEFFREY L STINSON
C07K16/12,C07K16/46,A61K39/40,C07K7/00,A61K39/02,C12Q1/18 CC
edness: Single;
Topology: Linear;
/desc = 'primer'.
Key Location/Qualifiers
source
1. .35
/organism='Unidentified'.
Location/Qualifiers
1. .35
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/db_xref="taxon:32644"

60.0%; Score 13.2; DB 6; Length 35;
larity 72.2%; Pred. No. 4.7e+04;
Conservative 3; Mismatches 2; Indels 0; Gaps 0;
ATCAGTCTCTGCGG 21
|||||:||||:|
|TCACHGTCTCYKAG 15

9738 47 bp. DNA linear PAT 12-JUN-2003
ance 1473 from patent US 6537751.
9738

```

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VERSION AR289738.1 GI:31677022
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 47)
Unclassified.
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 1473 25-MAR-2003;
FEATURES
Location/Qualifiers
1. 47
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 75.0%; Pred. No. 4.7e+04;
Matches 15; Conservative 1; Mismatches 4; Indels 0;

QY 2 GACAATCACAGTCTCTGCGG 21
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|GAGCAYCACACACTCTGCGG 38
Db

RESULT 23
AX199173 51 bp DNA linear PAT:
LOCUS Sequence 103 from Patent WO0151670.
ACCESSION AX199173
VERSION AX199173.1 GI:15389525
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

REFERENCE
1
AUTHORS Shinkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms
methods of use thereof
JOURNAL Patent: WO 0151670-A 103 19-JUL-2001;
Curagen Corporation (US)
FEATURES
Location/Qualifiers
source
1. .51
/organism="Homo sapiens"
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/db_xref="taxon:9606"

misc_feature 26
/note="1 of 2 allelic variants (104 is other en
Accession number CG43093113"

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Query Match 60.0%; Score 13.2; DB 6; Length 51;
Best Local Similarity 83.3%; Pred. No. 4.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGACAATCACAGTCTCTG 18
|||||:||||:|
|27 AGACAATCCATTGTCTG 44
Db

RESULT 24
AX199174 51 bp DNA linear PAT:
LOCUS Sequence 104 from Patent WO0151670.
ACCESSION AX199174
VERSION AX199174.1 GI:15389526
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

REFERENCE
1

```

kets,R.A. and Leach,M.D.  
 eic acids containing single nucleotide polymorphisms and  
 ods of use thereof  
 nt: WO 0151670-A 104 19-JUL-2001;  
 gen corporation (US)  
 Location/Qualifiers  
 1..51  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 26  
 /note="2 of 2 allelic variants (103 is other entry)"  
 Accession number CG43093113"

60.0%; Score 13.2; DB 6; Length 51;  
 ilarity 83.3%; Pred.No. 4.7e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACAAATCACAGTCTCTG 18  
 |||||  
 ACAATCCATGTCGTG 44

'2233 22 bp DNA linear PAT 28-AUG-2000  
 ence 36 from patent US 5948611.  
 '2233  
 '2233.1 GI:9998997

own.  
 own.  
 assified.  
 ases 1 to 22)  
 kop,D.J., Ala-Kokko,L., Williams,C.J., Ritvaniemi,P.,  
 twin,C., Hopkinson,I. and Ahmad,N.Nina.  
 ivers and methods for detecting mutations in the procollagen II  
 ; (COL2A1) that indicate a genetic predisposition for a  
 ?AI-associated disease  
 nt: US 5948611-A 36 07-SEP-1999;  
 Location/Qualifiers  
 1..22  
 /organism="unknown"  
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59.1%; Score 13; DB 6; Length 22;  
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 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACAAATCACAGTCTCTGCGG 21  
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 ACACCTGCAGTCTCACCTG 1

344 22 bp DNA linear PAT 07-OCT-1996  
 uence 36 from patent US 5558988.  
 344  
 344.1 GI:1606214

own.  
 own.  
 lassified.  
 (bases 1 to 22)  
 ckop,D.J., Ala-Kokko,L. and Ritvaniemi,P.  
 mers and methods for detecting mutations in the procollagen II  
 e that indicate a genetic predisposition for osteoarthritis  
 ent: US 5558988-A 36 24-SEP-1996;  
 Location/Qualifiers  
 1..22

/organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 59.1%; Score 13; DB 6; Length 22;  
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 Matches 16; Conservative 0; Mismatches 5; Indels 0;

Qy 1 AGACAATCACAGTCTCTGCGG 21  
 |||||  
 Db 21 AGACATCGCAGTCTCACCTG 1

RESULT 27  
 AX688870 25 bp DNA linear PAT  
 LOCUS  
 DEFINITION Sequence 1602 from Patent EP1281758.  
 ACCESSION AX688870  
 VERSION AX688870.1 GI:29411574  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

REFERENCE  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4,  
 mdz12  
 JOURNAL Patent: EP 1281758-A 1602 05-FEB-2003;  
 Aeomica, Inc. (US)

FEATURES  
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 /db\_xref="taxon:9606"

## ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 25;  
 Best Local Similarity 76.2%; Pred.No. 5.9e+04;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0;

Qy 1 AGACAATCACAGTCTCTGCGG 21  
 |||||  
 Db 5 AGTCATTCTCAGTCTCTCGG 25

RESULT 28  
 AX688875 25 bp DNA linear PAT  
 LOCUS  
 DEFINITION Sequence 1607 from Patent EP1281758.  
 ACCESSION AX688875  
 VERSION AX688875.1 GI:29411579  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

REFERENCE  
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.  
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4,  
 mdz12  
 JOURNAL Patent: EP 1281758-A 1607 05-FEB-2003;  
 Aeomica, Inc. (US)

FEATURES  
 source  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

## ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 25;  
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 Matches 16; Conservative 0; Mismatches 5; Indels 0;

AATCAGAGTCTCTCGCGA 22  
 |||||  
 ATTCTCAGTCTCTCTCGGA 21

1992 28 bp DNA linear PAT 07-SEP-2000  
 nce 1112 from patent US 5994076.

1992.1 GI:10017747

own.  
 own.  
 issified.  
 bases 1 to 28)  
 chik,A., Johhadze,G. and Bibilashvilli,R.  
 ods of assaying differential expression  
 t: US 5994076-A 1112 30-NOV-1999;  
 Location/Qualifiers  
 1. .28  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ilarity 59.1%; Score 13; DB 6; Length 28;  
 76.2%; Pred. No. 6e+04;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACATCAGAGTCTCTCGCG 21  
 |||||  
 ACAACACATTCTCAGTGG 28

3027 28 bp DNA linear PAT 20-APR-2002  
 nce 1112 from patent US 6352829.

9027  
 3027.1 GI:20247876

own.  
 own.  
 assified.  
 bases 1 to 28)  
 chik,A., Johhadze,G. and Bibilashvilli,R.  
 ods of assaying differential expression  
 nt: US 6352829-A 1112 05-MAR-2002;  
 Location/Qualifiers  
 1. .28  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ilarity 59.1%; Score 13; DB 6; Length 28;  
 76.2%; Pred. NO. 6e+04;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACATCAGAGTCTCTCGCG 21  
 |||||  
 ACAACACATTCTCAGTGG 28

0181 28 bp DNA linear PAT 20-DEC-2002  
 nce 1112 from patent US 6489455.

0181  
 0181.1 GI:27310692

own.  
 own.

Unclassified.  
 1 (bases 1 to 28)  
 Chenchik,A., Johhadze,G. and Bibilashvilli,R.  
 Methods of assaying differential expression  
 Patent: US 6489455-A 1112 03-DEC-2002;  
 Location/Qualifiers  
 1. .28  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 28;  
 Best Local Similarity 76.2%; Pred. No. 6e+04; 5; Indels 0;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCAGTCTCTCGCG 21  
 |||||  
 8 ACACAACACATTCTCAGTGG 28

Db

RESULT 32  
 AX794235 28 bp DNA linear PAT  
 LOCUS  
 DEFINITION Sequence 66 from Patent WO02092827.  
 ACCESSION AX794235  
 VERSION AX794235.1 GI:32959641  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.

REFERENCE 1  
 AUTHORS Rottier,P.J., de Haan,C.A., Haijema,B.J. and Bosch,B.J.  
 TITLE Corona-virus-like particles comprising functionally dele  
 JOURNAL Patent: WO 02092827-A 66 21-NOV-2002;  
 Universiteit Utrecht (NL) ; STICHTING VOOR DE TECHNISCHE  
 WETENSCHAPPEN (NL)

FEATURES  
 Location/Qualifiers  
 1. .28  
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 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="sequence of junction generated in recomb  
 MHV-virus"

ORIGIN

Query Match 59.1%; Score 13; DB 6; Length 28;  
 Best Local Similarity 76.2%; Pred. No. 6e+04; 5; Indels 0;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 2 GACAATCAGTCTCTCGCGA 22  
 |||||  
 8 GACTATCACAGCCCCCGCGCA 28

Db

RESULT 33  
 I92361 34 bp DNA linear PAT  
 LOCUS  
 DEFINITION Sequence 13 from patent US 5728519.  
 ACCESSION I92361  
 VERSION I92361.1 GI:3936831  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 34)  
 AUTHORS Levenbook,I.S., Chumakov,K.M., Norwood,L.P. and Roninson  
 TITLE Assay for virulent revertants of attenuated live vaccine  
 therefor  
 JOURNAL Patent: US 5728519-A 13 17-MAR-1998;  
 Location/Qualifiers  
 1. .34  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

09:38:24 2004

us-10-090-326-6.max.rge

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59.1%; Score 13; DB 6; Length 34;
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Conservative 0; Mismatches 0; Gaps 0;

CAATCAGTCTCTGCGGA 22
|||||
CAATCAGATTGTGAGCA 34
|||||

8476 40 bp DNA linear PAT 23-NOV-2002
ence 256 from Patent WO02072846.
8476 47 bp DNA linear PAT 28-AUG-2001
8476.1 GI:25270886
helic construct
helic construct
ficial sequences.

ourt, D., Reynes, J.P. and Tiraby, G.
helic genes and bacterial plasmids devoid of cpv
nt: WO 02072846-A 256 19-SEP-2002;
A (FR)
Location/Qualifiers
1..40
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="assembling oligo for CpG-free LacZ"

59.1%; Score 13; DB 6; Length 40;
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Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CAATCAGTCTCTGCGGA 22
|||||
CAATCAGTGGATGTGGA 38
|||||

35024 47 bp DNA linear PAT 28-AUG-2001
ence 494 from Patent WO0151659.
35024
35024.1 GI:15385671
o sapiens (human)
o sapiens
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

T., Blumenfeld, M. and Cohen, D.
helic markers derived from genomic regions carrying genes
olved in central nervous system disorders
ent: WO 0151659-A 494 19-JUL-2001;
SET (FR)
Location/Qualifiers
1..47
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
24
/note="18-856-85 : polymorphic base C or T"

59.1%; Score 13; DB 6; Length 47;
ilarity 100.0%; Pred. No. 6.1e+04;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 5 AATCAGTCTCT 17
Db 23 AATCAGTCTCT 11

RESULT 36
AX234381 50 bp DNA linear PAT
LOCUS
DEFINITION Sequence 31 from Patent WO0162942.
ACCESSION AX234381
VERSION AX234381.1 GI:15593382
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Alitalo, K.M. and Jeltsch, M.M.
TITLE Materials and methods involving hybrid vascular endothel
JOURNAL factor dhas and proteins and screening methods for modul
FEATURES PATENT: WO 0162942-A 31 30-AUG-2001;
source LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; Licentia OY
1..50 Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

ORIGIN
Query Match 59.1%; Score 13; DB 6; Length 50;
Best Local Similarity 76.2%; Pred. No. 6.1e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

Qy 2 GACATCAGTCTCTGCGGA 22
Db 1 GCCATCAGTCTCTGCGGA 21

RESULT 37
AX158793 51 bp DNA linear PAT
LOCUS
DEFINITION Sequence 2121 from Patent WO0140521.
ACCESSION AX158793
VERSION AX158793.1 GI:14540124
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shinkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphism
JOURNAL Patent: WO 0140521-A 2121 07-JUN-2001;
FEATURES Curagen Corporation (US)
source 1..51
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/mol_type="unassigned DNA"
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misc_feature 26
/note="1 of 2 allelic variants (2122 is other
Accession number CG38453366"

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Matches 16; Conservative 0; Mismatches 5; Indels 0;

Qy 2 GACATCAGTCTCTGCGGA 22
Db 29 GAAATCAGATCTCTCTGA 49
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09:38:24 2004

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794          51 bp      DNA      linear      PAT 22-JUN-2001
794.1  GI:14540125
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ets, R.A. and Leach, M.
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ds of use thereof
t: WO 0140521-A 2122 07-JUN-2001;
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ets, R.A. and Leach, M.
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DEFINITION     Sequence 40 from Patent WO0162942.
ACCESSION      AX234390
VERSION        AX234390.1  GI:15593391
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE
1
AUTHORS        Aliatalo, K.M. and Jeltsch, M.M.
TITLE          Materials and methods involving hybrid vascular endothel:
              factor dnas and proteins and screening methods for moduli:
              Patent: WO 0162942-A 40 30-AUG-2001;
              LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; Licentia OY
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DEFINITION     Sequence 12 from Patent WO0178773.
ACCESSION      AX285267
VERSION        AX285267.1  GI:17045949
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE
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AUTHORS        Denich, K.
TITLE          Dissociated pili, their production and use
              Patent: WO 0178773-A 12 25-OCT-2001;
              O'Hanley, Peter (US) ; Denich, Kenneth (CA)
JOURNAL        Location/Qualifiers
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DEFINITION     Sequence 32 from Patent WO0179277.
ACCESSION      AX302070
VERSION        AX302070.1  GI:17383021
KEYWORDS       synthetic construct
SOURCE         synthetic construct
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helic construct  
ficial sequences.

ch,K. and Schmidt,M.A.

nogenic pili presenting foreign peptides, their production and

nt: WO 0179277-A 32 25-OCT-2001;

nley, Peter (US) ; Denich, Kenneth (CA) ; Schmidt, M. Alexander

Location/Qualifiers

1. 20

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ACAATCACAGTCTC 16

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AGATCGCAGTCTC 3

7974 24 bp DNA linear PAT 11-MAY-2001

ence 3097 from Patent WO0129262.

7974

7974.1 GI:14034925

helic construct  
helic construct  
ficial sequences.

ult-Newburg,L. and Pohl,M.

typing reagents, kits and methods of use thereof

nt: WO 0129262-A 3097 26-APR-2001;

id BioSciences, Inc. (US)

Location/Qualifiers

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ACAGTCTTTGCAGA 4

9827 47 bp DNA linear PAT 12-JUN-2003

ence 1562 from patent US 6537751.

9827

9827.1 GI:31677111

OWN.

OWN.

assified.

bases 1 to 47)

n.D., Chumakov,I. and Blumenfeld,M.

lelic markers for use in constructing a high density

quilibrium map of the human genome

nt: US 6537751-A 1562 25-MAR-2003;

FEATURES source Location/Qualifiers  
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DEFINITION Sequence 235 from Patent WO0147942.

ACCESSION

AX190056

VERSION

AX190056.1

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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/mol\_type="unassigned DNA"

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/note="1 of 2 allelic variants (236 is other

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ORIGIN

Query Match

Best Local Similarity

Matches 14; Conservative

Qy 1 AGACATCACAGTCTC 16

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Db 33 AGACACTCACAGTTTC 18

Search completed: February 29, 2004, 09:42:52

Job time : 713.857 secs

09:38:24 2004

us-10-090-326-6.max.rng

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

leic search, using sw model

February 29, 2004, 07:46:14 ; Search time 187.714 Seconds  
(without alignments)  
497.886 Million cell updates/sec

JS-10-090-326-6  
22

1 agacaatcacagtctctgcgga 22

IDENTITY NUC

Japop 10.0 , Gapext 1.0

3373863 seqs, 212409041 residues

hits satisfying chosen parameters: 3308108

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001as:\*
- 5: Geneseq2001bs:\*
- 6: Geneseq2002as:\*
- 7: Geneseq2003as:\*
- 8: Geneseq2003bs:\*
- 9: Geneseq2003cs:\*
- 10: Geneseq2004s:\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

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70.9	30	2	AAT06506	Aat06506 Primer NH
69.1	31	4	AAF61364	Aaf61364 Thrombom
64.5	20	6	AAD34356	Aad34356 Human BSM
64.5	60	6	ABN43232	Abn43232 Human spl
63.6	25	7	ADB00617	Adb00617 Human MDZ
63.6	25	7	ADB00619	Adb00619 Human MDZ
63.6	25	7	ADB00620	Adb00620 Human MDZ
63.6	25	7	ADB00618	Adb00618 Human MDZ
62.7	25	8	ACI53991	Act53991 Human mic
62.7	41	6	ABQ77936	Abq77936 Human mac
61.8	24	2	AAQ27842	Aaq27842 Short tan
61.8	25	8	ACI61709	Act61709 Human mic
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61.8	53	7	ABX15587	Abx15587 MHV expre

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55.5	32	6	AbL56456	Primer VA	317	12	54.5	23	8	ADA21520	I
55.5	33	3	Aaz298724	PCR prime	318	12	54.5	23	8	ADA10307	I
55.5	33	3	Aaz29868	SYDV reia	319	12	54.5	23	8	ADA17851	I
55.5	36	2	Aaz23792	Reshaped	320	12	54.5	23	8	ADA27959	I
55.5	37	6	AbQ72442	PCR prime	321	12	54.5	23	8	ADA94539	I
55.5	38	6	AbQ72426	PCR prime	322	12	54.5	23	8	ADA38764	I
55.5	38	6	AbQ72443	PCR prime	323	12	54.5	23	8	ADA92885	I
55.5	38	6	AbQ72444	PCR prime	324	12	54.5	23	8	ACH65489	I
55.5	38	6	AbQ72448	PCR prime	325	12	54.5	23	8	ADA22446	I
55.5	38	6	AbQ72440	PCR prime	326	12	54.5	23	8	ADA22446	I
55.5	38	6	AbQ72441	PCR prime	327	12	54.5	23	8	ADA06612	I
55.5	41	6	AbQ77937	Human mac	328	12	54.5	23	8	ADA39305	I
55.5	41	6	AbK11520	Human oxy	329	12	54.5	23	8	ADB96331	I
55.5	42	6	AaQ23848	Primer RH	330	12	54.5	23	9	ADC57803	I
55.5	42	6	AaQ28862	Human ant	331	12	54.5	23	9	ADC55167	I
55.5	42	9	ADd67340	Human ant	332	12	54.5	23	9	ADCL2034	I
55.5	43	2	AaQ37845	Sequence	333	12	54.5	23	9	ADC56456	I
55.5	48	2	AaQ69258	Human cho	334	12	54.5	23	9	ADC07511	I
55.5	48	2	AaT63720	Human cho	335	12	54.5	23	9	ADCL1501	I
55.5	48	2	AaX17008	Test sequ	336	12	54.5	23	9	ADCL14623	I
55.5	48	6	AbK82499	DNA bindi	337	12	54.5	23	9	AD008155	I
55.5	48	10	AD880038	Duplex ol	338	12	54.5	23	9	AD081980	I
55.5	49	2	AaQ69329	Human cho	339	12	54.5	23	9	ADD07622	I
55.5	49	2	AaT63791	Human cho	340	12	54.5	23	9	ADC82513	I
55.5	49	2	AaX17079	Test sequ	341	12	54.5	23	9	AD008693	I
55.5	49	6	AbK82570	DNA bindi	342	12	54.5	23	9	ADC84362	I
55.5	49	10	AD880109	Duplex ol	343	12	54.5	23	9	ADC83863	I
55.5	50	2	AaX52154	Synthetic	344	12	54.5	23	9	AD006942	I
55.5	50	2	AaX52078	Synthetic	345	12	54.5	23	9	AD006942	I
55.5	50	4	AaL31473	Human SNP	346	12	54.5	23	9	ADC83189	I
55.5	50	6	AbZ04399	Human leu	347	12	54.5	23	9	ADD55296	I
55.5	50	6	AbZ03209	Human leu	348	12	54.5	23	9	ADD56254	I
55.5	51	4	AaH79418	Human DNA	349	12	54.5	23	9	AD26846	I
55.5	51	5	AbL00984	Human ami	350	12	54.5	23	9	AD26313	I
55.5	52	2	AaV79391	Staphyloc	351	12	54.5	24	2	AaT30775	I
55.5	60	6	AbN58889	Human spl	352	12	54.5	24	3	AaZ89686	I
55.5	60	6	AbN42164	Human spl	353	12	54.5	24	4	AaF60486	I
55.5	60	6	AbN58634	Human spl	354	12	54.5	24	7	AaL51450	I
55.5	60	6	AbN47836	Human spl	355	12	54.5	25	7	AD00615	I
55.5	60	6	AbN47944	Human spl	356	12	54.5	25	8	ACI66408	I
55.5	60	6	AbN43233	Human spl	357	12	54.5	25	8	ACI07223	I
55.5	60	6	AbN46474	Human spl	358	12	54.5	25	8	ACI12742	I
55.5	60	6	AbN45521	Human spl	359	12	54.5	25	8	ACI22801	I
55.5	60	6	AbN36252	Human spl	360	12	54.5	25	8	ACI97128	I
55.5	60	6	AbN36681	Human spl	361	12	54.5	25	8	ACI29320	I
55.5	60	6	AbN37178	Human spl	362	12	54.5	25	8	ACI22566	I
55.5	20	2	AaZ02867	PCR prime	363	12	54.5	25	8	ACI61708	I
54.5	20	6	AbL50603	Mouse Nap	364	12	54.5	25	8	ACI95431	I
54.5	20	9	AD24128	Cre recom	365	12	54.5	25	8	ACK26101	I
54.5	21	2	AaX36544	PCR prime	366	12	54.5	25	8	ACH53513	I
54.5	21	3	AaZ55812	Rat FGF-1	367	12	54.5	25	8	ACH53514	I
54.5	21	6	AbS61385	Plasmid d	368	12	54.5	25	8	ACH53977	I
54.5	23	3	AaZ65202	Primer am	369	12	54.5	26	2	AaZ00259	I
54.5	23	4	AaC90135	Human PRO	370	12	54.5	27	2	AaQ29062	I
54.5	23	5	AaF44359	Human PRO	371	12	54.5	29	3	AaZ89682	I
54.5	23	7	AbX77918	Human PRO	372	12	54.5	29	9	ADD40784	I
54.5	23	7	AbX80330	Human sec	373	12	54.5	30	2	AaT30494	I
54.5	23	7	AbX80330	Human sec	374	12	54.5	30	2	AaX36541	I
54.5	23	7	AbX90307	Human sec	375	12	54.5	30	3	AaZ55809	I
54.5	23	7	AbX64153	Human PRO	376	12	54.5	32	2	AaX88085	I
54.5	23	7	AbX64375	Novel hum	377	12	54.5	32	9	ADD15546	I
54.5	23	7	AbX58037	Human neo	378	12	54.5	33	4	AaH76938	I
54.5	23	7	AbX80834	Human sec	379	12	54.5	33	4	AaD03061	I
54.5	23	7	AbX80834	Human PRO	380	12	54.5	33	6	ABA05772	I
54.5	23	7	AbX79514	Human sec	381	12	54.5	33	6	ABA05339	I
54.5	23	7	AbX93535	Novel hum	382	12	54.5	34	2	AaX82046	I
54.5	23	7	AbX81217	Human sec	383	12	54.5	34	4	AaH43249	I
54.5	23	7	AbX93033	Novel hum	384	12	54.5	34	4	AaH43060	I
54.5	23	7	AbX17117	Human PRO	385	12	54.5	35	2	AaQ36176	I
54.5	23	8	AbX67972	Novel hum	386	12	54.5	35	6	AbX92545	I
54.5	23	8	AbX88421	Human sec	387	12	54.5	36	2	AaX82025	I
54.5	23	8	AbX81928	Human PRO	388	12	54.5	37	8	ADA15870	I



53.6	36	4	AAC66984	Aac66984 Bacteriop	608	11.6	52.7	20	3	AAC73804	Aac73804 I
53.6	37	2	AAQ80392	AAQ80392 Mouse hea	609	11.6	52.7	20	4	AAS15171	Aas15171 I
53.6	37	2	AAQ80670	AAQ80670 L243 VH r	610	11.6	52.7	20	6	ABV73630	Abv73630 I
53.6	37	2	AAT07333	Aat07333 Mab 39D10	611	11.6	52.7	20	7	ABX04458	Abx04458 I
53.6	37	2	AAT16943	Aat16943 Murine an	612	11.6	52.7	20	9	ADE14416	Adel14416 I
53.6	37	2	AAQ90430	Aaq90430 ChimERIC	613	11.6	52.7	21	6	ABQ79112	Abq79112 I
53.6	37	6	AAQ31320	Aad31320 Mouse hea	614	11.6	52.7	21	9	ADD05293	Add05293 I
53.6	38	6	ABQ72438	Abq72438 PCR prime	615	11.6	52.7	22	2	AAI16566	Aai16566 I
53.6	38	6	AAV57502	Aav57502 Antibody	616	11.6	52.7	22	2	AAV23624	Aav23624 I
53.6	38	6	ABQ72429	Abq72429 PCR prime	617	11.6	52.7	23	3	AAT15902	Aat15902 I
53.6	38	6	ABQ72439	Abq72439 PCR prime	618	11.6	52.7	23	3	AAI88508	Aai88508 I
53.6	39	4	AAH78402	Aah78402 PCR prime	619	11.6	52.7	24	6	ABQ08771	Abq08771 I
53.6	39	7	ACA49915	Acc49915 Synthetic	620	11.6	52.7	24	6	ABQ02436	Abq02436 I
53.6	40	7	ACA55229	Aca55229 Human IGE	621	11.6	52.7	24	6	ABQ08812	Abq08812 I
53.6	40	7	ACA55211	Aca55211 Human IGE	622	11.6	52.7	25	7	AAV62108	Aav62108 I
53.6	40	7	ACA55191	Aca55191 Canine Ig	623	11.6	52.7	25	7	ADB00624	Adb00624 I
53.6	40	7	ACA55218	Aca55218 Human IGE	624	11.6	52.7	25	8	ACK16869	Ack16869 I
53.6	41	2	AAV50774	Aav50774 Brassaica	625	11.6	52.7	25	8	ACI90111	ACI90111 I
53.6	41	3	AAZ87718	Aaz87718 Anti-huma	626	11.6	52.7	25	8	ACI77084	ACI77084 I
53.6	41	4	AAF70195	Aaf70195 Oligonucl	627	11.6	52.7	25	8	ACI57014	ACI57014 I
53.6	41	5	AAFC83900	Aac83900 PCR prime	628	11.6	52.7	25	8	ACI65779	ACI65779 I
53.6	41	6	AAI69209	Aai69209 Human tyr	629	11.6	52.7	25	8	ACI53105	ACI53105 I
53.6	41	7	ACC00157	Acc00157 Probe #2	630	11.6	52.7	25	8	ACK15711	ACK15711 I
53.6	42	6	ABQ72379	Abq72379 PCR prime	631	11.6	52.7	25	8	ACI47944	ACI47944 I
53.6	42	3	AAZ49551	Aaz49551 Anticense	632	11.6	52.7	25	8	ACI84694	ACI84694 I
53.6	43	2	AAT74974	Aat74974 Anti-tran	633	11.6	52.7	25	8	ACK17311	ACK17311 I
53.6	43	3	AAZ87717	Aaz87717 Anti-huma	634	11.6	52.7	25	8	ACI78125	ACI78125 I
53.6	43	4	AAF70194	Aaf70194 Oligonucl	635	11.6	52.7	25	8	ACK13930	ACK13930 I
53.6	44	2	AAQ37398	Aaq37398 Primer Mo	636	11.6	52.7	25	8	ACK18611	ACK18611 I
53.6	44	2	AAV44007	Aav44007 Human Mab	637	11.6	52.7	25	8	ACK189185	ACK189185 I
53.6	47	3	AAZ67762	Aaz67762 Human map	638	11.6	52.7	25	8	ACK23330	ACK23330 I
53.6	47	4	AAH88583	Aah88583 CNS disor	639	11.6	52.7	26	6	ACC47323	ACC47323 I
53.6	48	2	AAV03844	Aav03844 Mouse hea	640	11.6	52.7	28	6	ABT09646	Abt09646 I
53.6	48	2	AAV18533	Aav18533 Mouse hea	641	11.6	52.7	28	6	ABL41266	AbL41266 I
53.6	48	2	AAV18569	Aav18569 Mouse hea	642	11.6	52.7	29	7	ACC74146	Acc74146 I
53.6	48	2	AAV82320	Aav82320 Mouse imm	643	11.6	52.7	30	2	AAQ66532	AAQ66532 I
53.6	48	2	AAZ28184	Aaz28184 Chlamydia	644	11.6	52.7	30	2	AAV35354	AAV35354 I
53.6	48	3	AAZ99167	Aaz99167 Chlamydia	645	11.6	52.7	30	3	AAZ88333	AAZ88333 I
53.6	48	4	AAH21994	Aah21994 Mouse imm	646	11.6	52.7	30	3	AAA40187	Aaa40187 I
53.6	48	4	AAH22020	Aah22020 Mouse Ig	647	11.6	52.7	30	4	AAF88138	Aaf88138 I
53.6	48	9	ADC65080	Adc65080 Mouse imm	648	11.6	52.7	30	4	AAF88081	Aaf88081 I
53.6	48	9	ADC65054	Adc65054 Mouse imm	649	11.6	52.7	30	7	ABX13116	Abx13116 I
53.6	50	2	AAQ37397	Aaq37397 Primer Fo	650	11.6	52.7	30	7	ABX13122	Abx13122 I
53.6	50	2	AAQ37416	Aaq37416 Primer MO	651	11.6	52.7	31	2	AAI57793	Aai57793 I
53.6	50	4	AAI73211	Aai73211 Human sil	652	11.6	52.7	31	4	AAI30568	Aai30568 I
53.6	51	2	AAV77111	Aav77111 Staphyloc	653	11.6	52.7	31	6	ABN83750	Abn83750 I
53.6	51	2	AAV33750	Aav33750 Ig-like V	654	11.6	52.7	31	6	ABN83753	Abn83753 I
53.6	51	4	AAI29092	Aai29092 Human SNP	655	11.6	52.7	31	6	ABN83749	Abn83749 I
53.6	51	4	AAI77020	Aai77020 Human sil	656	11.6	52.7	33	2	AAQ68730	AAQ68730 I
53.6	51	4	AAI73210	Aai73210 Human sil	657	11.6	52.7	34	2	AAQ36969	AAQ36969 I
53.6	51	4	AAH40412	Aah40412 Human SNP	658	11.6	52.7	36	2	AAQ00980	AAQ00980 I
53.6	51	7	ABX88797	Abx88797 Corn ear-	659	11.6	52.7	36	2	AAI00981	Aai00981 I
53.6	53	7	ABZ21173	Abz21173 Variable	660	11.6	52.7	36	9	ADD29945	Add29945 I
53.6	54	2	AAQ78346	Aaq78346 Fv haptan	661	11.6	52.7	36	9	ADD35983	Add35983 I
53.6	54	2	AAQ86751	Aaq86751 Primer fo	662	11.6	52.7	38	7	ACD54088	ACD54088 I
53.6	54	2	AAV07645	Aav07645 anti-CD22	663	11.6	52.7	39	6	AAZ25718	Aaz25718 I
53.6	56	3	AAZ44228	Aaz44228 Murine CD	664	11.6	52.7	40	2	AAQ36508	AAQ36508 I
53.6	56	3	AAZ58686	Aaz58686 Anti-CD4	665	11.6	52.7	40	2	AAQ54753	Aaq54753 I
53.6	60	4	AAT85649	Aat85649 Canine im	666	11.6	52.7	40	2	AAQ75893	Aaq75893 I
53.6	60	4	AAI30706	Aai30706 Mouse JH	667	11.6	52.7	40	2	AAT70698	Aat70698 I
53.6	60	6	ABN47743	Abn47743 Human spl	668	11.6	52.7	40	2	AAT28128	Aat28128 I
53.6	60	6	ABN35548	Abn35548 Human spl	672	11.6	52.7	41	6	ABZ48181	Abz48181 I
53.6	60	6	ABN33859	Abn33859 Human spl	671	11.6	52.7	41	6	ABZ46007	Abz46007 I
53.6	60	6	ABN50576	Abn50576 Human spl	670	11.6	52.7	41	6	ABT12238	ABT12238 I
53.6	60	6	ABN58845	Abn58845 Human spl	671	11.6	52.7	41	6	ABT60017	ABT60017 I
53.6	60	6	ABN43038	Abn43038 Human spl	672	11.6	52.7	41	6	ABZ48181	Abz48181 I
53.6	60	6	ABN47127	Abn47127 Human spl	673	11.6	52.7	43	2	AAQ53769	Aaq53769 I
53.6	60	6	ABN49635	Abn49635 Human spl	674	11.6	52.7	43	2	AAT07970	Aat07970 I
53.6	60	6	AAZ70326	Aaz70326 Human bia	675	11.6	52.7	43	2	AAV00986	AAV00986 I
52.7	18	3	AAZ70326	Aaz70326 Human bia	676	11.6	52.7	43	2	AAV14771	Aav14771 I
52.7	19	6	ABSS59954	Abss59954 Human DNA	677	11.6	52.7	43	2	AAV79846	Aav79846 I
52.7	19	7	ABT33997	Abt33997 Human pig	678	11.6	52.7	43	3	AAZ92946	Aaz92946 I
52.7	20	2	AAZ72837	Aaz72837 SP24 gene	679	11.6	52.7	43	6	ABK61322	ABK61322 I
52.7	20	3	AAZ76305	Aaz76305 Human bia	680	11.6	52.7	45	2	AAT88664	Aat88664 I

52.7	45	7	ABT34060	Human pig	754	11.4	51.8	18	6	ABT06161	ABT06161
52.7	46	7	ACC47398	G. cirrat	755	11.4	51.8	19	2	AAV30474	AAV30474
52.7	47	2	AAL11953	Human pot	c 756	11.4	51.8	19	2	AAV58063	AAV58063
52.7	47	4	AAH88587	CNS disor	c 757	11.4	51.8	19	2	AAV81132	AAV81132
52.7	48	2	AAH86302	Primer ol	c 758	11.4	51.8	19	2	AAV81082	AAV81082
52.7	48	2	AAV03965	LDR probe	c 759	11.4	51.8	20	2	AAQ53353	AAQ53353
52.7	48	2	ADD27837	GLCNAc-ph	c 760	11.4	51.8	20	2	AAV28294	AAV28294
52.7	50	3	AA37231	Human DNA	c 761	11.4	51.8	20	2	AAV28224	AAV28224
52.7	50	4	AA313202	Tobacco r	c 762	11.4	51.8	20	2	AAV28224	AAV28224
52.7	50	4	AA128722	Human SNP	c 763	11.4	51.8	20	4	AAV28224	AAV28224
52.7	50	4	AA134141	Human SNP	c 764	11.4	51.8	20	4	AAV28224	AAV28224
52.7	50	4	AA129730	Human SNP	c 765	11.4	51.8	20	6	AAV28224	AAV28224
52.7	50	4	AA154340	Probe #30	c 766	11.4	51.8	20	7	AAV28224	AAV28224
52.7	50	4	AA154340	Probe #30	c 767	11.4	51.8	20	7	AAV28224	AAV28224
52.7	50	4	AA154340	Probe #30	c 768	11.4	51.8	20	9	AAV28224	AAV28224
52.7	50	6	AB201612	Human leu	c 769	11.4	51.8	21	6	ABK69607	ABK69607
52.7	50	6	AB207152	Human leu	c 770	11.4	51.8	21	7	ACC68851	ACC68851
52.7	50	6	AB203511	Human leu	c 771	11.4	51.8	22	2	AAZ07852	AAZ07852
52.7	50	6	AB204178	Human leu	c 772	11.4	51.8	22	6	ABK95503	ABK95503
52.7	50	6	AB206762	Human leu	c 773	11.4	51.8	22	6	ABT04310	ABT04310
52.7	50	6	AB207525	Human leu	c 774	11.4	51.8	22	9	ADC66100	ADC66100
52.7	50	6	AB202277	Human leu	c 775	11.4	51.8	23	6	AAV97990	AAV97990
52.7	50	6	AB207446	Human leu	c 776	11.4	51.8	24	2	AAV86450	AAV86450
52.7	50	6	AB203481	Human leu	c 777	11.4	51.8	24	2	AAV86611	AAV86611
52.7	50	8	ACD68377	Novel hum	c 778	11.4	51.8	24	3	AAV86611	AAV86611
52.7	50	8	ACD68377	Novel hum	c 779	11.4	51.8	24	5	AAV86611	AAV86611
52.7	50	8	ACD68377	Novel hum	c 780	11.4	51.8	24	7	ABX76693	ABX76693
52.7	50	9	ADD31781	Anti-CEA	c 781	11.4	51.8	24	8	ABX93096	ABX93096
52.7	50	9	ADD70707	Human sec	c 782	11.4	51.8	25	2	AAV84294	AAV84294
52.7	50	9	ADD39784	Human sec	c 783	11.4	51.8	25	4	AAV84294	AAV84294
52.7	50	9	ADD70230	Human sec	c 784	11.4	51.8	25	6	ABQ75556	ABQ75556
52.7	50	9	ADD38351	Human sec	c 785	11.4	51.8	25	6	ABK40427	ABK40427
52.7	50	9	ADD39307	Human sec	c 786	11.4	51.8	25	8	ACI60939	ACI60939
52.7	50	9	ADD38830	Human sec	c 787	11.4	51.8	25	8	ACI72655	ACI72655
52.7	50	9	ADD40261	Human sec	c 788	11.4	51.8	25	8	ACI52665	ACI52665
52.7	50	9	ADE50482	Human sec	c 789	11.4	51.8	25	8	ACI93231	ACI93231
52.7	50	9	ADE20094	Human sec	c 790	11.4	51.8	25	8	ACI65791	ACI65791
52.7	50	9	ADE50005	Human sec	c 791	11.4	51.8	25	8	ACK02422	ACK02422
52.7	50	9	ADE21563	Human sec	c 792	11.4	51.8	25	8	ACI09271	ACI09271
52.7	51	4	AAH7908	Human SNP	c 793	11.4	51.8	25	8	ACI28807	ACI28807
52.7	51	4	AAH7908	Human SNP	c 794	11.4	51.8	25	8	ACI64952	ACI64952
52.7	51	4	AAH7908	Human SNP	c 795	11.4	51.8	25	8	ACI00127	ACI00127
52.7	59	2	AA25558	Human gen	c 796	11.4	51.8	25	8	ACI77033	ACI77033
52.7	60	6	ABN42693	Human spl	c 797	11.4	51.8	25	8	ACI33719	ACI33719
52.7	60	6	ABN34962	Human spl	c 798	11.4	51.8	25	8	ACI54543	ACI54543
52.7	60	6	ABN41633	Human spl	c 799	11.4	51.8	25	8	ACK05619	ACK05619
52.7	60	6	ABN39456	Human spl	c 800	11.4	51.8	25	8	ACK07092	ACK07092
52.7	60	6	ABN47190	Human spl	c 801	11.4	51.8	25	8	ACK09503	ACK09503
52.7	60	6	ABN33052	Human spl	c 802	11.4	51.8	25	8	ACI93377	ACI93377
52.7	60	6	ABN49959	Human spl	c 803	11.4	51.8	25	8	ACI10924	ACI10924
52.7	60	6	ABN37902	Human spl	c 804	11.4	51.8	25	8	ACI14350	ACI14350
52.7	60	6	ABN33552	Human spl	c 805	11.4	51.8	25	8	ACI75034	ACI75034
52.7	60	6	ABN33725	Human spl	c 806	11.4	51.8	25	8	ACK07093	ACK07093
52.7	60	6	ABN40869	Human spl	c 807	11.4	51.8	25	8	ACI41690	ACI41690
52.7	60	6	ABN46183	Human spl	c 808	11.4	51.8	25	8	ACK26967	ACK26967
52.7	60	6	ABN45405	Human spl	c 809	11.4	51.8	25	8	ACI00322	ACI00322
52.7	60	6	ABN46240	Human spl	c 810	11.4	51.8	25	8	ACI04307	ACI04307
52.7	60	6	ABN38002	Human spl	c 811	11.4	51.8	25	8	ACI33626	ACI33626
52.7	60	6	ABN58902	Human spl	c 812	11.4	51.8	25	8	ACI41691	ACI41691
52.7	60	6	ABN38188	Human spl	c 813	11.4	51.8	25	7	ABZ84407	ABZ84407
52.7	60	6	ABN46890	Human spl	c 814	11.4	51.8	26	2	AAV07646	AAV07646
52.7	60	6	ABN40307	Human spl	c 815	11.4	51.8	27	2	AAZ09469	AAZ09469
52.7	60	6	ABN45400	Human spl	c 816	11.4	51.8	27	3	AAV87569	AAV87569
52.7	60	6	ABN40592	Human spl	c 817	11.4	51.8	27	6	ABK11610	ABK11610
52.7	60	6	ABN44042	Human spl	c 818	11.4	51.8	27	7	ABX56465	ABX56465
52.7	60	6	ABN46747	Human spl	c 819	11.4	51.8	28	2	AAV36143	AAV36143
52.7	60	6	ABN42468	Human spl	c 820	11.4	51.8	28	6	ABL54830	ABL54830
52.7	60	6	ABN47612	Human spl	c 821	11.4	51.8	28	6	ABK66449	ABK66449
51.8	17	2	AAA22930	Integrin	c 822	11.4	51.8	28	6	ABK66449	ABK66449
51.8	17	2	AAA22930	Integrin	c 823	11.4	51.8	30	2	AAQ65482	AAQ65482
51.8	17	3	AAA22929	Integrin	c 824	11.4	51.8	30	2	AAQ65482	AAQ65482
51.8	17	3	AAA22929	Integrin	c 825	11.4	51.8	30	2	AAV32409	AAV32409
51.8	17	9	ADB43442	Tumour su	c 826	11.4	51.8	30	3	AAZ35125	AAZ35125
51.8	18	6	ABT06166	Human lig	c 826	11.4	51.8	30	3	AAZ35125	AAZ35125



30	6	ABN83507	Human alp	900	11.4	51.8	50	6	ABZ03910
30	6	ABN83131	Molloney 1	901	11.4	51.8	50	6	ABZ07136
30	6	ABN83131	Vector pv	c 902	11.4	51.8	50	6	ABZ07430
31	2	AAQ62449	Human gen	c 903	11.4	51.8	50	6	ABZ05642
31	2	AAQ39003	Human sin	c 904	11.4	51.8	50	6	ABZ06746
31	4	AAI29711	Human CLA	c 905	11.4	51.8	50	9	ADC15776
31	6	AAI18910	Human CLA	c 906	11.4	51.8	51	2	AAZ28224
31	7	ACC69676	Antisense	c 907	11.4	51.8	51	3	AAA76893
31	7	ADB95122	Primer SK	c 908	11.4	51.8	51	3	AAA76906
31	9	AAV56631	Feline FL	c 909	11.4	51.8	51	3	AAA76323
32	2	AAV56631	Human c-f	c 910	11.4	51.8	51	3	AAA77435
32	3	AAAC63829	Human c-f	c 911	11.4	51.8	51	3	AAA76322
32	5	AAH78297	PCR prime	c 912	11.4	51.8	51	3	AAA76892
32	6	ABs66558	Primer as	c 913	11.4	51.8	51	3	AAA76892
32	6	ABs65205	Glub-1 PC	c 914	11.4	51.8	51	3	AAA77434
32	6	ABs65205	Primer of	c 915	11.4	51.8	51	3	AAA77783
32	9	ADC84589	Primer of	c 916	11.4	51.8	51	4	AAAL29672
33	2	AAQ92010	Oligomer	c 917	11.4	51.8	51	4	AAAL29672
33	2	AAQ92010	Sense pri	c 918	11.4	51.8	51	4	AAAI77989
33	2	AAQ91813	Porphorym	c 919	11.4	51.8	51	4	AAAI77989
33	2	AAQ10952	15D3 VH c	c 920	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	15D3 VH c	c 921	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 922	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 923	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 924	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 925	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 926	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 927	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 928	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 929	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 930	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 931	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 932	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 933	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 934	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 935	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 936	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 937	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 938	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 939	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 940	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 941	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 942	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 943	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 944	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 945	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 946	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 947	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 948	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 949	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 950	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 951	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 952	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 953	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 954	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 955	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 956	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 957	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 958	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 959	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 960	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 961	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 962	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 963	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 964	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 965	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 966	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 967	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 968	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 969	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 970	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 971	11.4	51.8	51	4	AAAI75183
33	2	AAQ10952	Oligonucle	c 972	11.4	51.8	51	4	AAAI75183

50.9 18 7 ABZ81724  
 50.9 18 8 ADB12819  
 50.9 19 2 AAV10708  
 50.9 20 2 AAQ82523  
 50.9 20 2 AAQ88018  
 50.9 20 2 AAV14498  
 50.9 20 2 AAZ05811  
 50.9 20 2 AAX95167  
 50.9 20 2 AAX93019  
 50.9 20 3 AAA40876  
 50.9 20 3 AAA56679  
 50.9 20 3 AAA56677  
 50.9 20 4 AAF83344  
 50.9 20 4 AAF62056  
 50.9 20 5 ABA82070  
 50.9 20 6 ABK13149  
 50.9 20 6 ABK13359  
 50.9 20 6 ABK22867  
 50.9 20 6 ABQ74717  
 50.9 20 7 ABQ83431  
 50.9 20 7 ABX95291  
 50.9 20 7 ACC45450  
 50.9 20 7 ACF57067  
 50.9 20 8 ACD05104  
 50.9 20 9 ADB98148  
 50.9 20 9 ADC35609  
 50.9 20 9 ADD42146  
 50.9 20 9 ADD42148

## ALIGNMENTS

standard; DNA; 22 BP.

2 (first entry)

PCR primer SEQ ID NO:6.

; carcinoembryonic antigen; adenocarcinoma; oesophagus;  
 ; PCR primer; ss.

ns.

1-A1.

2.

2; 2002WO-US006504.

1; 2001US-0273277P.

IV PITTSBURGH.

, Luketich JD, Raja S, Kelly LA, Finkelstein SD;

732795/79.

PCR method for detecting malignancies, e.g. adenocarcinoma of  
 igus comprises conducting a PCR amplification on a DNA sample in  
 ition mixture.

page 33; 141pp; English.

it invention describes a multiplex polymerase chain reaction  
 comprising conducting PCR on a DNA sample in a reaction  
 ducted in first and second amplification stages, each with one  
 r cycles comprising denaturing, annealing and elongating steps  
 elongating step may be conducted at the same temperature as the

CC annealing step. The second amplification stage of (M1) is condu  
 CC different reaction conditions from that of the first amplificat  
 CC to modulate the relative rate of production of the first amplif  
 CC first primer set and a second amplicon by a second primer set d  
 CC first and second amplification stages. Also described: (1) an  
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) intr  
 CC PCR diagnostic; (3) rapid detection of a malignancy or of metas  
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use in  
 CC automated PCR system. (M1) is useful for detecting malignancies  
 CC adenocarcinoma of the oesophagus. (M1) eliminates contaminatio  
 CC decreases the time it takes to carry out a PCR reaction. The pr  
 CC sequence represents a PCR primer for human CEA (carcinoembryoni  
 CC antigen), which is used in an example from the present inventio  
 XX  
 SQ Sequence 22 BP; 7 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0;  
 Matches 22; Conservative 0; Mismatches 0;

OY 1 AGACAATCACAGTCTCTCGGA 22  
 |||||  
 Db 1 AGACAATCACAGTCTCTCGGA 22

## RESULT 2

AAT36494/c

ID AAT36494 standard; DNA; 46 BP.

XX AAT36494;

XX 13-NOV-1996 (first entry)

XX Carcinoembryonic antigen gene 3' PCR primer.

XX Carcinoembryonic antigen; immunogen; breast cancer; lung cancer;  
 KW colon cancer; therapy; immunotherapy; vaccine; baculovirus; ve  
 KW Autographa californica nuclear-polyhedrosis virus; Spodoptera f  
 KW insect; pA9080 AcNPV-CEA; primer; PCR; polymerase chain reacti  
 XX Synthetic.

XX WO9532286-A2.

XX 30-NOV-1995.

XX 19-MAY-1995; 95WO-US006373.

XX 20-MAY-1994; 94US-00246981.

XX (MICR-) MICROGENESYS INC.

XX Smith G, Volvovitz F, Hackett C;

XX WPI; 1996-02C581/02.

XX Immunogenic carcinoembryonic antigen produced using insect cel  
 PT baculovirus expression system - useful in cancer therapy.

XX Disclosure; Page 18; 61pp; English.

XX A 3' PCR primer (AAT36494) contains sequences complementary to  
 CC KpnI and BamHI sites and a stop codon and sequences designed t  
 CC the last 72 bp of the human carcinoembryonic antigen (CEA) gen  
 CC codes for the hydrophobic C-terminal region of CEA that is not  
 CC mature CEA expressed in tumour cells. It was used with a 5' pr  
 CC (AAT36493) designed to delete the CEA signal sequence for the  
 CC amplification of human colon adenocarcinoma LS174T (ATCC CL 18  
 CC The PCR product was used to construct vector pA9080 AcNPV-CEA  
 CC AAT36495) which allows prodn. of soluble, immunogenic CEA (AAF  
 CC insect cells

XX Sequence 46 BP; 9 A; 9 C; 15 G; 13 T; 0 U; 0 Other;

71.8%; Score 15.8; DB 2; Length 46;  
 ilarity 89.5%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 ACAATCACAGTCTCTGC 19  
 |||||  
 AGCATCACAGTCTCTGC 26

undard; DNA; 30 BP.

(first entry)

rin cytoplasmic domain PCR primer NH beta-7 3.

in-like beta 7 integrin binding protein; human; inflammation;  
 .eukocyte; polymerase chain reaction; PCR; primer; ss.

L.

97WO-US000100.  
 96US-00583562.  
 ; CORP.

Harris EA;  
 72863/34.

n-like beta 7 integrin binding protein FLP-1 - used to  
 ulators of inflammatory processes involving leukocytes.

age 10; 84pp; English.

beta-7 3 (AAT73719) and NH beta-7 5 (AAT73718) were used in  
 ification of the beta-7 integrin cytoplasmic domain. The PCR  
 utilised in a 'bait' plasmid in a two-hybrid screening for  
 pressed in a human B cell library which interacted with the C-  
 oplasmic domain of the beta-7 integrin. A claimed coding  
 e AAT73717) for human filamin-like beta-7 integrin binding  
 -1 (AAWI9327) was deduced from isolated clones

BP; 4 A; 9 C; 10 G; 7 T; 0 U; 0 Other;  
 70.9%; Score 15.6; DB 2; Length 30;  
 larity 81.8%; Pred. No. 4.7e+02;  
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 ACAATCACAGTCTCTGCGGA 22  
 |||||  
 ACAGTCCCACTCTCTGAGGA 5

andard; DNA; 30 BP.

(first entry)

a:7 (3') for PCR of beta-7 integrin cytoplasmic domain.

KW inflammatory bowel disease; IBD; mucosal tissue; leukocyte; int  
 KW filamin; lymphocyte; inflammation; PCR; primer; cytoplasmic dom  
 XX Synthetic.  
 OS Homo sapiens.  
 XX US5948891-A.  
 XX 07-SEP-1999.  
 XX 06-JAN-1997; 97US-00779113.  
 XX 05-JAN-1996; 96US-00583562.  
 XX (ICOS-) ICOS CORP.  
 XX Salot Harris EA, Staunton DB;  
 XX WPI; 1999-517974/43.  
 XX Cytoplasmic modulators of integrin binding are able to modulate  
 inflammatory response.  
 XX Example 1; Col 6; 51pp; English.  
 XX This is the 3' primer for the PCR of the beta 7 integrin cytopl  
 CC domain. The 5' primer is sequence AAZ06505. The product from th  
 CC used in the identification of genes in a B cell library which c  
 CC beta 7 interacting proteins. This invention relates to a novel  
 CC like beta 7 integrin binding protein designated FLP-1. Two beta  
 CC associated integrins have been identified (alpha-4,beta-7 and a  
 CC e,beta-7). Both are expressed on a sub population of peripheral  
 CC lymphocytes and their expression is inducible. Both are express  
 CC macrophages but not monocytes and both appear to function in ho  
 CC localisation of lymphocytes to mucosal tissue (Jutila, J. J. Leu  
 CC Biol. 55:133-140 (1994)). Due to the nature of the binding of o  
 CC beta 7 integrins to their respective counter-receptor, they may  
 CC contribute to mucosal immune response as well as inflammatory  
 CC inflammatory bowel disease, IBD) and autoimmune responses at th  
 CC Filamin is thought to be important in cell locomotion, cells th  
 CC low levels of this protein do not form the lamella structures r  
 CC for locomotion. FLP-1 is structurally similar to filamin, and t  
 CC observation that integrins cluster in point contacts, gives ris  
 CC possibility that the beta 7 interaction with FLP-1 and/or filam  
 CC a crucial step in cell locomotion. Disrupting this interaction  
 CC useful in preventing the homing of beta 7 positive cells, which  
 CC certain inflammatory responses such as IBD  
 XX Sequence 30 BP; 4 A; 9 C; 10 G; 7 T; 0 U; 0 Other;  
 SQ Query Match 70.9%; Score 15.6; DB 2; Length 30;  
 Best Local Similarity 81.8%; Pred. No. 4.7e+02;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0;  
 QY 1 AGACAATCACAGTCTCTGCGGA 22  
 |||||  
 Db 26 AGACAGTCCCACTCTCTGAGGA 5

RESULT 5  
 AAF61364  
 ID AAF61364 standard; DNA; 31 BP.  
 XX AC  
 XX AAF61364;  
 XX DT 25-MAY-2001 (first entry)  
 XX DE Thrombomodulin antisense PCR primer.  
 XX PCR primer; expression plasmid; leptin; thrombomodulin; NO synt  
 KW prostacyclin synthase; vasotropic; gene therapy; neovasculariza  
 KW restenosis; peripheral arterial occlusive disease; VEGF;  
 KW vascular endothelial growth factor; ss.

d.

A1.

; 99DE-01040012.

; 99DE-01040012.

RBER K.

SEN P.

HOEPE D.

Roesen P, Tschoepe D;

45983/26.

expression plasmid useful for treating peripheral arterial disease, comprises two expression cassettes, one containing the man vascular endothelial growth factor VEGF165.

Page 10; 16pp; German.

ion describes a novel eukaryotic expression plasmid, in presson cassettes, a coding sequence for human VEGF<sub>165</sub> in with at least one human coding sequence selected from leptin, lin, prostacyclin synthase and/or constitutive NO synthase. s of the invention have vasotropic activity and can be used erapy. The plasmid is useful for inducing neovascularization ing restenosis in the treatment of peripheral arterial disease, e.g. in diabetics

BP; 3 A; 11 C; 10 G; 7 T; 0 U; 0 Other;

ularity 69.1%; Score 15.2; DB 4; Length 31;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACATCAGTCTCTGGG 21

CGATCAGTCTCTGGG 28

standard; DNA; 20 BP.

; (first entry)

gene polymorphism detecting PCR primer, LRGEN17R.

; strength and mineralisation regulatory protein; BSMR; jth; mineralisation; ophthalmological; antidiabetic; y regulating transmembrane receptor; prosthetic device; nplant; diabetic retinopathy; hypertensive retinopathy; steoporosis; prematurity; ocular vessel; eye disorder; ; PCR; primer; ss.

ns.

3-A2.

2.

1; 2001WO-US041788.

0; 2000US-0226119P.

0; 2000US-0234337P.

1; 2001US-0304851P.

XX

PA (AVET ) AVENTIS PHARMA SA.

PA (HARD ) HARVARD COLLEGE.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

XX

PI Warman ML, Gong Y, Olsen BR, Rawadi G, Roman-Roman S;

XX

WPI; 2002-329694/36.

DR

Polynucleotide encoding bone strength and mineralization regula protein useful for diagnosis or therapy of osteoporosis.

XX

PS Disclosure; Fig 5; 124pp; English.

XX

CC The invention relates to bone strength and mineralisation regul protein (BSMR) and its corresponding nucleic acid sequence. BSM useful for the diagnosis or therapy of osteoporosis and for reg (increasing) bone strength and mineralisation in a human subjec CC activating a bone density regulating transmembrane receptor (B protein). An expression vector comprising a promoter that is of CC linked to BSMR DNA is useful for modulating bone density and f CC enhancing bone strength and mineralisation in a mammal cell. CC comprising a BSMR effector is useful for treating osteoporosis CC useful particularly as a coating for prosthetic devices and su CC implants. BSMR is useful for screening lead pharmaceutical age CC effectors, which may be used to treat a range of eye disorders CC diabetic retinopathy, hypertensive retinopathy and retinopathy CC prematurity, in which normal vascular growth and integrity of C vessels is disrupted. The present sequence is a PCR primer use CC amplify cDNA and gDNA molecules useful for detecting polymorph CC genes in human

XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match

Best Local Similarity 64.5%; Score 14.2; DB 6; Length 20;

Matches 16; Conservative 84.2%; Pred. No. 2.2e+03;

Indels 0;

QY 3 ACAATCAGTCTCTGGG 21

Db 20 AAAATCAGTCTCTGGG 2

RESULT 7

ABN43232/c

ID ABN43232 standard; DNA; 60 BP.

XX

AC ABN43232;

XX

DT 15-JUL-2002 (first entry)

XX

DE Human spliced transcript detection oligonucleotide SEQ ID NO:11

XX

KW Human; mouse; rat; splice transcript; detection; RNA transcript/ splice variant; transcriptome; oligonucleotide library; ss.

XX

OS Homo sapiens.

XX

FN WO200210449-A2.

XX

PD 07-FEB-2002.

XX

PF 20-JUL-2001; 2001WO-IB001903.

XX

PR 28-JUL-2000; 2000US-0221607P.

PR

02-MAY-2001; 2001US-0287724P.

XX

PA (COMP-) COMPUGEN INC.

XX

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX

DR WPI; 2002-257363/30.

XX

09:38:24 2004

us-10-090-326-6.max.rng

cleotide libraries comprising oligonucleotides which hybridize to mRNAs transcribed from a transcription unit of a full for detecting tissue-, pathology-, and developmental-nes.

SEQ ID NO 15980; 47pp; English.

invention describes oligonucleotide libraries for detecting NAs that populate a (sub-)transcriptome, where the (sub-)ome comprises messenger RNAs transcribed from multiple on units that populate a genome. The library comprises several tides, each capable of hybridising selectively to a set of NAs transcribed from a given transcription unit of the genome, es one or more messenger RNA splice variants. The tide libraries are useful for detecting mRNAs from a sample, in expression profiling studies, in qualitatively or ely characterising the corresponding transcriptome, and in NA transcripts and splice variants of human or animal mes. The libraries may also be used as specialised mini o detect transcripts of a sub-transcriptome under a particular or pathological state, and so allowing the detection of tissue ology-specific genes such as those genes only expressed in sue under a specific pathological condition; to detect al specific genes; and to detect RNA transcripts and splice a transcriptome of a patient suffering from a particular .BN27253 to ABN59589 represent oligonucleotide sequences from s and mice, which are used in the exemplification of the ention. N.B. The sequence data for this patent did not form : printed specification, but was obtained in electronic format om WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

BP; 16 A; 13 C; 20 G; 11 T; 0 U; 0 Other;

64.5%; Score 14.2; DB 6; Length 60;

ilarity 84.2%; Pred. No. 2.7e+03; Indels 0; Gaps 0;

Conservative 0; Mismatches 3;

ACAACTACAGTCTCTGC 19

|||||

ACAACTACAGTCTGCAGC 42

andard; DNA; 25 BP.

(first entry)

scanning oligonucleotide SEQ ID 1603.

; immunostimulant; gene therapy; vaccine; human;  
; protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
; al disorder; ss.

15.

12.

3.

2; 2002EP-00016874.

1; 2001US-00922181.

OMICA INC.

Gu Y, Nguyen C;

423107/40.

PT New zinc finger-containing proteins and nucleic acids, useful i  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity c  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 1603; 103pp; English.

XX The present invention relates to novel human zinc finger-conta  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. N  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p2  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at c  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful i  
CC or in manufacturing a medicament for treating or preventing a c  
CC associated with decreased or increased expression or activity c  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. T  
CC acids and proteins are also useful for diagnosing or monitoring  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The  
CC acids can also be used as probes to detect and characterize grc  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The p  
CC useful in constructing microarrays for measuring gene expressio  
CC proteins are useful as therapeutic agents for gene therapy or e  
CC vaccines. The present sequence was used to illustrate the inver

XX Sequence 25 BP; 4 A; 8 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 63.6%; Score 14; DB 7; Length 25;

Best Local Similarity 77.3%; Pred. No. 2.9e+03;

Matches 17; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGAATTCACAGTCTCTGC 22

|||||

4 AGTATTCTCAGTCTCTCGGA 25

RESULT 9

ADB00619

ID ADB00619 standard; DNA; 25 BP.

XX ADB00619;

XX 20-NOV-2003 (first entry)

XX Human MDZ3 scanning oligonucleotide SEQ ID 1605.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1  
KW developmental disorder; ss.

XX Homo sapiens.

XX EP1281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 1605; 103pp; English.

XX The present invention relates to novel human zinc finger-conta

their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2, MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome 15q26.1. MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy, acturing a medicament for treating or preventing a disorder with decreased or increased expression or activity of MDZ3, or MDZ12, e.g. cancer or developmental disorders. The nucleic acids are also useful for diagnosing or monitoring a disease in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are so be used as probes to detect and characterize gross alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The present sequence was used to illustrate the invention.

BP; 4 A; 8 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 63.6%; Score 14; DB 7; Length 25;  
Best Local Similarity 77.3%; Pred. No. 2.9e+03;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACATTCACAGTCTCTCGGGA 22  
|||||  
TCATTCACAGTCTCTCGGGA 23

standard; DNA; 25 BP.

(first entry)

scanning oligonucleotide SEQ ID 1606.

immunostimulant; gene therapy; vaccine; human;  
protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
a disorder; ss.

S.

2.

; 2002EP-00016874.

; 2001US-00922181.

MTCA INC.

Gu Y, Nguyen C;

23107/40.

nger-containing proteins and nucleic acids, useful in  
ng a medicament for treating or preventing a disorder  
with decreased or increased expression or activity of MDZ3,  
or MDZ12, e.g. cancer.

SEQ ID NO 1606; 103pp; English.

invention relates to novel human zinc finger-containi  
d their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
15q26.1. MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
acturing a medicament for treating or preventing a disorder  
with decreased or increased expression or activity of MDZ3,  
or MDZ12, e.g. cancer or developmental disorders. The nucleic  
acids are also useful for diagnosing or monitoring a disease

CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The  
CC acids can also be used as probes to detect and characterize gro  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The pr  
CC useful in constructing microarrays for measuring gene expressio  
CC proteins are useful as therapeutic agents for gene therapy or a  
CC vaccines. The present sequence was used to illustrate the inven  
CC  
XX Sequence 25 BP; 4 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

SQ

Query Match 63.6%; Score 14; DB 7; Length 25;  
Best Local Similarity 77.3%; Pred. No. 2.9e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0;

OY 1 AGACAATCACAGTCTCTCGGGA 22  
|||||  
Db 1 AGTCATTCACAGTCTCTCGGGA 22

RESULT 11

ADB00618

ID ADB00618 standard; DNA; 25 BP.

XX ADB00618;

XX 20-NOV-2003 (first entry)

XX Human MDZ3 scanning oligonucleotide SEQ ID 1604.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1  
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1;  
XX developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful i  
XX manufacturing a medicament for treating or preventing a disorde  
XX associated with decreased or increased expression or activity o  
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 1604; 103pp; English.

XX The present invention relates to novel human zinc finger-contai  
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. M  
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p2  
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at c  
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful i  
XX or in manufacturing a medicament for treating or preventing a d  
XX associated with decreased or increased expression or activity o  
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. T  
XX acids and proteins are also useful for diagnosing or monitoring  
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The  
XX acids can also be used as probes to detect and characterize gro  
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The pr  
XX useful in constructing microarrays for measuring gene expressio  
XX proteins are useful as therapeutic agents for gene therapy or a  
XX vaccines. The present sequence was used to illustrate the inven  
XX  
XX Sequence 25 BP; 4 A; 8 C; 6 G; 7 T; 0 U; 0 Other;

SQ

us-10-090-326-6.max.rng

Best Local Similarity 88.2%; Pred. NO. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0;

```

      1 AGACAATCACAGTCTCT 17
      |||||
      6 ATACAATCACAGTTTCT 22

```

XX AC ABQ77936;

DT 30-JAN-2003 (first entry)

DE Human macroprotein 21.01 probe, SEQ ID NO:8.

Human; macroprotein 21.01; recombinant production; gene therapy; dementia; facial paralysis; probe: ss.

PD 29-MAY-2002.

26-OCT-2000; 2000CN-00125816.

26-OCT-2000: 2000CN-00125816.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

Human macroprotein 21.01.

Example 6: Page 21 (Disclosure); 34pp; Chinese.

PS Example 6; Page 21 (Disclosure); 34pp; Chinese.

XX

CC The invention relates to human macroprotein 21.01 (AB989891) and acids encoding it (ABQ7931). The protein has a molecular weight of 1 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the gene and antagonist in therapeutic applications. Macroprotein 21.01 can be used in the treatment of a variety of diseases such as dementia and facial paralysis. Sequences ABQ7936-ABQ7937 represent human macroprotein 21.01 probes used in an exemplification of the invention.

CC Sequence 41 BP; 12 A; 8 C; 10 G; 11 T; 0 U; 0 Other

XX

SQ

[illegible]

DE Short tandem repeat sequence primer.

STR; polymorphism detection; DNA profiling; typing; identification;

09:38:24 2004

us-10-090-326-6.max.rng

forensic; medical; ss.

L.

92WO-US000736.

91US-00647655.

JOR COLLEGE MEDICINE.

Edwards AO;

00053/36.

g assay - by detecting polymorphisms in a short tandem repeat and characterising DNA.

ye 49; 75pp; English.

is that of a primer used in a DNA profiling assay for polymorphisms in a short tandem repeat (STR). The assay is internal or external standards, provides higher sensitivity, shorter analysis time, lowers expense, and enables precise identification of alleles. The STRs are amplified with great fidelity and patterns are easily interpreted. The method can be used for STR sequences which show polymorphisms in the number of repeats action or identification of medical and forensic samples, sample origin and tissue origin. See also AAQ27841-Q27864. 25-MAR-2003 to correct PN field.)

BP; 5 A; 6 C; 6 G; 7 T; 0 U; 0 Other;

61.8%; Score 13.6; DB 2; Length 24;

ilarity 80.0%; Pred.No. 4.6e+03;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

TAATCAGCTCTCTCGG 21

||||| ||||| |||||

TAATCGCTCTCTCGAG 23

andard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 61700.

be; expressed sequence tag; microarray; gene expression; ation; biallelic marker; polymorphism; human; as comparison.

s.

0-A1.

; 2002US-00098263.

; 2001US-0276759P.

YMETRIX INC.

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization Southern, Northern or dot-blot hybridization to identify or detect sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 61700; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA array. The array is used in analysis of genetic variation or in hybridisation of tag-labeled compounds. The nucleic acid probes are specifically designed for at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises gene expression levels, identifying biallelic markers or polymorphisms or family members of a gene and a cross-species comparison. Each nucleic acid further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules, primer extensions or in screening cDNA or genomic libraries or for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is on a nucleic acid probe incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Sequence 25 BP; 5 A; 9 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 61.8%; Score 13.6; DB 8; Length 25;

Best Local Similarity 80.0%; Pred. No. 4.6e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 2 GACAATCACAGTCTCTCGG 21

||||| ||||| |||||

Db 4 GACAACCTCAGTGTCTCGG 23

RESULT 16

ACK26100/c

ID ACK26100 standard; DNA; 25 BP.

XX ACK26100;

XX AC

XX 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 126081.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX



us-10-090-326-6.max.rng

PT New probe array useful e.g. for monitoring gene expression level  
PT analyzing genetic variations, or for hybridizing tag-labeled com  
PT comprises multiple nucleic acid probes.

Claim 1: SEO ID NO 2524; 9pp; English.

The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of the nucleotide sequences defined in the patent, or their perfect or sense mismatch, antisense match or antisense mismatch oligonucleotide. The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression variations, and in hybridising tag-labelled compounds. The probes are useful for identifying family members of a gene. The probes are useful for identifying family members, in screening cDNA or genomic DNA (or derived subclones) for additional clones containing segments that have been previously isolated and sequenced, in Southern, Northern or dot-blot hybridisation of genomic DNA to identify or detect a sequence of any gene or detect specific mutations in any gene, or mapping the 5' termini of mRNA molecules by primer extensions. The nucleic acid sequences of the invention are also useful as PCR sequences. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical applications. ACH50865-ACH5260 represent the target sequences of the invention. The sequence data for this patent was obtained in electronic form directly from the USPTO web site at [seqdata.uspto.gov/patseqDB01/](http://seqdata.uspto.gov/patseqDB01/)

Sequence 25 BP: 5 A: 4 C: 9 G: 7 T: 0 U: 0 Other:

```
Query Match      61.8%; Score 13.6; DB 8; Length 25;
Best Local Similarity 80.0%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0;
```

Qy 3 ACAATCACAGTCTCTGCGGA 22  
|||||  
nb 23 ACATTCAACCGTCTCACCGGA 4

CH53387/C      CH53387 standard: DNA: 25 BP.

16-OCT-2003 (first entry)

DNA target sequence #2523 useful in array for genetic analyses.

Gene expression analysis; array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR; primer; ss.

Unidentified.

US2003082596-A1.

08-AUG-2002: 2002US-00215112.

08-AUG-2001: 2001US-0311040P.

(MITT/) MITTMANN M.

WPT: 2003-576608/54.

ray useful e.g. for monitoring gene expression levels, for  
nucleic variations, or for hybridizing tag-labeled compounds,  
multiple nucleic acid probes.

ID NO 2523; 9pp; English.

invention relates to nucleic acid sequences that are  
y to particular genes, and can be used as probes for a  
analyses such as gene expression analysis. Each probe  
or more consecutive nucleotides from at least one of 14936  
sequences defined in the patent, or their perfect sense match,  
ch, antisense match or antisense mismatch oligonucleotides.  
may be used in an array comprising at least 10 distinct  
probes. The array is useful in monitoring gene expression  
/bridisation to a DNA library, in analysing genetic  
and in hybridising tag-labeled compounds. The probes are  
identifying family members of a gene. The probes are also  
in situ hybridisations, in screening cDNA or genomic libraries  
subclones) for additional clones containing segments of DNA  
previously isolated and sequenced, in Southern, northern,  
hybridisation of genomic DNA to identify or detect the  
any gene or detect specific mutations in any gene, and in  
5' termini of mRNA molecules by primer extensions. The  
sequences of the invention are also useful as PCR primers.  
n provides a large collection of nucleic acid sequences  
y to particular genes with a wide range of analytical uses.  
#65260 represent the target sequences of the invention. Note:  
# data for this patent was obtained in electronic format  
on the USPTO web site at [seqdata.uspto.gov/psipdIDEntry.html](http://seqdata.uspto.gov/psipdIDEntry.html)

BP; 5 A; 4 C; 9 G; 7 T; 0 U; 0 Other;

61.8%; Score 13.6; DB 8; Length 25;

ilarity 80.0%; Pred. No. 4.6e+03;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCACAGTCTCTGCGGA 22

||||| |||||

ATTCACCGTCTCACCGGA 4

andard; DNA; 33 BP.

(first entry)

ription aporepressor CTCF 10.23 PCR primer SEQ ID NO 6.

scription aporepressor; CCCTC-conjugated factor; CTCF;

/; tumour; development; PCR; primer; ss.

s.

; 2000CN-00116361.

; 2000CN-00116361.

E GENE DEV CO LTD SHANGHAI.

Y;

17567/28.

tide-human transcription arrestin CCCTC-conjugated factor  
and polynucleotide for encoding such polypeptide.

PS Example 4; Page 19 (Disclosure); 34pp; Chinese.

XX The invention relates to human transcription aporepressor CCCTC-  
CC conjugated factor (CTCF) 10.23, the polynucleotide encoding this  
CC polypeptide and DNA recombinant processes to produce the polypep  
CC present invention also discloses the application of the polynuc  
CC for gene therapy. The present invention discloses the antagonis  
CC resisting the polypeptide and its treatment effect. The present  
CC also discloses the method of applying the polypeptide in treati  
CC diseases, such as common tumours, development disturbance disea  
CC present sequence is that of a PCR primer, useful in examples of  
CC invention

SQ Sequence 33 BP; 11 A; 8 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 61.8%; Score 13.6; DB 6; Length 33;

Best Local Similarity 80.0%; Pred. No. 4.8e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACAATCACAGTCTCTGCGGA 22

||||| |||||

Db 13 ACAGTCACATCTCTATGAGGA 32

RESULT 20

AAV40070

ID AAV40070 standard; DNA; 37 BP.

XX

AC AAV40070;

XX

DT 09-NOV-1998 (first entry)

XX

DE PCR primer A3 from WO9829453 Example 2.

XX

KW Drug; cell membrane-directed drug; phospholipid; lipid bilayer;

KW cell cortex; blood coagulation; inflammation; immunological dis

KW PCR primer; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9829453-A1.

XX

PD 09-JUL-1998.

XX

PF 05-JAN-1998; 98WO-JP000002.

XX

PR 27-DEC-1996; 96JP-00359053.

XX

PA (MOCH ) MOCHIDA PHARM CO LTD.

XX

PI Kuriyama S, Hasegawa T;

XX

XX WPI; 1998-388051/33.

XX

PT Drugs containing peptide(s) with specific affinity to phospholi  
PT such as phosphatidyl serine, for treatment of blood coagulation  
PT inflammatory and immunological disorders.

PS Example 2; Fig 2; 117pp; Japanese.

XX

CC The present invention describes drug compositions which contain  
CC active component a peptide which has specific affinity to parti  
CC phospholipids (such as phosphatidyl ethanolamine or phosphatid  
CC especially to phospholipids which constitute a lipid bilayer of  
CC cortex and of which the concentration in the bilayer increases  
CC which are abnormal (e.g. through injury, denaturation or activa  
CC particular, the peptide contains a sequence having phospholipid  
CC and a structure of formula (I): (A1)a-(A2)b-(A3)c, where (A1) i  
CC two specific sequences (see AAW69516 and AAW69519), (A2) and (A  
CC TRYLRHPSQSWHQALR, LRYLRHPSQSWHQALR (see AAW69517) or MEVLGC  
CC (see AAW69518); a = 0-5; b = 1-5, and c = 0-5. Preferred are th  
CC A1-A2-A3, A2-A3, A2-A2-A3, A2-A2-A2-A3 or A2-A2 (especially A2-

A2-A2). The sequence is linked to a peptide such as a blood cially thrombo-modulin, urina-statin or membrane cofactor drugs are used for the treatment and prevention of diseases ood coagulation, inflammatory and immunological disorders. sequence represents a PCR primer used in an example from the ntion

BP; 6 A; 12 C; 10 G; 9 T; 0 U; 0 Other;

61.8%; Score 13.6; DB 2; Length 37;

larity 80.0%; Pred. No. 4.9e+03; Length 37;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

AATCACAGTCTCTGCGG 21

|||||

CCTCAGAGTCTCTGCGG 28

ndard; DNA; 48 BP.

(revised)  
(revised)  
(first entry)

s gingivalis protein PCR primer #21.

s gingivalis; PG; periodontal disease; gingivitis; vaccine;  
CR primer; ss.

s gingivalis.

98WO-AU001023.

97AU-00000839.

97AU-00001182.

98AU-00001546.

98AU-00002264.

98AU-00002911.

98AU-00003128.

98AU-00003338.

98AU-00003654.

98AU-00004917.

98AU-00004963.

98AU-00005028.

LTD.

rr IG, Patterson MA, Agius CT, Rothel LJ, Margetts MB;  
Webb EA;

5613/32.

orphorymonas gingivalis peptides for preventing gingivitis.

Page 48; 588pp; English.

AA91801 encode two hundred and sixty six antigenic s gingivalis (PG) polypeptide sequences given in AA91801 to X91802 to AA91899 represent PCR primers used in the the PG polypeptides. The PG polypeptides have antibacterial h a vaccine mechanism of action. The PG polypeptides can be ines especially against Porphyromonas gingivalis. Probes can etect Porphyromonas gingivalis in standard hybridisation horymonas gingivalis is involved in periodontal disease

CC especially gingivitis. (Updated on 20-MAR-2003 to correct PR file  
CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 48 BP; 16 A; 12 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 61.8%; Score 13.6; DB 2; Length 48;

Best Local Similarity 80.0%; Pred. No. 5.2e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 2 GACAATCACAGTCTCTGCGG 21

|||||

Db 28 GACAATCACAGTCTCTGCGG 47

RESULT 22

ABX15582

ID ABX15582 standard; DNA; 50 BP.

XX AC ABX15582;

XX 27-MAR-2003 (first entry)

XX MHV expression plasmid junction region #1.

XX MHV; ds; virucide; antibacterial; antiparasitic; VLP;

XX virus-like particle; coronavirus; attenuated virus; structural f

XX nucleocapsid protein; membrane protein; envelope protein; spike

XX immunogen; vaccine; FIPV.

XX Mouse hepatitis virus strain A59.

XX WO200292827-A2.

XX 21-NOV-2002.

XX 17-MAY-2002; 2002WO-NL000318.

XX 17-MAY-2001; 2001EP-00201861.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX (TEWE-) STICHTING TECH WETENSCHAPPEN.

XX Rottier PJM, De Haan CAM, Haijema BJ, Bosch BJ;

XX WPI; 2003-120691/11.

XX Novel isolated or recombinant virus-like particle derived from

XX coronavirus for therapeutic and diagnostic purposes, and as immu

XX vaccine, has functionally deleted fragments and is capable of

XX replication.

XX Disclosure; Fig 1A; 138pp; English.

XX The invention relates to isolated or recombinant virus-like part

XX (VLP) capable of replication, derived from coronavirus (e.g. mou

XX hepatitis virus, MHV), having functionally deleted genomes. The

XX functional fragment from nucleic acid encoding viral gene produc

XX than polymerase or structural protein (SP) like nucleocapsid (N)

XX membrane (M), envelope (E) or spike (S) protein, is deleted, or

XX SP do not occur in the order 5'-S-E-M-N-3'. Also included are a

XX composition comprising the VLP, and a carrier for therapeutic an

XX diagnostic use, as an immunogen or vaccine and inhibiting or blo

XX infection with a coronavirus or corona-VLP, by treating an organ

XX a heptad repeat peptide or its functional fragment. The VLP comp

XX is useful for therapeutic and diagnostic purposes, and as an imm

XX vaccine. The VLP is also useful as gene delivery vehicle, and fo

XX eliciting immune response against proteins e.g. viral, bacterial

XX parasitic, and cellular origins. Attenuated MHV VLPs were constr

XX with the ectodomain of the S protein replaced by the correspondi

XX sequence from FIPV (feline infectious peritonitis virus) allowin

XX replication in feline cells. The present sequence is a plasmid j

XX region for the construct

XX



AAATCAGAGTCTCTCGGA 22  
|||||  
AAATCAGAGTCTCTCGGA 7

andard; DNA; 60 BP.

(first entry)

ed transcript detection oligonucleotide SEQ ID NO:10366.

e; rat; splice transcript; detection; RNA transcript;  
ant; transcriptome; oligonucleotide library; ss.

S.

-A2.

; 2001WO-IB001903.

; 2000US-0221607P.

; 2001US-0287724P.

PUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

57383/30.

cleotide libraries comprising oligonucleotides which  
hybridize to mRNAs transcribed from a transcription unit of a  
ful for detecting tissue-, pathology-, and developmental-  
nes.

SEQ ID NO 10366; 47pp; English.

invention describes oligonucleotide libraries for detecting  
NAs that populate a (sub-)transcriptome, where the (sub-  
one comprises messenger RNAs transcribed from multiple  
on units that populate a genome. The library comprises several  
tides, each capable of hybridizing selectively to a set of  
NAs transcribed from a given transcription unit of the genome,  
es one or more messenger RNA splice variants. The  
tide libraries are useful for detecting mRNAs from a  
sample, in expression profiling studies, in qualitatively or  
sily characterizing the corresponding transcriptome, and in  
NA transcripts and splice variants of human or animal  
nes. The libraries may also be used as specialised mini-  
o detect transcripts of a sub-transcriptome under a particular  
or pathological state, and so allowing the detection of tissue  
logy-specific genes such as those genes only expressed in  
ssue under a specific pathological condition; to detect  
al specific genes; and to detect RNA transcripts and splice  
a transcriptome of a patient suffering from a particular  
3N27253 to ABN59589 represent oligonucleotide sequen-  
s and mice, which are used in the exemplification of the  
ntion. N.B. The sequence data for this patent did not form  
printed specification, but was obtained in electronic format  
m WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 20 A; 11 C; 17 G; 12 T; 0 U; 0 Other;

61.8%; Score 13.6; DB 6; Length 60;  
ilarity 80.0%; Pred. No. 5.4e+03;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

AAATCAGAGTCTCTCGG 21

Db 56 GACAATCAGTCTCTATACAG 37  
|||||

RESULT 26

ABN41535/c

ID ABN41535 standard; DNA; 60 BP.

XX AC ABN41535;

XX DT 15-JUL-2002 (first entry)

XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:14

XX KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
XX KW splice variant; transcriptome; oligonucleotide library; ss.

XX OS Homo sapiens.

XX PN WO200210449-A2.

XX PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-IB001903.

XX PR 28-JUL-2000; 2000US-0221607P.

XX PR 02-MAY-2001; 2001US-0287724P.

XX PA (COMP-) COMPUEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX DR WPI; 2002-257383/30.

XX PT New oligonucleotide libraries comprising oligonucleotides which  
selectively hybridize to mRNAs transcribed from a transcription  
genome, useful for detecting tissue-, pathology-, and developme  
specific genes.

XX PS Example 1; SEQ ID NO 14283; 47pp; English.

XX CC The present invention describes oligonucleotide libraries for d  
messenger RNAs that populate a (sub-)transcriptome, where the (s  
)transcriptome comprises messenger RNAs transcribed from multip  
transcription units that populate a genome. The library compris  
oligonucleotides, each capable of hybridizing selectively to a  
messenger RNAs transcribed from a given transcription unit of t  
which encodes one or more messenger RNA splice variants. The  
oligonucleotide libraries are useful for detecting mRNAs from a  
biological sample, in expression profiling studies, in qualit  
detecting RNA transcripts and splice variants of human or anima  
transcriptomes. The libraries may also be used as specialised m  
libraries to detect transcripts of a sub-transcriptome under a  
biological or pathological state, and so allowing the detection  
- and pathology-specific genes such as those genes only express  
specific tissue under a specific pathological condition; to det  
developmental specific genes; and to detect RNA transcripts and  
variants of a transcriptome of a patient suffering from a parti  
disorder. ABN27253 to ABN59589 represent oligonucleotide sequen  
rats, humans and mice, which are used in the exemplification of  
present invention. N.B. The sequence data for this patent did n  
part of the printed specification, but was obtained in electron  
directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 60 BP; 15 A; 14 C; 12 G; 19 T; 0 U; 0 Other;

Query Match 61.8%;

Best Local Similarity 80.0%; Pred. No. 5.4e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACAATCAGAGTCTCTCGGA 22  
|||||

CATTGACAGTCTCTGGCGA 41

tandard; DNA; 36 BP.

4 (first entry)

in Fv polypeptide associated VH PCR primer #22.

in Fv polypeptide; human albumin; immune diagnostic agent; VH;  
r; ss.

ed.

78-A.

2.

1; 2001JP-00260411.

3; 2000JP-00259436.

FO LTD.

124058/40.

ain Fv polypeptide having human albumin combining activity.

Fig 2; 1lpp; Japanese.

: invention relates to a single chain Fv polypeptide having  
activity specific to human albumin. Also disclosed is the  
:ide sequence encoding the single chain Fv polypeptide, an  
vector containing the polynucleotide, a host cell transformed  
re expression vector, and preparation of a single chain Fv  
; in which the above host cell is cultured and the above single  
lypeptide is separated from the culture. The polypeptide can  
: the preparation of immune diagnostic agents. The present  
presents a PCR primer used in the examples of the present

BP; 9 A; 10 C; 13 G; 4 T; 0 U; 0 Other;

ilarity 60.9%; Score 13.4; DB 9; Length 36;

Conservative 93.3%; Pred. No. 6.2e+03;

0; Mismatches 1; Indels 0; Gaps 0;

ACAGTCTCTGCGG 21

ACTGCTCTGCGG 15

andard; DNA; 50 BP.

(first entry)

ligonucleotide #3230.

essive; immunostimulatory; antiinflammatory; cytostatic;  
tive; antimicrobial; gene therapy; vaccine; amylose; cancer;  
tein; angiotensin; apoptosis related protein; cadherin;  
ymerase; oncogene; histone; kinase; colony stimulating factor;  
related protein; cytochrome; kinesin; cytokine; interferon;  
; G-protein coupled receptor; thioesterase; inflammation;  
ial disease; autoimmune disease; infection;

KW nervous system disease; ss.  
XX Homo sapiens.  
XX WO200147944-A2.  
XX 05-JUL-2001.  
XX 28-DEC-2000; 2000WO-US035498.  
XX 28-DEC-1999; 99US-0173419P.  
PR 27-DEC-2000; 2000US-00173419.  
XX (CURA-) CURAGEN CORP.  
XX Shimkets RA, Leach M;  
XX WPI; 2001-465210/50.  
XX

Polymorphic nucleic acids encoding e.g. amylases, cyclins, pol-  
PT oncogenes and histones, useful for diagnosing and treating, e.  
PT autoimmune diseases and infections.

Claim 1; Page 2312; 4143pp; English.

XX The present invention relates to oligonucleotides encoding pol-  
CC variants of proteins related to amylases, amyloid proteins, an-  
CC apoptosis related proteins, cadherin, cyclin, polymerase, onco-  
CC histones, kinases, colony stimulating factors, complement rela-  
CC proteins, cytochromes, kinesins, cytokines, interferons, inter-  
CC protein coupled receptors and thioesterases. The present sequ-  
CC such oligonucleotide. The oligonucleotides and the peptides en-  
CC them may be used in the prevention, diagnosis and treatment of  
CC associated with inappropriate expression of the proteins listed  
CC Disorders that may be prevented, diagnosed and/or treated incl-  
CC multifactorial diseases with a genetic component, such as auto-  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabet-  
CC systemic lupus erythematous and Grave's disease), inflammati-  
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
CC leukaemia), diseases of the nervous system and an infection of  
CC organisms

XX Sequence 50 BP; 7 A; 19 C; 10 G; 14 T; 0 U; 0 Other;

Query Match 60.9%; Score 13.4; DB 4; Length 50;

Best Local Similarity 93.3%; Pred. No. 6.5e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 4 CAATCACAGTCTCTG 18

DB 19 CACTCACAGTCTCTG 33

RESULT 29

ABN36160/c

ID ABN36160 standard; DNA; 60 BP.

XX ABN36160;

XX 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:89

XX Human; mouse; rat; splice transcript; detection; RNA transcript

XX splice variant; transcriprome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB001903.

09:38:24 2004

us-10-090-326-6.max.rng

2000US-0221607P.  
2001US-0287724P.

UGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

7383/30.

leotide libraries comprising oligonucleotides which hybridize to mRNAs transcribed from a transcription unit of a gene for detecting tissue-, pathology-, and developmental-  
ies.

SEQ ID NO 9908; 47pp; English.

invention describes oligonucleotide libraries for detecting  
as that populate a (sub-)transcriptome, where the (sub-  
me comprises messenger RNAs transcribed from multiple  
n units that populate a genome. The library comprises several  
:ides, each capable of hybridising selectively to a set of  
as transcribed from a given transcription unit of the genome,  
as one or more messenger RNA splice variants. The  
ide libraries are useful for detecting mRNAs from a  
sample, in expression profiling studies, in qualitatively or  
ly characterising the corresponding transcriptome, and in  
NA transcripts and splice variants of human or animal  
nes. The libraries may also be used as specialised mini  
o detect transcripts of a sub-transcriptome under a particular  
or pathological state, and so allowing the detection of tissue  
logy-specific genes such as those genes only expressed in  
ssue under a specific pathological condition; to detect  
al specific genes; and to detect RNA transcripts and splice  
a transcriptome of a patient suffering from a particular  
BN27253 to ABN59589 represent oligonucleotide sequences from  
s and mice, which are used in the exemplification of the  
ention. N.B. The sequence data for this patent did not form  
printed specification, but was obtained in electronic format  
om WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 13 A; 12 C; 14 G; 21 T; 0 U; 0 Other;

ilarity 60.9%; Score 13.4; DB 6; Length 60;

Conservative 93.3%; Pred No. 6.8e-03;

Mismatches 0; Indels 1; Gaps 0;

CAGTCTCTGCGGA 22  
|||||  
CAGTCTCTGAGGA 2

andard; DNA; 18 BP.

3 (first entry)

is casselliflavus vanC-2 gene PCR primer vanC2-2.

indicator group; PCR; primer; ss.

us casselliflavus.

43-A2.

3.

2; 2002WO-NO000490.

1; 2001NO-00006251.

PR 19-DEC-2001; 2001US-0340872P.

XX (DAUR/) ANGLES D'AURIAC M B.

XX Angles D'auriac MB, Sirevag R;

XX WPI; 2003-523534/49.

XX New oligonucleotide primers, useful for detecting bacterial indi-  
PT groups and/or virulence factors and/or for determining the subt;  
PT virulence factors.

XX Disclosure; Page 19; 48pp; English.

XX The present sequence is that of PCR primer vanC2-2 for the vanC  
CC Enterococcus casselliflavus. The primer was used in a previous m  
CC protocol for detection of Enterococcus. The present invention p  
CC methods for the detection and/or subtyping of 3 bacterial indic  
CC groups (Escherichia coli, Enterococcus faecalis and Enterococu  
CC used in food microbiology and/or virulence factors associated w  
CC aetiology of diarrhoea, using simplex or multiplex PCR

XX Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 8; Length 18;

Best Local Similarity 83.3%; Pred No. 6.9e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 3 ACAATCACAGTCTCTGCG 20

DB 18 AATATCACCTGCTGCG 1

RESULT 31

AAC66297/c

ID AAC66297 standard; DNA; 22 BP.

XX AAC66297;

XX 20-FEB-2001 (first entry)

XX Primer EVENR2 used in EIAV DNA isolation.

XX Equine infectious anemia virus; EIAV; donkey leukocyte strain;

XX gene therapy; human immunodeficiency virus; HIV; primer; ss.

XX Synthetic.

XX WO2000063387-A1.

XX 26-OCT-2000.

XX 21-APR-2000; 2000WO-CN000096.

XX 21-APR-1999; 99CN-00105852.

XX (NAAI-) NAT CENT AIDS PREVENTION & CONTROL.

XX (HARB-) HARBIN VETERINARY RES INST CHINESE ACAD.

XX Shao Y, Shen R, Chen G, Yu K, Pan P, Jia B, Feng Y, Xue

XX Xiang W, Fan X, Lue X, Zhao L;

XX WPI; 2000-672738/65.

XX Full-length DNA sequence of provirus genomes, sequences of var-  
PT functional genes and protein of donkey leukocyte strain of equ  
PT infectious anemia virus, used for preparing vaccines and study

XX Example 1; Page 7; 26pp; Chinese.

XX This invention relates to a full length provirus genomic DNA s  
CC AAC66281 of equine infectious anemia virus (EIAV) from the don  
CC leukocyte strain. Included in the invention are the gag, pol,

2 gene sequences AAC66314 - AAC66319 and their encoded proteins  
 AAC65759. The invention also relates to PCR primers AAC66282 -  
 AAC66289 - AAC66313 are also used in the course of the  
 for the isolation and characterisation of the DNA sequences  
 in the invention. The genes and proteins can be used for  
 gene mutation and deletion vaccines, DNA vaccines and  
 in producing an equine infectious anemia virus gene  
 system for gene therapy. The proteins and polynucleotides may  
 be used in the study of HIV

2 BP; 4 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

60.0%; Score 13.2; DB 3; Length 22;  
 Similarity 83.3%; Pred. No. 7.1e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3ACAAATCAGTCTCTG 18  
 ||||| ||||| |||||  
 3ACAACTCAGTACTG 1

standard; DNA; 22 BP.

(revised)  
 (first entry)

ie PCR primer SKB-8.

AT; Atropis; ATR; 5-methylcytosine glycosylase; ss;  
 lation; transgenic plant; transcription modulation;  
 ime; endosperm development; MEDEA; PCR primer.

d.

-Al.

; 2001WO-US013059.

; 2000US-00553690.

V CALIFORNIA.

Choi Y, Hannon M, Okamuro JK, Tatarinova TV;

55307/07.

leotide that control plant development comprising a sequence  
 specific homology to DEMETER domains A, B or C.

Page 23; 109pp; English.

on relates to an isolated polynucleotide sequence or their  
 encoding a polypeptide having a sequence at least 40%  
 o DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B  
 ir combinations. Also included are an expression cassette  
 the polynucleotide or comprising a heterologous polynucleotide  
 control of a promoter at least 70% identical to DMT 5' flanking  
 MT 3' flanking sequence or an 5' untranslated region of DMT, a  
 comprising an exogenous polynucleotide encoding a DMT-like  
 a transgenic plant comprising a polynucleotide encoding a DMT  
 in. The expression cassette is useful for modulating  
 on. The method comprises introducing the cassette into a host  
 ably Agrobacterium by sexual cross, and selecting a host cell  
 ted transfection, where the protein is capable of exhibiting  
 e of the following biological activities, which include  
 pression of the protein in a plant results in a delay in

CC flowering time, introduction of the protein into a cell result;  
 CC modulation of methylation of chromosomal DNA in the cell, redu  
 CC expression of the protein in a plant results in enhanced endos  
 CC development and expressing of the protein in an Arabidopsis le  
 CC in expression of the MEDEA gene. The polynucleotide is useful  
 CC in detecting a nucleic acid in a sample. DEMETER is related to 5-  
 CC methylcytosine glycosylases and regulates transcription of tar  
 CC by demethylation. The present sequence represents a PCR primer  
 CC isolate the nucleic acids encoding the DMT-like proteins of th  
 CC invention. (Updated on 07-AUG-2003 to correct OS field.)

XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 6; Length 22;  
 Best Local Similarity 83.3%; Pred. No. 7.1e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 GACATCAGTCTCTGC 19  
 ||||| ||||| |||||  
 Db 18 GACAATAACCGTCTCTCC 1

RESULT 33

ABL59611/c

ID ABL59611 standard; DNA; 22 BP.

XX

AC ABL59611;

XX

DT 17-JUL-2002 (first entry)

XX

DE Human glutathione S-transferase GSTM2 gene PCR primer SEQ ID NC

XX

KW Human; glutathione S-transferase; GST; enzyme; differentiation;

XX

OS PCR primer; ss.

XX

OS Homo sapiens.

XX

PN JP2002058483-A.

XX

PD 26-FEB-2002.

XX

PF 14-AUG-2000; 2000JP-00245951.

XX

PR 14-AUG-2000; 2000JP-00245951.

XX

PA (SAKA ) OTSUKA SEIYAKU KOGYO KK.

XX

DR WPI; 2002-398775/43.

XX

PT Differentiation and quantitative determination of glutathione S

PT transferase comprises the use of oligonucleotide probes.

XX

PS Claim 8; Page 11; 12pp; Japanese.

XX

CC The present invention describes a method for the differentiatio

CC quantitative determination of glutathione S-transferase using

CC oligonucleotide probes (ABL59585 to ABB59601). The method allow

CC and sensitive determination of glutathione S-transferase for

CC investigation of interaction and incompatibility of proposed dr

CC present sequence represents a PCR primer for a human glutathion

CC transferase gene, which is used in an method for the differenti

CC quantitative determination of glutathione S-transferase

XX

SQ Sequence 22 BP; 5 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

XX

Query Match 60.0%; Score 13.2; DB 6; Length 22;

Best Local Similarity 83.3%; Pred. No. 7.1e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 5 AATCAGTCTCTGCGGA 22

Db 22 ACTCAGTCTCTGCGGA 5



09:38:24 2004

us-10-090-326-6.max.rng

ACK23331/c  
ID ACK23331 standard; DNA; 25 BP.  
XX  
AC ACK23331;  
XX  
DT 14-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 123312.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Mittmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization; Southern, Northern or dot-blot hybridization to identify or detect sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 123312; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, perfect match, antisense match or antisense mismatch. The array is used in monitoring gene expression levels by hybridisation to a DNA library. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises gene expression levels, identifying biallelic markers or polymorphisms of a gene and a cross-species comparison. Each nucleic acid further comprises a tag sequence. The array of nucleic acids is useful in situ hybridisation, in Southern, Northern blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules or in screening cDNA or genomic libraries or for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one nucleic acid probe incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html  
SQ Sequence 25 BP; 5 A; 4 C; 8 G; 8 T; 0 U; 0 Other;  
  
Query Match 60.0%; Score 13.2; DB 8; Length 25;  
Best Local Similarity 83.3%; Pred. No. 7.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
  
QY 3 ACAATCAGTCTCTCGG 20  
DB 18 ACAAACTCACTCTCTCGG 1  
  
RESULT 36  
ACK13931/c  
ID ACK13931 standard; DNA; 25 BP.  
  
BP; 9 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
  
Similarity 60.0%; Score 13.2; DB 8; Length 25;  
Conservative 83.3%; Pred. No. 7.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
TACAGTCTCTCTCGG 22  
TAAATGCTCTCTCGG 23

```

XX      14-OCT-2003 (first entry)
DT      Human microarray DNA oligonucleotide SEQ ID NO 115691.
XX
XX      EST, ss; probe; expressed sequence tag; microarray; gene expres
DE      iation; biallelic marker; polymorphism; human;
XX      es comparison.
KW
KW      Homo sapiens.
XX
OS      US2003104410-A1.
XX
FN      05-JUN-2003.
XX
PD      15-MAR-2002; 2002US-00098263.
XX
PF      16-MAR-2001; 2001US-0276759P.
XX
PR      (AFFY-) AFFYMETRIX INC.
XX
PA      Mittmann MP;
XX
PI      WPI; 2003-567953/53.
XX
DR      New array of nucleic acid probes, useful for in situ hybridizat
PT      ion, Northern or dot-blot hybridization to identify or dete
PT      ct sequence or specific mutations of any gene.
XX
XX      Claim 1; SEQ ID NO 115691; 9pp; English.
XX
XX      The invention discloses a microarray comprising a plurality of
CC      acid probes including one of 2,018,500 fully defined sequences,
CC      each, perfect mismatch, antisense match or antisense mismatch.
CC      Also disclosed is a method of gene expression analysis. The ar
CC      ray is a method of gene expression analysis. The array is used
CC      in monitoring gene expression levels by hybridisation to a DNA
CC      library. The nucleic acid probes are specifically designed for
CC      analysis of genetic variation or in hybridisation of tag-label
CC      ed probes and detecting the hybridisation. The nucleic acid
CC      probes are attached to a solid support. The analysis comprises
CC      gene expression levels, identifying biallelic markers or polym
CC      or family members of a gene and a cross-species comparison. Ea
CC      ch nucleic acid further comprises a tag sequence. The array of n
CC      ucleic acids is useful in situ hybridisation, in Southern, Northe
CC      rn blot hybridisation to identify or detect the sequence or spec
CC      ific mutations of any gene, in mapping the 5' termini of mRNA molec
CC      ules, primer extensions or in screening cDNA or genomic libraries or
CC      for additional subclones containing segments of DNA that have b
CC      een isolated and previously sequenced. The sequence presented is o
CC      ne of the nucleic acid probes incorporated in the microarray. Note: The
CC      data for this patent can also be obtained in electronic format
CC      from USPTO at seqdata.uspto.gov/sequence.html
XX
XX      Sequence 25 BP; 4 A; 7 C; 3 G; 11 T; 0 U; 0 Other;
SQ

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```

XX      array DNA oligonucleotide SEQ ID NO 113912.
DT      (first entry)
XX
XX      obe; expressed sequence tag; microarray; gene expression;
DE      iation; biallelic marker; polymorphism; human;
XX      es comparison.
KW
KW      Homo sapiens.
XX
OS      US.
XX
FN      0-A1.
XX
PD      .
XX
PF      ; 2002US-00098263.
XX
PR      ; 2001US-0276759P.
XX
PA      YMETRIX INC.
XX
PI      ;
XX
DR      .67953/53.
XX
PT      f nucleic acid probes, useful for in situ hybridization, in
PT      Northern or dot-blot hybridization to identify or detect the
XX      specific mutations of any gene.
XX
XX      Q ID NO 113912; 9pp; English.
XX
XX      on discloses a microarray comprising a plurality of nucleic
CC      acids including one of 2,018,500 fully defined sequences, or its
CC      ch, perfect mismatch, antisense match or antisense mismatch.
CC      used is a method of gene expression analysis. The array is used
CC      ing gene expression levels by hybridisation to a DNA library.
CC      of genetic variation or in hybridisation of tag-labelled
CC      The nucleic acid probes are specifically designed for analysis
CC      : one target sequence. The method of analysis comprises
CC      at least one or more nucleic acids to at least two or more
CC      d probes and detecting the hybridisation. The nucleic acid
CC      attached to a solid support. The analysis comprises monitoring
CC      sion levels, identifying biallelic markers or polymorphisms,
CC      members of a gene and a cross-species comparison. Each of the
CC      ds further comprises a tag sequence. The array of nucleic acid
CC      useful in situ hybridisation, in Southern, Northern or dot-
CC      lisation to identify or detect the sequence or specific
CC      if any gene, in mapping the 5' termini of mRNA molecules by
CC      nsions or in screening cDNA or genomic libraries or subclones
CC      nal subclones containing segments of DNA that have been
CC      id previously sequenced. The sequence presented is one of the
CC      d probes incorporated in the microarray. Note: The sequence
CC      his patent can also be obtained in electronic format directly
CC      at seqdata.uspto.gov/sequence.html
XX
XX      ; BP; 5 A; 4 C; 8 G; 8 T; 0 U; 0 Other;
SQ

```

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```

XX      Query Match      60.0%; Score 13.2; DB 8; Length 25;
DT      Best Local Similarity 83.3%; Pred. No. 7.3e+03;
XX      Matches 15; Conservative 0; Mismatches 3; Indels 0;
XX
XX      QY      4 CAATCAGTCTCTGCG 21
XX      |||||
XX      DB      2 CAATCATATCTCTGCG 19
XX
XX      RESULT 38
XX      AAT08014/c
XX      ID AAT08014 standard; DNA; 35 BP.
XX
XX      AC AAT08014;
XX
XX      XX 24-JUL-1996 (first entry)
DT

```

heavy chain back primer JS160.

chain reaction; PCR; primer; amplify; traa; leader sequence; in; hormone; enzyme; inhibitor; receptor; antigen; antibody; library; specific binding pair; epitope mapping; vaccine; al vaccine; bacterial display; phage display; TA1; SBP; fication; alpha-CKMB; creatine kinase-MB; ss.

95WO-US007541.

94US-00258026.

: INT INC.

thode PR, Stinson JR, Wong HC;

9677/05.

target protein on bacterial cell as fusion protein - with it(s) and peptide leader, used e.g. to select members of ding pairs.

age 42; 74pp; English.

AAT08014 represent amplification primers for the heavy chain lonal antibody alpha-CKMB. Alpha-CKMB is directed against ase-MB. The amplified sequence is used as the DNA encoding a in, for insertion into a chimaeric DNA sequence of the he chimaeric sequence contains a target protein coding when the DNA encoding the traa leader sequence (amplified by AAT08007) and the traa gene product coding sequence sing AAT08006 and AAT08008). The target protein is then a bacterial host cell transformed with a vector containing c sequence. The chimaeric sequence is useful for displaying ins such as hormones, enzymes, inhibitors, receptors, antibodies. It is particularly useful for selecting a target protein from a DNA library, especially members of a ding pair (SBP) or compounds that affect SBP interactions. may also be used for epitope mapping or for use in live cines. The method combines the advantages of bacterial and y and makes possible protein purification without the need ng, panning, etc

BP; 6 A; 10 C; 10 G; 4 T; 0 U; 5 Other;

60.0%; Score 13.2; DB 2; Length 35;

larity 72.2%; Pred. No. 7.7e+03;

Conservative 3; Mismatches 2; Indels 0; Gaps 0;

TCACAGTCTCTGCGG 21

|||||:|||||:

TCACAGTCTCTCYKAG 15

ndard; DNA; 35 BP.

(first entry)

chain back primer JS160.

ntibody; MAb; lipoteichoic acid; gram positive; bacteria; in; phagocytosis; infection; epitope; peptide mimic;

KW MAb 96-110; panning; PCR primer; ss.  
XX Synthetic.  
OS Mus sp.  
XX WO9857994-A2.  
PN  
XX 23-DEC-1998.  
PD  
XX 16-JUN-1998; 98WO-US012402.  
PF  
XX 16-JUN-1997; 97US-0049871P.  
PR  
XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.  
PA  
XX Fischer GW, Schuman RF, Wong H, Stinson JL;  
PI  
XX WPI; 1999-095329/08.  
DR  
XX  
XX New antibodies to lipoteichoic acid of gram positive bacteria -  
PT develop products for the diagnosis, prevention and treatment of  
PT infections caused by gram positive bacteria.  
XX  
XX Example 8; Fig 11; 150pp; English.  
PS  
XX The invention relates to a monoclonal antibody (MAb) to lipoteic  
CC of gram positive bacteria, where the MAb is a chimeric immunogl  
CC comprising at least part of a human immunoglobulin constant reg  
CC least part of a non-human immunoglobulin variable region having  
CC specificity to lipoteichoic acid of gram positive bacteria. The  
CC antibodies bind to whole bacteria and enhance phagocytosis and  
CC the bacteria and enhance protection from lethal infection. The  
CC or peptides (encoded by a DNA of the variable region of anti-lif  
CC acid antibody or characterised by amino acids corresponding to c  
CC more of the complementarity determining regions (CDRs) of the v  
CC region of the antibody) can be used for treating or preventing i  
CC caused by gram positive bacteria. They can also be used for the  
CC of gram positive bacterial infections. Sequences AAX0561-78 re  
CC PCR primers used for cloning the variable region gene fragments  
CC MAb 96-100 antibody of the invention  
XX  
SQ Sequence 35 BP; 6 A; 10 C; 10 G; 4 T; 0 U; 5 Other;  
Query Match 60.0%; Score 13.2; DB 2; Length 35;  
Best Local Similarity 72.2%; Pred. No. 7.7e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0;  
QY 4 CAATCAGTCTCTGCGG 21  
|||:|||||:  
DB 32 CACTCAGTCTCYKAG 15  
RESULT 40  
AAX82036/c  
ID AAX82036 standard; DNA; 35 BP.  
XX  
AC AAX82036;  
XX  
DT 10-SEP-1999 (first entry)  
XX  
DE Mouse heavy chain back primer JS160.  
XX  
KW Humanised; monoclonal antibody; MAb; Shiga toxin; immunoglobulin  
KW Ig constant region; enterohemorrhagic Escherichia coli; EHEC; ur  
KW edema; bloody diarrhoea; hemorrhagic colitis; hemolytic uremic s  
KW thrombocytopenia; EHEC-mediated disease; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
XX WO9932645-A1.  
PN  
XX 01-JUL-1999.  
PD  
XX

98WO-US027267.

97US-0068635P.

98US-00215163.

NISON J L.

S H.

NIEN A D.

MITT C K.

TON-CELSA A.

Wong H, O'Brien AD, Schmitt CK, Melton-Celsa A;

18935/35.

monoclonal antibodies against Shiga toxins, useful for  
against enterohemorrhagic *Escherichia coli* or other Shiga  
toxin-producing bacteria.

J 5A; 75pp; English.

on relates to humanised monoclonal antibodies (MAB) against  
s. The humanised MAB that binds to Shiga toxin comprises a  
variable region, where: (a) the constant region contains  
part of a human immunoglobulin (Ig) constant region; and (b) the  
region contains at least part of a non-human Ig variable region.  
transformed with vectors encoding a humanised MAB against  
type 2 is useful for treating a patient with an infection  
enterohemorrhagic *Escherichia coli* (EHEC) or other Shiga toxin  
producing bacteria. The humanised MAB can also be used to reduce illness  
caused by food-borne outbreaks of bloody diarrhoea (hemorrhagic  
shock) or other Shiga toxin-producing bacteria. EHEC are  
responsible for food-borne outbreaks of bloody diarrhoea (hemorrhagic  
shock) and hemolytic uremic syndrome. In particular, the humanised  
rate edema, thrombocytopenia and uremia associated with EHEC-  
sease. Sequences AAX82030-48 represent PCR primers for  
the variable regions of 11E10 antibody

BP; 6 A; 10 C; 10 G; 4 T; 0 U; 5 Other;

Identity 60.0%; Score 13.2; DB 2; Length 35;

Conservative 3; Mismatches 2; Indels 0; Gaps 0;

ATCACAGTCTCTGCGG 21

|||||:|||||

STCAGGTCTCTGCGG 15

standard; DNA; 47 BP.

(first entry)

related bi-allelic marker SEQ ID NO:1562.

e; bi-allelic marker; high density disequilibrium map;  
; haplotype; phenotype; polymorphic base; genotyping;  
; hybridisation; identification; characterisation; diagnosis;  
eotide polymorphism; SNP; ds.

s.

Location/Qualifiers

replace(24,T)

/\*tag= a

/standard\_name= "single nucleotide polymorphism"

2.

XX 21-APR-1999; 99WO-IB000822.  
XX 21-APR-1998; 98US-0082614P.  
XX 23-NOV-1998; 98US-0109732P.  
XX (GEST ) GENSET.  
XX Cohen D, Blumenfeld M, Chumakov I;  
XX WPI; 2000-013267/01.  
XX Novel bi-allelic markers used to construct a high density disequilibrium  
map of the human genome.  
XX  
XX Claim 1; Page 563; 2745pp; English.  
XX AAZ65654 to AAZ69578 represent human bi-allelic markers from the  
invention, which contain a polymorphic base at position 24 of the  
nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
primers for the bi-allelic markers. The bi-allelic markers of the  
invention have a variety of uses: they can be used for high density mapping  
of a human genome, and in complex association studies and haplotyping  
which are useful in determining the genetic basis for disease susceptibility  
and in the development of the invention can also be useful for  
comparisons and methods of the targets for the development of pharmaceutical  
agents and diagnostic methods, as well as the characterisation of  
differential efficacious responses to and side effects from  
pharmaceutical agents acting on a disease as well as other treatments.  
N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3  
3367, are not actually given a sequence in the Sequence Listing  
present invention  
XX Sequence 47 BP; 14 A; 10 C; 17 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 60.0%; Score 13.2; DB 3; Length 47;  
Best Local Similarity 83.3%; Pred. No. 8.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
Qy 4 CAATCACAGTCTCTGCGG 21  
|||:|||||  
Db 38 CAGTCTCAGTCTCTGCGG 21  
|||:|||||  
RESULT 42  
ABZ00861/c  
ID ABZ00861 standard; DNA; 50 BP.  
XX AC ABZ00861;  
XX AC  
XX 09-JAN-2003 (first entry)  
XX Human leukocyte gene expression profiling probe SEQ ID NO 852.  
XX T7; leukocyte; gene expression profiling; allograft rejection;  
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infectious  
ss.  
XX Homo sapiens.  
XX WO200257414-A2.  
XX 25-JUL-2002.  
XX 22-OCT-2001; 2001WO-US047856.  
XX 20-OCT-2000; 2000US-0241994P.  
XX 08-JUN-2001; 2001US-0296764P.  
XX (BIOC-) BIOTEC INC.  
XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips

09:38:24 2004

us-10-090-326-6.max.rng

ard R, Quertermous T, Johnson F;

6525/68.

or leukocyte expression profiling, diagnosing a disease, or the rate of) progression of a disease, e.g. atherosclerosis, e heart failure, comprises diagnostic oligonucleotides.

e 352; Opp; English.

n relates to a system for detecting gene expression, which e or two isolated DNA molecules that detect expression of a the gene corresponds to any of 8143 oligonucleotides Z08152) each having 50 base pairs (bp). The system is useful e expression profiling. It is particularly useful for e disease, monitoring (rate of) progression of a disease, herapeutic outcome, determining prognosis for a patient, isease complications in an individual or monitoring response in an individual. The diseases include cardiac allograft idney allograft rejection, liver allograft rejection, sis, congestive heart failure, systemic lupus erythematosus, rthritis, osteoarthritis or cytomegalovirus infection

BP; 12 A; 10 C; 9 G; 19 T; 0 U; 0 Other;

60.0%; Score 13.2; DB 6; Length 50;

arity 83.3%; Pred. No. 8.3e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

'CAGAGTCTCTGCGGA 22

|||||

'CATAGTCTCTGGGTA 4

undard; DNA; 51 BP.

(first entry)

oietin coding sequence polymorphic site SEQ ID NO: 104.

e nucleotide polymorphism; SNP; paternity test;

it; aberrant protein expression; ds.

;

-A2.

2001WO-US000322.

2000US-0174962P.

AGEN CORP.

Leach MD;

51871/48.

30214.

nan polymucleotides containing single nucleotide

ns, useful for the treatment and diagnosis of e.g. cancer,

nd diabetes.

ge 137; 475pp; English.

invention relates to human nucleic acids containing single polymorphisms (SNPs). These can be used in forensic and asets, and to aid in the treatment of diseases associated with

CC aberrant protein expression, including cancer, amyloidosis, dial  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vascu  
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arth  
CC meningitis, muscular disorders, dementia, neurological diseases,  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disc  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obes  
CC autoimmunity. The present sequence is a polymorphism-containing  
CC oligonucleotide fragment of the invention

XX

SQ Sequence 51 BP; 13 A; 17 C; 8 G; 13 T; 0 U; 0 Other;

Query Match

60.0%; Score 13.2; DB 4; Length 51;

Best Local Similarity 83.3%; Pred. No. 8.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGACATATCACAGTCTCTG 18

|||||

Db 27 AGACATATCCATTTGCTG 44

RESULT 44

AAH89322

ID AAH89322 standard; DNA; 51 BP.

XX

AC AAH89322;

XX

DT 01-OCT-2001 (first entry)

XX

DE Human angiotensin coding sequence polymorphic site SEQ ID NO: 1

XX

XW Human; single nucleotide polymorphism; SNP; paternity test;

XW forensic test; aberrant protein expression; ds.

XX

OS Homo sapiens.

XX

FN WO200151670-A2.

XX

PD 19-JUL-2001.

XX

PF 05-JAN-2001; 2001WO-US000322.

XX

PR 07-JAN-2000; 2000US-0174962P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach MD;

XX

DR WPI: 2001-451871/48.

DR

DR P-PSDB; AM00213.

XX

Isolated human polymucleotides containing single nucleotide

polymorphisms, useful for the treatment and diagnosis of e.g. c

infection and diabetes.

XX

PS Claim 1; Page 137; 475pp; English.

XX

The present invention relates to human nucleic acids containing

nucleotide polymorphisms (SNPs). These can be used in forensic

paternity tests, and to aid in the treatment of diseases associ

aberrant protein expression, including cancer, amyloidosis, dial

Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vascu

glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arth

meningitis, muscular disorders, dementia, neurological diseases,

sclerosis, male infertility, hypercalcaemia, blood pressure dis

osteoporosis, pathogenic infections, hypercholesterolaemia, obes

autoimmunity. The present sequence is a polymorphism-containing

oligonucleotide fragment of the invention

XX

SQ Sequence 51 BP; 14 A; 16 C; 8 G; 13 T; 0 U; 0 Other;

Query Match

60.0%; Score 13.2; DB 4; Length 51;

Best Local Similarity 83.3%; Pred. No. 8.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

09:38:24 2004

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ACAATCACAGTCTCTG 18  
|||||  
ACAATCCCATTTGCTG 44

Qy 4 CAATCACAGTCTCTGCGG 21  
Db 41 CTATCATAGTCTCTGCTG 24

Search completed: February 29, 2004, 09:02:36  
Job time : 224.714 secs

andard; DNA; 60 BP.

(first entry)

ed transcript detection oligonucleotide SEQ ID NO:19346.

a; rat; splice transcript; detection; RNA transcript;  
ant; transcriptome; oligonucleotide library; ss.

S.

-A2.

; 2001WO-IB001903.

; 2000US-0221607P.

; 2001US-0287724P.

PUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

57383/30.

cleotide libraries comprising oligonucleotides which  
hybridize to mRNAs transcribed from a transcription unit of a  
ful for detecting tissue-, pathology-, and developmental-  
nes.

3SEQ ID NO 19346; 47pp; English.

invention describes oligonucleotide libraries for detecting  
NAs that populate a (sub-)transcriptome, where the (sub-  
me comprises messenger RNAs transcribed from multiple  
on units that populate a genome. The library comprises several  
tides, each capable of hybridising selectively to a set of  
NAs transcribed from a given transcription unit of the genome,  
es one or more messenger RNA splice variants. The  
side libraries are useful for detecting mRNAs from a  
sample, in expression profiling studies, in qualitatively or  
aly characterising the corresponding transcriptome, and in  
NA transcripts and splice variants of human or animal  
nes. The libraries may also be used as specialised mini  
o detect transcripts of a sub-transcriptome under a particular  
or pathological state, and so allowing the detection of tissue  
logy-specific genes such as those genes only expressed in  
ssue under a specific pathological condition; to detect  
al specific genes; and to detect RNA transcripts and splice  
a transcriptome of a patient suffering from a particular  
3N27253 to ABN59589 represent oligonucleotide sequences from  
s and mice, which are used in the exemplification of the  
ention. N.B. The sequence data for this patent did not form  
printed specification, but was obtained in electronic format  
om WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 17 A; 12 C; 19 G; 12 T; 0 U; 0 Other;

ilarity 60.0%; Score 13.2; DB 6; Length 60;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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us-10-090-326-6.max.rni

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

eic search, using sw model

February 29, 2004, 08:44:24 ; Search time 41.4286 Seconds  
(without alignments)  
294.698 Million cell updates/sec

S-10-090-326-6  
2

agacaatcacagtctctcgga 22

IDENTITY NUC

apopt 10.0 , Gapext 1.0

82709 seqs, 277475446 residues

its satisfying chosen parameters: 874574

ngth: 0  
ngth: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents NA: \*  
: /cgn2\_6/prodata/2/ina/5A\_COMB.seq.\*  
: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*  
: /cgn2\_6/prodata/2/ina/6A\_COMB.seq.\*  
: /cgn2\_6/prodata/2/ina/6B\_COMB.seq.\*  
: /cgn2\_6/prodata/2/ina/PCRUS\_COMB.seq.\*  
: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

s the number of results predicted by chance to have a  
er than or equal to the score of the result being printed,  
ved by analysis of the total score distribution.

# SUMMARIES

Query match	Length	DB	ID	Description
71.8	46	1	US-08-217-299-3	Sequence 3, Appli
71.8	46	1	US-08-217-299-4	Sequence 4, Appli
70.9	30	2	US-08-583-562B-4	Sequence 4, Appli
70.9	30	2	US-08-779-113-4	Sequence 4, Appli
61.8	24	1	US-07-647-655C-4	Sequence 41, Appl
61.8	37	4	US-09-331-793-41	Sequence 2, Appli
61.8	44	3	US-08-666-354A-2	Sequence 8, Appli
61.8	52	1	US-07-647-655C-2	Sequence 10, Appl
60.0	22	4	US-09-553-690-8	Sequence 10, Appl
60.0	35	1	US-08-258-026A-10	Sequence 10, Appl
60.0	35	4	US-09-057-055B-73	Sequence 10, Appl
60.0	35	5	PCT-US95-07541-10	Sequence 1473, Ap
60.0	47	4	US-09-422-978-1473	Sequence 36, Appl
59.1	22	1	US-07-977-284A-36	Sequence 36, Appl
59.1	22	2	US-08-256-426B-36	Sequence 1112, Ap
59.1	28	2	US-08-859-998-1112	Sequence 1112, Ap
59.1	28	4	US-09-225-928-1112	Sequence 1112, Ap
59.1	28	4	US-09-225-201B-1112	Sequence 13, Appl
59.1	34	1	US-08-361-337-13	Sequence 1562, Ap
58.2	47	4	US-09-422-978-1562	Sequence 74, Appl
57.3	35	4	US-09-097-055B-74	Sequence 3196, Ap
57.3	47	4	US-09-422-978-3196	Sequence 29, Appl
57.3	48	1	US-08-472-194A-29	Sequence 29, Appl
57.3	48	3	US-08-262-142-29	Sequence 28, Appl
57.3	48	4	US-08-849-567A-29	Sequence 8, Appli
57.3	49	1	US-08-424-874-8	Sequence 11, Appl
57.3	59	3	US-08-983-607-11	

56.4	12.4	C	28	4	US-09-586-376-19	Sequence
56.4	12.4		29	4	US-10-082-260-8	Sequence
56.4	12.4		30	4	US-10-082-260-10	Sequence
56.4	12.4		31	4	US-08-815-783-8	Sequence
56.4	12.4		32	4	US-08-815-783-10	Sequence
56.4	12.4		33	4	US-09-879-919-8	Sequence
56.4	12.4		34	4	US-09-879-919-10	Sequence
56.4	12.4		35	4	US-08-871-488A-6	Sequence
56.4	12.4	C	36	4	US-09-123-030-4	Sequence
56.4	12.4		37	4	US-08-779-113-43	Sequence
56.4	12.4	C	38	2	US-08-779-113-44	Sequence
56.4	12.4		39	2	US-08-899-241-220	Sequence
56.4	12.4	C	40	2	US-08-483-695-19	Sequence
56.4	12.4		41	2	US-07-965-285-19	Sequence
56.4	12.4		42	2	US-08-487-231-19	Sequence
56.4	12.4		43	2	US-09-201-912-19	Sequence
56.4	12.4	C	44	4	US-09-422-978-2788	Sequence
56.4	12.4		45	2	US-08-949-155-45	Sequence
56.4	12.2	C	46	2	US-09-819-964-45	Sequence
56.4	12.2		47	2	US-08-949-155-23	Sequence
56.4	12.2	C	48	2	US-08-949-155-23	Sequence
56.4	12.2		49	2	US-09-301-593-70	Sequence
56.4	12.2	C	50	2	US-09-116-032-9	Sequence
56.4	12.2		51	2	US-09-301-593-69	Sequence
56.4	12.2	C	52	2	US-09-874-547-78	Sequence
56.4	12.2		53	2	US-09-874-547-62	Sequence
56.4	12.2	C	54	2	US-09-874-547-76	Sequence
56.4	12.2		55	2	US-09-874-547-77	Sequence
56.4	12.2	C	56	2	US-09-874-547-79	Sequence
56.4	12.2		57	2	US-09-874-547-80	Sequence
56.4	12.2	C	58	2	US-09-874-547-84	Sequence
56.4	12.2		59	2	US-08-071-601-10	Sequence
56.4	12.2	C	60	2	US-08-621-100-10	Sequence
56.4	12.2		61	2	US-08-171-389-8	Sequence
56.4	12.2	C	62	2	US-08-123-936-8	Sequence
56.4	12.2		63	2	US-08-475-228A-8	Sequence
56.4	12.2	C	64	2	US-08-482-080A-8	Sequence
56.4	12.2		65	2	US-09-354-947-8	Sequence
56.4	12.2	C	66	2	PCT-US93-12388-8	Sequence
56.4	12.2		67	2	US-08-171-389-79	Sequence
56.4	12.2	C	68	2	US-08-123-936-79	Sequence
56.4	12.2		69	2	US-08-475-228A-79	Sequence
56.4	12.2	C	70	2	US-08-482-080A-79	Sequence
56.4	12.2		71	2	US-09-354-947-79	Sequence
56.4	12.2	C	72	2	PCT-US93-12388-79	Sequence
56.4	12.2		73	2	US-09-554-929-59	Sequence
56.4	12.2	C	74	2	US-09-554-929-135	Sequence
56.4	12.2		75	2	US-08-956-171B-5080	Sequence
56.4	12.2	C	76	2	US-08-943-915-24	Sequence
56.4	12.2		77	2	US-09-019-160-54	Sequence
56.4	12.2	C	78	2	US-08-697-610-4	Sequence
56.4	12.2		79	2	US-08-349-357-4	Sequence
56.4	12.2	C	80	2	US-09-786-256C-19	Sequence
56.4	12.2		81	2	US-09-786-256C-14	Sequence
56.4	12.2	C	82	2	US-08-943-915-21	Sequence
56.4	12.2		83	2	US-08-348-548-44	Sequence
56.4	12.2	C	84	2	PCT-US95-15716-44	Sequence
56.4	12.2		85	2	US-09-668-113A-9	Sequence
56.4	12.2	C	86	2	US-08-170-290A-35	Sequence
56.4	12.2		87	2	US-08-133-011-57	Sequence
56.4	12.2	C	88	2	US-08-322-730A-57	Sequence
56.4	12.2		89	2	US-08-387-874-55	Sequence
56.4	12.2	C	90	2	US-08-383-619-57	Sequence
56.4	12.2		91	2	US-09-293-823-19	Sequence
56.4	12.2	C	92	2	US-08-907-739-57	Sequence
56.4	12.2		93	2	US-09-729-597-57	Sequence
56.4	12.2	C	94	2	US-09-726-653-68	Sequence
56.4	12.2		95	2	PCT-US93-08364-55	Sequence
56.4	12.2	C	96	2	US-08-461-286-1	Sequence
56.4	12.2		97	2	US-08-627-151A-1	Sequence
56.4	12.2	C	98	2	US-08-627-151A-1	Sequence
56.4	12.2		99	2	US-09-646-691B-2	Sequence
56.4	12.2	C	100	2	US-08-250-859-13	Sequence

54.5	42	1	US-08-490-803-13	Sequence 13, Appl	c 174	11.6	52.7	20	4	US-09-422-978-10661	Sequence
54.5	42	2	US-08-379-057-22	Sequence 22, Appl	175	11.6	52.7	22	1	US-08-546-130A-18	Sequence
54.5	42	2	US-08-457-254-24	Sequence 24, Appl	176	11.6	52.7	22	2	US-08-680-395-26	Sequence
54.5	42	2	US-08-484-257-13	Sequence 13, Appl	177	11.6	52.7	22	3	US-09-066-641-28	Sequence
54.5	42	5	PCT-US94-08806-13	Sequence 13, Appl	c 178	11.6	52.7	22	4	US-09-431-705-44	Sequence
54.5	42	5	PCT-US95-01775-13	Sequence 13, Appl	179	11.6	52.7	30	1	US-08-244-376-20	Sequence
54.5	42	5	PCT-US95-16626-24	Sequence 24, Appl	180	11.6	52.7	30	5	PCT-US93-11527-20	Sequence
54.5	48	4	US-09-538-709-998	Sequence 998, App	c 181	11.6	52.7	36	1	US-07-842-349-22	Sequence
54.5	49	2	US-08-627-695-8	Sequence 8, Appl	182	11.6	52.7	36	1	US-07-842-349-23	Sequence
54.5	52	1	US-07-647-655C-1	Sequence 1, Appl	c 183	11.6	52.7	36	1	US-07-756-251A-6	Sequence
54.5	57	1	US-08-050-319B-6	Sequence 6, Appl	184	11.6	52.7	38	4	US-09-474-432B-1366	Sequence
54.5	57	2	US-08-465-902-6	Sequence 6, Appl	185	11.6	52.7	38	4	US-09-476-387-1365	Sequence
54.5	20	1	US-08-167-113-5	Sequence 5, Appl	c 186	11.6	52.7	40	3	US-08-563-501A-33	Sequence
53.6	20	1	US-08-886-161-5	Sequence 5, Appl	c 187	11.6	52.7	42	2	US-09-205-231-33	Sequence
53.6	20	3	US-09-050-159-37	Sequence 37, Appl	188	11.6	52.7	42	2	US-08-389-423-25	Sequence
53.6	20	4	US-09-198-452A-2262	Sequence 2262, Ap	189	11.6	52.7	42	2	US-08-389-423-25	Sequence
53.6	20	4	US-09-198-452A-2265	Sequence 2265, Ap	190	11.6	52.7	42	4	US-09-189-028-25	Sequence
53.6	20	4	US-09-679-299A-155	Sequence 155, App	191	11.6	52.7	42	4	US-09-189-028-25	Sequence
53.6	20	4	US-09-679-299A-156	Sequence 156, App	192	11.6	52.7	43	1	US-07-931-473B-246	Sequence
53.6	24	4	US-09-382-552-180	Sequence 180, App	193	11.6	52.7	43	1	US-07-714-131C-246	Sequence
53.6	27	1	US-08-331-398A-6	Sequence 6, Appl	194	11.6	52.7	43	1	US-08-412-110-246	Sequence
53.6	27	1	US-08-331-397B-6	Sequence 6, Appl	c 195	11.6	52.7	43	1	US-08-467-420A-38	Sequence
53.6	27	2	US-08-759-804A-6	Sequence 6, Appl	c 196	11.6	52.7	43	1	US-08-470-110A-38	Sequence
53.6	27	3	US-09-227-693-6	Sequence 6, Appl	c 197	11.6	52.7	43	1	US-08-409-442A-246	Sequence
53.6	28	2	US-08-859-998-1184	Sequence 1184, Ap	c 198	11.6	52.7	43	1	US-08-667-769A-38	Sequence
53.6	28	4	US-09-225-928-1184	Sequence 1184, Ap	c 199	11.6	52.7	43	2	US-08-469-609A-246	Sequence
53.6	28	4	US-09-225-201B-1184	Sequence 1184, Ap	c 200	11.6	52.7	43	2	US-08-940-371-38	Sequence
53.6	29	4	US-09-304-234-285	Sequence 285, App	c 201	11.6	52.7	43	3	US-09-143-190-246	Sequence
53.6	30	2	US-08-743-637B-148	Sequence 148, App	c 202	11.6	52.7	43	3	US-08-637-647-38	Sequence
53.6	30	2	US-08-526-840B-148	Sequence 148, App	c 203	11.6	52.7	43	4	US-09-502-344-246	Sequence
53.6	31	2	US-08-483-528B-12	Sequence 12, Appl	c 204	11.6	52.7	43	5	PCT-US95-17082A-38	Sequence
53.6	31	2	US-08-673-799C-12	Sequence 12, Appl	c 205	11.6	52.7	45	1	US-08-447-169A-229	Sequence
53.6	31	3	US-09-393-385B-12	Sequence 8, Appl	c 206	11.6	52.7	47	4	US-09-336-643A-61	Sequence
53.6	32	1	US-07-977-696C-8	Sequence 8, Appl	c 207	11.6	52.7	47	4	US-08-778-570B-39	Sequence
53.6	32	1	US-08-129-930B-8	Sequence 8, Appl	c 208	11.6	52.7	47	4	US-09-422-978-1483	Sequence
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53.6	32	3	US-08-783-853A-107	Sequence 107, App	c 210	11.6	52.7	48	3	US-09-440-523-2	Sequence
53.6	32	4	US-08-976-288A-8	Sequence 8, Appl	c 211	11.4	51.8	16	2	US-08-448-418-93	Sequence
53.6	32	4	US-09-344-050-107	Sequence 2, Appl	c 212	11.4	51.8	16	2	US-09-146-979-93	Sequence
53.6	32	4	US-09-313-350-2	Sequence 41, Appl	c 213	11.4	51.8	20	4	US-09-198-452A-1520	Sequence
53.6	33	3	US-08-427-569-41	Sequence 14, Appl	c 214	11.4	51.8	20	4	US-09-198-452A-1525	Sequence
53.6	33	4	US-09-874-547-14	Sequence 11, Appl	c 215	11.4	51.8	22	2	US-08-899-371-17	Sequence
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53.6	35	1	US-08-024-253-21	Sequence 75, Appl	c 217	11.4	51.8	24	1	US-08-445-265A-3	Sequence
53.6	35	4	US-09-097-055B-75	Sequence 6, Appl	c 218	11.4	51.8	24	3	US-08-990-442-3	Sequence
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53.6	37	2	US-08-765-783A-33	Sequence 33, Appl	c 223	11.4	51.8	25	4	US-08-671-573B-28	Sequence
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53.6	37	3	US-08-902-201-33	Sequence 35, Appl	c 227	11.4	51.8	28	4	US-09-225-928-537	Sequence
53.6	37	3	US-08-569-147-35	Sequence 33, Appl	c 228	11.4	51.8	28	4	US-09-225-201B-537	Sequence
53.6	37	3	US-09-416-557-33	Sequence 2, Appl	c 229	11.4	51.8	30	1	US-08-273-362-5	Sequence
53.6	37	4	US-09-347-061-2	Sequence 65, Appl	c 230	11.4	51.8	30	1	US-08-273-362-7	Sequence
53.6	38	4	US-08-874-547-55	Sequence 75, Appl	c 231	11.4	51.8	30	3	US-08-975-084-9	Sequence
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53.6	41	2	US-08-350-260A-579	Sequence 579, App	c 233	11.4	51.8	32	4	US-09-302-495-13	Sequence
53.6	41	4	US-09-104-337A-579	Sequence 15, Appl	c 234	11.4	51.8	32	4	US-10-079-616-13	Sequence
53.6	42	4	US-09-874-547-15	Sequence 5, Appl	c 235	11.4	51.8	33	1	US-08-475-000-7	Sequence
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53.6	46	2	US-09-649-083-29	Sequence 20, Appl	c 237	11.4	51.8	33	2	US-08-902-623-22	Sequence
53.6	47	4	US-09-724-138-10	Sequence 10, Appl	c 238	11.4	51.8	33	2	US-08-484-508-7	Sequence
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53.6	48	4	US-09-724-138-10	Sequence 4, Appl	c 240	11.4	51.8	34	2	US-08-458-356-167	Sequence
53.6	50	2	US-08-190-199A-4	Sequence 7257, Ap	c 241	11.4	51.8	34	3	US-08-460-736-167	Sequence
53.6	51	4	US-09-313-294A-7257	Sequence 2800, Ap	c 242	11.4	51.8	34	4	US-09-535-370-167	Sequence
53.6	51	4	US-08-956-171E-2800	Sequence 4682, Ap	c 243	11.4	51.8	38	6	5494663-28	Patent I
52.7	18	4	US-09-422-978-4682	Sequence 157, App	c 244	11.4	51.8	39	2	US-08-193-039B-3	Sequence
52.7	20	3	US-09-280-789-157	Sequence 21, Appl	c 245	11.4	51.8	39	4	US-09-860-761-3	Sequence
52.7	20	3	US-09-277-020-21		246	11.4	51.8	40	2	US-08-857-946-73	Sequence



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31.8	41	4	US-09-104-337A-580	Sequence 580, App	322	11.2	50.9	43	4	US-09-464-453-45	Sequence
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31.8	47	4	US-09-671-317-888	Sequence 888, App	c 328	11.2	50.9	45	4	US-09-969-192-30	Sequence
31.8	47	4	US-09-422-978-2109	Sequence 2109, Ap	329	11.2	50.9	47	4	US-09-671-317-748	Sequence
31.8	47	4	US-09-422-978-3741	Sequence 3741, Ap	c 330	11.2	50.9	47	4	US-09-422-978-815	Sequence
31.8	47	4	US-09-422-978-3852	Sequence 3852, Ap	c 331	11.2	50.9	48	1	US-08-399-696-19	Sequence
31.8	47	4	US-09-724-138-33	Sequence 33, Appl	332	11.2	50.9	59	4	US-09-698-286A-4	Sequence
31.8	50	1	US-08-374-641-40	Sequence 40, Appl	c 333	11.2	50.9	60	2	US-08-765-512-1	Sequence
31.8	51	4	US-09-443-199C-5	Sequence 5, Appl	c 334	11.2	50.9	60	2	US-08-914-828-1	Sequence
31.8	51	4	US-09-443-199C-6	Sequence 6, Appl	c 335	11.2	50.9	60	3	US-08-907-392A-1	Sequence
31.8	51	4	US-09-443-199C-575	Sequence 575, App	336	11.2	50.9	60	3	US-09-121-286-10	Sequence
31.8	51	4	US-09-443-199C-576	Sequence 576, App	c 337	11	50.0	18	1	US-07-947-120-5	Sequence
31.8	51	4	US-09-443-199C-576	Sequence 576, App	c 338	11	50.0	18	1	US-08-472-893A-5	Sequence
31.8	51	4	US-09-443-199C-1117	Sequence 1117, Ap	c 339	11	50.0	18	3	US-08-947-492-5	Sequence
31.8	51	4	US-09-443-199C-1118	Sequence 1118, Ap	340	11	50.0	20	1	US-07-828-444-3	Sequence
31.8	55	3	US-09-264-737-4	Sequence 4, Appl	341	11	50.0	20	2	US-08-117-952-280	Sequence
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50.9	26	2	US-08-331-389A-52	Sequence 52, Appl	359	11	50.0	24	4	US-09-724-138-48	Sequence
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50.9	30	4	US-09-225-201B-226	Sequence 226, App	c 367	11	50.0	28	3	US-08-129-686-23	Sequence
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50.9	31	3	US-09-246-277A-9	Sequence 9, Appl	c 369	11	50.0	28	4	US-09-486-072-27	Sequence
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50.9	39	3	US-09-130-225-32	Sequence 32, Appl	387	11	50.0	33	4	US-07-955-726A-34	Sequence
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50.0	39	4	US-09-548-372D-37	Sequence 37, Appl	c 482	10.8	49.1	20	4	US-09-980-052-124	Sequence
50.0	39	4	US-09-548-372D-38	Sequence 38, Appl	c 483	10.8	49.1	21	1	US-07-869-380B-8	Sequence
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50.0	42	3	US-09-042-353-315	Sequence 315, App	c 493	10.8	49.1	21	4	US-09-060-299-186	Sequence
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9.1	35	2	US-08-833-622-3	Sequence 3, Appli	665	10.6	48.2	20	4	US-09-183-636-2	Sequence
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47.3 39 5 PCT-US91-08525-17  
47.3 39 5 PCT-US93-04384-33  
47.3 39 5 PCT-US93-04384-41  
47.3 40 3 US-08-675-773B-12  
47.3 40 4 US-09-485-773B-103  
47.3 41 1 US-08-081-539-62  
47.3 41 1 US-08-466-647-62  
47.3 41 1 US-08-122-546-5  
47.3 41 1 US-08-137-117D-7  
47.3 41 1 US-08-436-717-7  
47.3 41 2 US-08-764-938-5  
47.3 41 2 US-08-553-501A-7  
47.3 41 2 US-08-350-260A-588  
47.3 41 2 US-08-765-783A-7  
47.3 41 3 US-08-921-100-7

ALIGNMENTS

lication US/08217299  
2513  
ATION:  
Mach, J. P.  
Pelegriin, A.  
Tersklkh, A.  
VENTION: Carcinoembryonic Antigen Derivatives  
SEQUENCES: 4  
NCE ADDRESS:  
: Hoffmann-La Roche Inc.  
340 Kingsland Street  
tley  
J  
USA  
10  
ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patentin Release #1.0, Version #1.25  
LICATION DATA:  
ON NUMBER: US/08/217,299  
TE:  
ATION: 435  
CATION DATA:  
ON NUMBER: EP 93810214.2  
TE: 25-MAR-1993  
ENT INFORMATION:  
kzas, Bruce A.  
ION NUMBER: 32,748  
DOCKET NUMBER: RAN 4093/096  
CATION INFORMATION:  
: (201) 235-5801  
OR SEQ ID NO: 3:  
46 base pairs  
ucleic acid  
ESS: single  
: linear  
?PE: CDNA  
AL: NO

ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-217-299-3  
Query Match 71.8%; Score 15.8; DB 1; Length 46;  
Best Local Similarity 89.5%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 2; Indels 0;  
QY 1 AGACATCAGCTCTCTGC 19  
Db 23 AGACATCAGCTCTCTGC 41  
RESULT 2  
US-08-217-299-4/c  
Sequence 4, Application US/08217299  
Patent No. 5672513  
GENERAL INFORMATION:  
APPLICANT: Mach, J. P.  
APPLICANT: Pelegriin, A.  
APPLICANT: Tersklkh, A.  
TITLE OF INVENTION: Carcinoembryonic Antigen Derivatives  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: NJ  
COUNTRY: USA  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/217,299  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 93810214.2  
FILING DATE: 25-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pokras, Bruce A.  
REGISTRATION NUMBER: 32,748  
REFERENCE/DOCKET NUMBER: RAN 4093/096  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-5801  
TELEFAX: (201) 235-3500  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-217-299-4  
Query Match 71.8%; Score 15.8; DB 1; Length 46;  
Best Local Similarity 89.5%; Pred. No. 63;  
Matches 17; Conservative 0; Mismatches 2; Indels 0;  
QY 1 AGACATCAGCTCTCTGC 19  
Db 28 AGACATCAGCTCTCTGC 10  
RESULT 3

us-10-090-326-6.max.rni

```

/ APPLICATION NUMBER: US/08/779,113
/ FILING DATE:
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Greta E. No. 594899land
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 27866/33773
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ US-08-779-113-4

Query Match 70.9%; Score 15.6; DB 2; Length 30;
Best Local Similarity 81.8%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 4; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGA 22
      ||||| ||||| |||||
DB 26 AGAGAGTCCCACTCTCTGAGGA 5

RESULT 5
US-07-647-655C-4
/ Sequence 4, Application US/07647655C
/ Patent No. 5364759
/ GENERAL INFORMATION:
/ APPLICANT: Albert O. Edwards and
/ APPLICANT: Charles Thomas Caskey
/ TITLE OF INVENTION: DNA profiling with short
/ TITLE OF INVENTION: tandem repeat polymorphisms and identifier
/ TITLE OF INVENTION: STRS
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fulbright & Jaworski Patent Department
/ STREET: 1301 McKinney, Suite 5100
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: U.S.A.
/ ZIP: 77010-3095
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Disk, 3.5 inch (1.44MB)
/ COMPUTER: IBM PC/AT
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: BASIC
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/647,655C
/ FILING DATE: 19910131
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: THOMAS D. PAUL
/ REGISTRATION NUMBER: 32,714
/ REFERENCE/DOCKET NUMBER: D-5217
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (713) 651-5325
/ TELEFAX: (713) 651-5246
/ TELE: WESTERN UNION 762829
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 24
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: Single
/ TOPOLOGY: Linear
/ MOLECULE TYPE: Synthetic DNA

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us-10-090-326-6.max.rni

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61.8%; Score 13.6; DB 1; Length 24;
ilarity 80.0%; Pred. No. 6.9e+02;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CAATCAGTCTCTGCGG 21
|||||
GAATCGTGTCTCTGCGG 23

pplication US/09331793
0646
ATION:
URIYAMA, Shinichi
ASEGAWA, Takashi
NTION: CELL MEMBRANE DIRECTED DRUGS
E: 1110-253P
CATION NUMBER: US/09/331,793
G DATE: 1999-06-25
ID NOS: 67
tentin version 3.0

nthetic DNA Primers

61.8%; Score 13.6; DB 4; Length 37;
ilarity 80.0%; Pred. No. 7.4e+02;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CAATCAGTCTCTGCGG 21
|||||
TCTCAGTCTCTGCGG 28

/c
pplication US/08666354A
0141
MATION:
KLAUSER, THOMAS
KRAMER, JOACHIM
MEYER, THOMAS F.
POHLNER, JOHANNES
VENTION: BACTERIA USED TO PRODUCE STABLE FUSION
VENTION: PROTEINS AND METHOD FOR THEIR IDENTIFICATION
SEQUENCES: 18
NCE ADDRESS:
: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
P.O. BOX 747
LLS CHURCH
A
USA
140-0747
ADABLE FORM:
PE: Floppy disk
SYSTEM: PC-DOS/MS-DOS
Patent In Release #1.0, Version #1.30
PLICATION DATA:
ION NUMBER: US/08/666,354A
TE: 23-SEP-1996
ATION: 435
ENT INFORMATION:
FENSON, LEONARD R.
TION NUMBER: 30,330
DOCKET NUMBER: 147-157P
CATION INFORMATION:
: 703-205-8000

TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "OLIGONUCLEOTIDE PRIMER"
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-666-354A-2

Query Match 61.8%; Score 13.6; DB 3; Length 44;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACAATCACAGTCTCTGCGG 22
DB 29 ACTGTCACTGTCTCTGCGAA 10

RESULT 8
US-07-647-655C-2
Sequence 2, Application US/07647655C
Patent No. 5364759
GENERAL INFORMATION:
APPLICANT: Albert O. Edwards and
APPLICANT: Charles Thomas Caskey
TITLE OF INVENTION: DNA profiling with short
TITLE OF INVENTION: tandem repeat polymorphisms and identific
TITLE OF INVENTION: STRS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski Patent Department
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3.5 inch (1.44MB)
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: BASIC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/647,655C
FILING DATE: 19910131
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: THOMAS D. PAUL
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-5325
TELEFAX: (713) 651-5246
TELEX: WESTERN UNION 762829
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 52
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Synthetic DNA
US-07-647-655C-2

Query Match 61.8%; Score 13.6; DB 1; Length 52;
Best Local Similarity 80.0%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0;
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AATCAGTCTCTGCGG 21  
|||||  
AATCGTGTCTCTGCGAG 51

lication US/09553690  
296

TION:  
scher, Robert L.  
oi, Yeonhee  
mon, Mike  
e Regents of the University of California  
TION: Nucleic Acids That Control Seed and  
TION: Fruit Development in Plants  
: 023070-099900US  
ATION NUMBER: US/09/553,690  
DATE: 2000-04-21  
ID NOS: 50  
tSEQ for Windows Version 3.0

ificial Sequence

TION: primer SKB-8

60.0%; Score 13.2; DB 4; Length 22;  
larity 83.3%; Pred.No.1.1e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AATCAGTCTCTGCG 19  
|||||  
AATACCGTCTCTCC 1

/c  
plication US/08258026A  
637

ATION:  
Huang, Grace P.  
Rhode, Peter R.  
Stinson, Jeffrey R.  
Wong, Hing C.  
ENTION: A METHOD FOR DISPLAYING PROTEINS  
QUENCES: 26  
CE ADDRESS:  
David G. Conlin; DIKE, BRONSTEIN, ROBERTS &  
CUSHMAN  
30 WATER STREET  
TON  
SSACHUSETTS  
US  
9

DABLE FORM:  
E: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.25  
ICATION DATA:  
N NUMBER: US/08/258,026A  
E: 10-JUN-1994  
TION: 435

NT INFORMATION:  
nick, David R.  
ON NUMBER: 34235  
DOCKET NUMBER: 42838  
ATION INFORMATION:  
(617) 523-3400  
(617) 523-6400

TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
US-08-258-026A-10

Query Match 60.0%; Score 13.2; DB 1; Length 35;  
Best Local Similarity 72.2%; Pred.No.1.2e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0;

QY 4 CAATCAGTCTCTGCGG 21  
|||  
DB 32 CASTCAGTCTCYKAG 15

RESULT 11

US-09-097-055B-73/c  
; Sequence 73, Application US/09097055B  
; Patent No. 6610293  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Gerald W.  
; Schuman, Richard F.  
; Wong, Hing  
; Stinson, Jeffrey L.  
; TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND  
; CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEI  
; POSITIVE BACTERIA

NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
DUNNER, LLP

STREET: 1300 I Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/097,055B  
FILING DATE: 15-Jun-1998

ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carol P.  
REGISTRATION NUMBER: 32,220  
REFERENCE/DOCKET NUMBER: 04995.0041-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-09-097-055B-73

Query Match 60.0%; Score 13.2; DB 4; Length 35;  
Best Local Similarity 72.2%; Pred.No.1.2e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0;

QY 4 CAATCAGTCTCTGCGG 21  
|||  
DB 32 CASTCAGTCTCYKAG 15

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us-10-090-326-6.max.rni

Application PC/TUS9507541  
ATION: Huang, Grace P.  
Rhode, Peter R.  
Stinson, Jeffrey R.  
Wong, Hing C.  
VENTION: A METHOD FOR DISPLAYING  
SEQUENCES: 24  
NCE ADDRESS:  
: David G. Conlin; DIKE, BRONSTEIN,  
: ROBERTS & CUSHMAN  
130 WATER STREET  
STON  
ASSACHUSETTS  
US  
09  
ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patentin Release #1.0, Version #1.25  
ICATION DATA:  
ON NUMBER: PCT/US95/07541  
TE:  
ATION:  
ATION DATA:  
ON NUMBER: US 08/258,026  
TE: 10-JUN-1994  
ENT INFORMATION:  
snick, David R.  
ION NUMBER: 34235  
/DOCKET NUMBER: 42838  
ATION INFORMATION:  
: (617) 523-3400  
(617) 523-6400  
00291 STRE UR  
OR SEQ ID NO: 10:  
ARACTERISTICS:  
35 base pairs  
cleic acid  
SSS: unknown  
unknown  
0  
ilarity 60.0%; Score 13.2; DB 5; Length 35;  
Conservative 72.2%; Pred. No. 1.2e+03;  
Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
ATCACAGTCTCTGCGG 21  
STCACHGTCTCYKAG 15  
73  
Application US/09422978  
7751  
ATION:  
hen, Daniel  
umenfeld, Marta  
umakov, Ilya  
NTION: Biallelic markers for use in constructing a high density...  
E: GENSET.020CPI  
CATION NUMBER: US/09/422,978  
G DATE: 1999-10-20  
CATION NUMBER: US 09/298,850  
G DATE: 1999-04-21  
CATION NUMBER: US 60/109,732  
G DATE: 1998-11-23

EARLIER APLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 1473  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 99-25379-389 : polymorphic base C or T  
US-09-422-978-1473  
Query Match 60.0%; Score 13.2; DB 4; Length 47;  
Best Local Similarity 75.0%; Pred. No. 1.2e+03;  
Matches 15; Conservative 1; Mismatches 4; Indels 0;  
QY 2 GACAATCACAGTCTCTGCGG 21  
DB 19 GAGCAYCACACTCTGCGG 38  
RESULT 14  
US-07-977-284A-36/c  
Sequence 36, Application US/07977284A  
Patent No. 5558988  
GENERAL INFORMATION:  
APPLICANT: Prockop, Darwin J.  
APPLICANT: Ala-Kokko, Leena  
APPLICANT: Williams, Charlene J.  
APPLICANT: Ritvaniemi, Pertti  
APPLICANT: Baldwin, Clinton  
APPLICANT: Hopkinson, Ian  
APPLICANT: Ahmad, Nilofar Nina  
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC  
TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS  
NUMBER OF SEQUENCES: 261  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 55589  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,284A  
FILING DATE: 13-NOV-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: DeLuca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-0697  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
ANTI-SENSE: YES  
US-07-977-284A-36  
Query Match 59.1%; Score 13; DB 1; Length 22;

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,928  
FILING DATE: 05-Jan-1999  
ASSIGNATION: <Unknown>  
APPLICATION DATA:  
APPLICATION NUMBER: 08/859,998  
FILING DATE: 21-MAY-1997  
Y/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
COMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
FOR SEQ ID NO: 1112:  
E CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
POLYMER: DNA  
E TYPE: DNA  
:  
OTHER INFORMATION: oligonucleotide primer  
E DESCRIPTION: SEQ ID NO: 1112:  
12  
59.1%; Score 13; DB 4; Length 28;  
ilarity 76.2%; Pred. No. 1.4e+03;  
Conservative 0; Mismatches 5; Indels 0;  
ACAATCACAGTCTCTGCGG 21  
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ACAAACACATCTCAGTGG 28  
112  
Application US/09225201B  
9455  
INVENTOR:  
NAME: Chenchik, Alex  
Jokhadze, George  
Hiblasavili, Robert  
INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
EXPRESSION  
OF SEQUENCES: 1375  
SEQUENCE ADDRESS:  
DRESSEE: Fish & Richardson, P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: US  
ZIP: 94025  
READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,201B  
FILING DATE: 05-Jan-1999  
ASSIGNATION: <Unknown>  
APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,998  
FILING DATE: 21-MAY-1997  
Y/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
COMMUNICATION INFORMATION:

TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875  
INFORMATION FOR SEQ ID NO: 1112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
SEQUENCE DESCRIPTION: SEQ ID NO: 1112:  
US-09-225-201B-1112  
Query Match 59.1%; Score 13; DB 4; Length 28;  
Best Local Similarity 76.2%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;  
QY 1 AGACATCACAGTCTCTGCGG 21  
| | | | | | | | | | | | | | | | | | | | | |  
DB 8 ACACAAACATCTCAGTGG 28  
| | | | | | | | | | | | | | | | | | | | | |  
RESULT 19  
US-08-361-337-13  
Sequence 13, Application US/08361337  
Patent No. 5728519  
GENERAL INFORMATION:  
APPLICANT: Levenbook, Inessa S.  
APPLICANT: Chumakov, Konstantin M.  
APPLICANT: No. 5728519wood, Laurie P.  
APPLICANT: Roninson, Igor  
TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF  
TITLE OF INVENTION: ATTENUATED LIVE VACCINES  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NEEDLE & ROSENBERG, P.C.  
STREET: 127 Peachtree Street, N.E.  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,337  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perityman, David G.  
REGISTRATION NUMBER: 33,438  
REFERENCE/DOCKET NUMBER: 1414.634  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 688-0770  
TELEFAX: (404) 688-9880  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-361-337-13  
Query Match 59.1%; Score 13; DB 1; Length 34;  
Best Local Similarity 76.2%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;  
QY 2 GACAATCACAGTCTCTGCGGA 22  
| | | | | | | | | | | | | | | | | | | | | |

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us-10-090-326-6.max.rni

AATCACAGATTCTGAGCA 34

2/c  
Application US/09422978

751

ION:

en, Daniel

nenfeld, Marta

nakov, Ilya

FIION: Biallelic markers for use in constructing a high density...

: GENSET.020CPI

ATION NUMBER: US/09/422,978

DATE: 1999-10-20

ATION NUMBER: US 09/298,850

DATE: 1999-04-21

ATION NUMBER: US 60/109,732

DATE: 1998-11-23

ATION NUMBER: US 60/082,614

DATE: 1998-04-21

ID NOS: 11796

o Sapiens

ele

TION: 99-4679-240 : polymorphic base C or T

2

larity 58.2%; Score 12.8; DB 4; Length 47;

Conservative 1; Mismatches 3; Indels 0; Gaps 0;

TCACAGTCTCTCGGG 21

|||||

TCTCAGTCTCTCCG 21

/c  
plication US/09097055B

293

MATION:

T: Fischer, Gerald W.

Schuman, Richard F.

Wong, Hing

Stinson, Jeffrey L.

INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND

CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM

POSITIVE BACTERIA

F SEQUENCES: 89

NDENCE ADDRESS:

RESSEE: FINNEGAN, HENDERSON, PARABOW, GARRETT &

DUNNER, LLP

ET: 1300 I Street, NW

TE: DC

NTY: USA

: 20005-3315

READABLE FORM:

IUM TYPE: Floppy disk

RATING SYSTEM: PC-DOS/MS-DOS

WARE: Patent in Release #1.0, Version #1.30

APPLICATION DATA:

LICATION NUMBER: US/09/097,055B

ING DATE: 15-Jun-1998

/AGENT INFORMATION:

E: Einaudi, Carol P.

ISTRATION NUMBER: 32,220

; REFERENCE/DOCKET NUMBER: 04995-0041-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 74:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 35 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "primer"

; SEQUENCE DESCRIPTION: SEQ ID NO: 74:

US-09-097-055B-74

Query Match

Best Local Similarity 57.3%; Score 12.6; DB 4; Length 35;

Matches 13; Conservative 3; Mismatches 3; Indels 0;

QY 3 ACAATCACAGTCTCTGCGG 21

|||||

Db 33 ACKSTCACHGTCTCYKAG 15

RESULT 22

US-09-422-978-3196/c

; Sequence 3196, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a hi

; FILE REFERENCE: GENSET.020CPI

; CURRENT APPLICATION NUMBER: US/09/422,978

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 3196

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: allele

; LOCATION: 24

; OTHER INFORMATION: 99-24480-44 : polymorphic base A or C

US-09-422-978-3196

Query Match

Best Local Similarity 57.3%; Score 12.6; DB 4; Length 47;

Matches 12; Conservative 2; Mismatches 1; Indels 0;

QY 8 CACAGTCTCTCTGCGGA 22

|||||

Db 16 CACAGTCTCTGCGSM 2

RESULT 23

US-08-472-194A-29

; Sequence 29, Application US/08472194A

; Patent No. 5807718

; GENERAL INFORMATION:

; APPLICANT: Joyce, Gerald F

; APPLICANT: Breaker, Ronald R

; TITLE OF INVENTION: ENZYMAIC DNA MOLECULES

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

09:38:24 2004

us-10-090-326-6.max.rni

Patent Counsel  
.0550 No. 5807718th Torrey Pines Road, TPC 8  
Jolla

USA  
ADABLE FORM:  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.25  
ICATION DATA: US/08/472,194A

IN NUMBER: US/07-JUN-1995

ATION: 536

ATION DATA:

IN NUMBER: US 08/349,023

IE: 02-DEC-1994

NT INFORMATION:

iting, Thomas

ON NUMBER: 34,163

DOCKET NUMBER: TSRI 463.1

ATION INFORMATION:

619-784-2937

619-784-9399

OR SEQ ID NO: 29:

ARACTERISTICS:

18 base pairs

leic acid

3SS: single

linear

2E: DNA (genomic)

,

57.3%; Score 12.6; DB 1; Length 48;  
ilarity 78.9%; Pred. No. 2.4e+03;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACATCAGTCTCTGC 19

||||| ||| |||

TCCATCAGTCTCTGC 29

pplication US/09262142B

0462

ATION:

bas, Carlos F.

/ce, Gerald

atoro, Stephen W.

idasamy, Sakthivel

ATION: ENZYMATIC DNA MOLECULES THAT CONTAIN MODIFIED

ATION: NUCLEOTIDES

3: SCR21448

ATION NUMBER: US/09/262,142B

3 DATE: 1999-03-03

ID NOS: 58

antIn Ver. 2.1

tificial Sequence

ATION: Description of Artificial Sequence: DNA enzyme

57.3%; Score 12.6; DB 3; Length 48;  
ilarity 78.9%; Pred. No. 2.4e+03;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACAATCAGTCTCTGC 19

||||| ||| |||

Db 11 AGTCCATCAGTCTCTGC 29

RESULT 25

US-08-849-567A-29

; Sequence 29, Application US/08849567A

; Patent No. 6326174

; GENERAL INFORMATION:

; APPLICANT: Joyce, Gerald F.

; APPLICANT: Breaker, Ronald R.

; TITLE OF INVENTION: ENZYMATIC DNA MOLECULES

; FILE REFERENCE: SCR1943S

; CURRENT APPLICATION NUMBER: US/08/849,567A

; CURRENT FILING DATE: 1997-08-25

; PRIOR APPLICATION NUMBER: PCT/US95/15580

; PRIOR FILING DATE: 1995-12-01

; PRIOR APPLICATION NUMBER: 08/472,194

; PRIOR FILING DATE: 1995-06-07

; PRIOR APPLICATION NUMBER: 08/349,023

; PRIOR FILING DATE: 1994-12-02

; NUMBER OF SEQ ID NOS: 101

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 29

; LENGTH: 48

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: DNA enzy

US-08-849-567A-29

Query Match 57.3%; Score 12.6; DB 4; Length 48;

Best Local Similarity 78.9%; Pred. No. 2.4e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 1 AGACAATCAGTCTCTGC 19

||||| ||| |||

Db 11 AGTCCATCAGTCTCTGC 29

RESULT 26

US-08-424-874-8/c

; Sequence 8, Application US/08424874

; Patent No. 5718915

; GENERAL INFORMATION:

; APPLICANT: Virtanen, Jorma A.

; APPLICANT: Virtanen, Sinikka

; TITLE OF INVENTION: BINDING MOLECULE MULTI ENZYME COMPLEXES

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/424,874

; FILING DATE: 19-APR-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Halluin, Albert P.

; REGISTRATION NUMBER: 25,227

; REFERENCE/DOCKET NUMBER: 8218-006

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-854-3660

; TELEFAX: 415-854-3694

; INFORMATION FOR SEQ ID NO: 8:

09:38:24 2004

us-10-090-326-6.max.rni

RACTERISTICS:

9 base pairs  
leic acid  
SS: unknown  
unknown  
E: DNA (genomic)

misc feature

25..26

RMATION: /note= "Where Y =

RMATION: FMOC-DMT-SER-CEDIPPA = N-Fluorenylmethoxycarbonyl

RMATION: O-dimethoxytriphenyl serinyl cyanoethyl

RMATION: N,N-diisopropylphosphoramidite"

57.3%; Score 12.6; DB 1; Length 49;

larity 71.4%; Pred. No. 2.4e+03;

Conservative 1; Mismatches 5; Indels 0; Gaps 0;

AATCAGAGTCTGCGGA 22

|||||

AATCTAGACTGCGCA 12

plication US/08983607

470

ATION:

Alan Garen

Xiaohong Cai

ENTION: Human Anti-Tumor Monoclonal Anti-

ENTION: bodies

QUENCES: 51

CE ADDRESS:

Department of Molecular Biophysics

and Biochemistry, Yale University

66 Whitney Avenue

Haven

nnecticut

United States of America

0-8114

DABLE FORM:

E: 3.5" 1.44 Mb diskette

IBM PC

SYSTEM: MS DOS

Word Processing

ICATION DATA:

N NUMBER: US/08/983,607

E: April 27, 1998

TION: 435

ATION DATA:

N NUMBER: PCT/IB96/01032

E: June 28, 1996

TION: 435

NT INFORMATION:

/ M. Krinsky

ON NUMBER: 32423

DOCKET NUMBER: OCR-679

ATION INFORMATION:

203-773-9544

203-773-1183

R SEQ ID NO: 11:

RACTERISTICS:

9 residues

leic acid

SS: single

linear

E: DNA

N: primer used in constructs

57.3%; Score 12.6; DB 3; Length 59;

Best Local Similarity 70.6%; Pred. No. 2.5e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0;

QY 6 ATCAGAGTCTGCGGA 22

|||||

Db 33 ATCAGAGTCTGCGGA 49

RESULT 28

US-09-586-376-19/c

; Sequence 19, Application US/09586376

; Patent No. 6492115

; GENERAL INFORMATION:

; APPLICANT: Guida, Marco

; APPLICANT: Hall, Jeff

; TITLE OF INVENTION: GENETIC TYPING OF THE HUMAN CYTOCHROME P450 2

; TITLE OF INVENTION: AND RELATED MATERIALS AND METHODS

; FILE REFERENCE: 4389-20

; CURRENT APPLICATION NUMBER: US/09/586,376

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-586-376-19

Query Match

56.4%; Score 12.4; DB 4; Length 17;

Best Local Similarity 92.9%; Pred. No. 2.5e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 1 AGACAATCACAGTC 14

|||||

Db 17 AGACCATCACAGTC 4

RESULT 29

US-10-082-260-8

; Sequence 8, Application US/10082260

; Patent No. 6506882

; GENERAL INFORMATION:

; APPLICANT: Yu, Guo-Liang, et al.

; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon

; FILE REFERENCE: PF253D1

; CURRENT APPLICATION NUMBER: US/10/082,260

; CURRENT FILING DATE: 2002-02-26

; PRIOR APPLICATION NUMBER: 08/815,783

; PRIOR FILING DATE: 1997-03-12

; PRIOR APPLICATION NUMBER: 60/016,812

; PRIOR FILING DATE: 1996-03-14

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 29

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

US-10-082-260-8

Query Match

56.4%; Score 12.4; DB 4; Length 29;

Best Local Similarity 92.9%; Pred. No. 2.8e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 3 ACAATCACAGTCTC 16

|||||

Db 10 ACAATCACAGTTTC 23

RESULT 30

US-10-082-260-10

; Sequence 10, Application US/10082260

16882  
 TATION:  
 GUO-LIANG, et al.  
 INTION: Human Tumor Necrosis Factor Delta and Epsilon  
 E: PF253D1  
 CATION NUMBER: US/10/082,260  
 IG DATE: 2002-02-26  
 TION NUMBER: 08/815,783  
 DATE: 1997-03-12  
 TION NUMBER: 60/016,812  
 DATE: 1996-03-14  
 ID NOS: 10  
 entIn Ver. 2.1

tificial Sequence  
 ATION: Primer

56.4%; Score 12.4; DB 4; Length 29;  
 ilarity 92.9%; Pred. No. 2.8e-03;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AATCACAGTCTC 16  
 |||||  
 AATCACAGTTTC 23

plication US/08815783  
 9170

MATION:  
 NI, JIAN  
 YU, GUO-LIANG  
 GENTZ, REINER  
 DILLON, PATRICK  
 VENTION: HUMAN TUMOR NECROSIS FACTOR DELTA AND  
 VENTION: EPSILON  
 EQUENCES: 10  
 NCE ADDRESS:  
 : HUMAN GENOME SCIENCES, INC.  
 9410 KEY WEST AVENUE  
 CKVILLE  
 D

US  
 50  
 ADABLE FORM:  
 PE: Floppy disk  
 IBM PC compatible  
 SYSTEM: PC-DOS/MS-DOS  
 PatentIn Release #1.0, Version #1.30  
 LICATION DATA:  
 ON NUMBER: US/08/815,783  
 RE:

ATION: 514  
 ENT INFORMATION:  
 EBALL, PAUL C  
 ION NUMBER: 34,610  
 /DOCKET NUMBER: PF253  
 CATION INFORMATION:  
 : (301) 309-8504  
 (301) 309-8512  
 OR SEQ ID NO: 8:  
 ARACTERISTICS:  
 29 base pairs  
 leic acid  
 3SS: single  
 linear  
 PE: DNA (genomic)

Query Match 56.4%; Score 12.4; DB 4; Length 29;  
 Best Local Similarity 92.9%; Pred. No. 2.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 3 ACAATCACAGTCTC 16  
 |||||  
 Db 10 ACAATCACAGTTTC 23

## RESULT 32

US-08-815-783-10  
 ; Sequence 10, Application US/08815783  
 ; Patent No. 6509170  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NI, JIAN  
 ; APPLICANT: YU, GUO-LIANG  
 ; APPLICANT: GENTZ, REINER  
 ; APPLICANT: DILLON, PATRICK  
 ; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR DELTA AND  
 ; TITLE OF INVENTION: EPSILON  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
 ; STREET: 9410 KEY WEST AVENUE  
 ; CITY: ROCKVILLE  
 ; STATE: MD  
 ; COUNTRY: US  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/815,783  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KIMBALL, PAUL C  
 ; REGISTRATION NUMBER: 34,610  
 ; REFERENCE/DOCKET NUMBER: PF253  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (301) 309-8504  
 ; TELEFAX: (301) 309-8512  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 29 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-815-783-10

Query Match 56.4%; Score 12.4; DB 4; Length 29;  
 Best Local Similarity 92.9%; Pred. No. 2.8e+03;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 3 ACAATCACAGTCTC 16  
 |||||  
 Db 10 ACAATCACAGTTTC 23

## RESULT 33

US-09-879-919-8  
 ; Sequence 8, Application US/09879919  
 ; Patent No. 6541224  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yu, Guo-Liang, et al.  
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon  
 ; FILE REFERENCE: PF253P1  
 ; CURRENT APPLICATION NUMBER: US/09/879,919  
 ; CURRENT FILING DATE: 2001-06-14



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us-10-090-326-6.max.rn1

ION NUMBER: 60/293,499  
DATE: 2001-05-25  
ION NUMBER: 60/277,978  
DATE: 2001-03-23  
ION NUMBER: 60/276,248  
DATE: 2001-03-16  
ION NUMBER: 60/254,875  
DATE: 2000-12-13  
ION NUMBER: 60/241,952  
DATE: 2000-10-23  
ION NUMBER: 60/211,537  
DATE: 2000-06-15  
ION NUMBER: 08/815,783  
DATE: 1997-03-12  
ION NUMBER: 60/016,812  
DATE: 1996-03-14  
ID NOS: 26  
ntIn Ver. 2.1

no sapiens

56.4%; Score 12.4; DB 4; Length 29;  
larity 92.9%; Pred. No. 2.8e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LATCACAGTCTC 16  
|||||  
LATCACAGTCTC 23

pplication US/09879919

(224

ATION:

Guo-Liang, et al.

ATION: Human Tumor Necrosis Factor Delta and Epsilon

3: PF253p1

ATION NUMBER: US/09/879,919

; DATE: 2001-06-14

ION NUMBER: 60/293,499

DATE: 2001-05-25

ION NUMBER: 60/277,978

DATE: 2001-03-23

ION NUMBER: 60/276,248

DATE: 2001-03-16

ION NUMBER: 60/254,875

DATE: 2000-12-13

ION NUMBER: 60/241,952

DATE: 2000-10-23

ION NUMBER: 60/211,537

DATE: 2000-06-15

ION NUMBER: 08/815,783

DATE: 1997-03-12

ION NUMBER: 60/016,812

DATE: 1996-03-14

ID NOS: 26

ntIn Ver. 2.1

no sapiens

56.4%; Score 12.4; DB 4; Length 29;  
larity 92.9%; Pred. No. 2.8e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

LATCACAGTCTC 16  
|||||

Db 10 ACAATCACAGTCTC 23

RESULT 35

US-08-871-488A-6

; Sequence 6, Application US/08871488A

; Patent No. 6358710

; GENERAL INFORMATION:

; APPLICANT: Graves, Scott S.

; APPLICANT: Reno, John M.

; APPLICANT: Mallett, Robert W.

; APPLICANT: Hylarides, Mark D.

; APPLICANT: Searle, Stephen M.J.

; APPLICANT: Henry, Andrew H.

; APPLICANT: Pedersen, Jan T.

; APPLICANT: Rees, Anthony R.

; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE

; TITLE OF INVENTION: ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THE

; TITLE OF INVENTION: PRETARGETING METHODS

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; City: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/871,488A

; FILING DATE: 09-JUN-1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey Ph.D., Richard G.

; REGISTRATION NUMBER: 32,629

; REFERENCE/DOCKET NUMBER: 690022.527C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-871-488A-6

Query Match 56.4%; Score 12.4; DB 4; Length 30;

Best Local Similarity 92.9%; Pred. No. 2.8e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 3 ACAATCACAGTCTC 16

|||||

Db 15 ACCATCACAGTCTC 28

RESULT 36

US-09-123-030-4/c

; Sequence 4, Application US/09123030

; Patent No. 6365337

; GENERAL INFORMATION:

; APPLICANT: Letts, Verity A.

; APPLICANT: Frankel, Wayne N.

; APPLICANT: Campbell, Kevin P.

; APPLICANT: Felix, Ricardo

; APPLICANT: Biddlecome, Gloria

; TITLE OF INVENTION: Genes Encoding Neuronal Voltage-Gated Calcium

; TITLE OF INVENTION: Gamma Subunits

; FILE REFERENCE: US App. 09/123,030

09:38:24 2004

us-10-090-326-6.max.rni

ATION NUMBER: US/09/123,030  
; DATE: 1998-07-27  
ID NOS: 40  
ntIn Ver. 2.0

inae gen. sp.

56.4%; Score 12.4; DB 4; Length 30;  
ilarity 72.7%; Pred. No. 2.8e+03;  
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ACAAATCACAGTCTCTGCGGA 22  
|||||  
3CCCTCAGCGCCCTGCGGA 9

application US/08779113  
3891

MATION:  
Staunton, Donald E.  
Harris, Edith S.  
VENTION: Cytoplasmic Modulators of Integrin  
VENTION: Binding  
SEQUENCES: 65

NCE ADDRESS:  
: Marshall, O'Toole, Gerstein, Murray & Borun  
233 South Wacker Drive, 6300 Sears Tower  
icago  
llinois  
United States of America

06  
ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.25  
LOCATION DATA:  
ON NUMBER: US/08/779,113

TE:  
ATION: 536  
ENT INFORMATION:  
eta E. No. 594889land  
ION NUMBER: 35,302  
/DOCKET NUMBER: 27866/33773  
CATION INFORMATION:  
: 312-474-6300  
312-474-0448  
OR SEQ ID NO: 43:  
ARACTERISTICS:  
34 base pairs  
cleic acid  
ESS: single  
linear  
PE: other nucleic acid

56.4%; Score 12.4; DB 2; Length 34;  
ilarity 72.7%; Pred. No. 2.9e+03;  
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ACAAATCACAGTCTCTGCGGA 22  
|||||  
ACTGACCCACTCTCTGAGGA 34

i/c  
application US/08779113

; Patent No. 5948891  
; GENERAL INFORMATION:  
; APPLICANT: Staunton, Donald E.  
; APPLICANT: Harris, Edith S.  
; TITLE OF INVENTION: Cytoplasmic Modulators of Integrin  
; TITLE OF INVENTION: Binding  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,113  
; FILING DATE:  
; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:  
; NAME: Greca E. No. 594889land  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33773  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid

US-08-779-113-44

Query Match 56.4%; Score 12.4; DB 2; Length 34;  
Best Local Similarity 72.7%; Pred. No. 2.9e+03;  
Matches 16; Cconservative 0; Mismatches 6; Indels 0;

Qy 1 AGACAATCACAGTCTCTGCGGA 22  
|||||  
Db 22 AGACTGACCCACTCTCTGAGGA 1

RESULT 39

US-08-899-241-220/c  
; Sequence 220, Application US/08899241A  
; Patent No. 6322995  
; GENERAL INFORMATION:  
; APPLICANT: Hohmann, Hans-Peter  
; APPLICANT: Huemelin, Markus  
; APPLICANT: van Loon, Adolphus  
; APPLICANT: Schurter, Walter  
; TITLE OF INVENTION: Improved Riboflavin Production  
; FILE REFERENCE: Improved Riboflavin Prod  
; CURRENT APPLICATION NUMBER: US/08/899,241A  
; CURRENT FILING DATE: 1997-07-23  
; EARLIER APPLICATION NUMBER: 96111905.4  
; EARLIER FILING DATE: 1996-07-24  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 220  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Bacillus subtilis  
US-08-899-241-220

Query Match 56.4%; Score 12.4; DB 4; Length 35;  
Best Local Similarity 92.9%; Pred. No. 2.9e+03;

09:38:24 2004

us-10-090-326-6.max.rni

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Application US/08483695  
;139

ATION:  
Brechot, Christian  
Kremsdorf, Dina

Porchon, Colette

ENTION: Nucleotide and Peptide Sequences of a  
ENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic

ENTION: Applications  
SEQUENCES: 46

ICE ADDRESS:  
Finnegan, Henderson, Farabow, Garrett &  
Dunner  
300 I Street, N.W.  
Washington

USA

5-3315

ADABLE FORM:

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.25

ICATION DATA:

N NUMBER: US/08/483,695

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ATION:

N NUMBER: US/07/965,285

E: 18-MAR-1993

N NUMBER: FR 91 06 882

E: 06-JUN-1991

NT INFORMATION:

ers, Kenneth J.

ON NUMBER: 25,146

DOCKET NUMBER: 05286-0001-00000

ATION INFORMATION:

202-408-4000

202-408-4400

R SEQ ID NO: 19:

ACTERISTICS:

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leic acid

SS: single

linear

E: Other

N: DNA probe

56.4%; Score 12.4; DB 2; Length 40;

larity 72.7%; Pred. No. 2.9e+03;

Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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plication US/07965285

904

ATION:

Brechot, Christian

APPLICANT: Kremsdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLYING DATE: 18-MAR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 06 882

FILING DATE: 06-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 05286-0001-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other

DESCRIPTION: DNA probe

US-07-965-285-19

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Best Local Similarity 72.7%; Pred. No. 2.9e+03;

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Db 13 AGACAATCACAGTCTCTGCGGA 34

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US-08-487-231-19

Sequence 19, Application US/08487231

Patent No. 5919454

GENERAL INFORMATION:

APPLICANT: Brechot, Christian

APPLICANT: Kremsdorf, Dina

APPLICANT: Porchon, Colette

TITLE OF INVENTION: Nucleotide and Peptide Sequences of a

TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and T

TITLE OF INVENTION: Applications

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

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Patentin Release #1.0, Version #1.25  
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TE: 07-JUNE-1995  
ACTION: 435  
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TE: 18-MAR-1993  
ACTION: 435  
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TE: 06-JUN-1991  
ENT INFORMATION:  
yers, Kenneth J.  
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CATION INFORMATION:  
: 202-408-4000  
: 202-408-4400  
OR SEQ ID NO: 19:  
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40 base pairs  
cleic acid  
ESS: single  
linear  
PE: Other  
ON: DNA probe  
56.4%; Score 12.4; DB 2; Length 40;  
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Conservative 0; Mismatches 6; Indels 0;  
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Application US/09201912  
0962  
INATION:  
Brechot, Christian  
Kremsdorf, Dina  
Porchon, Colette  
VENTION: Nucleotide and Peptide Sequences of a  
VENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
VENTION: Applications  
SEQUENCES: 46  
NCE ADDRESS:  
3: Finnegan, Henderson, Farabow, Garrett &  
3: Dunner  
1300 I Street, N.W.  
ashington  
DC  
USA  
005-3315  
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: Patentin Release #1.0, Version #1.25  
PLICATION DATA:  
ION NUMBER: US/09/201,912  
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ICATION DATA:  
ION NUMBER: 07/965,285  
ATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: DNA probe  
US-09-201-912-19  
Query Match 56.4%; Score 12.4; DB 3; Length 40;  
Best Local Similarity 72.7%; Pred. No. 2.9e+03;  
Matches 16; Conservative 0; Mismatches 6; Indels 0;  
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Sequence 2788, Application US/09422978  
Patent No. 6537751  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a  
FILE REFERENCE: GENSET 020CPI  
CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 2788  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
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OTHER INFORMATION: 99-18717-319 : polymorphic base T or A  
US-09-422-978-2788  
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Best Local Similarity 81.2%; Pred. No. 3e+03;  
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DB 34 TCACATTCCTGCTGA 19  
RESULT 45  
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Sequence 45, Application US/08949155  
Patent No. 6271436  
GENERAL INFORMATION:  
APPLICANT: Piedrahita, Jorge A  
APPLICANT: Bazer, Fuller W  
TITLE OF INVENTION: Compositions and Methods for the  
TITLE OF INVENTION: Generation of Transgenic Animal Species

09:38:24 2004

us-10-090-326-6.max.rni

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SE ADDRESS:  
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O. Box 4433  
Ston  
JS  
J-4433  
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IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
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ler, David W.  
ON NUMBER: 41,071  
DOCKET NUMBER: TANK:177  
ATION INFORMATION:  
(512) 418-3000  
(713) 789-2679  
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SS: single  
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55.5%; Score 12.2; DB 3; Length 22;  
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09:38:24 2004

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GenCore version 5.1.6  
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February 29, 2004, 09:43:45 ; Search time 135.143 Seconds  
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Listing first 1000 summaries

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61.8	25	14	US-10-215-112-2523			Sequence 2523, Ap
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61.8	25	14	US-10-098-263B-126081			Sequence 126081,
61.8	37	15	US-10-298-796-41			Sequence 41, Appl
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60.9	60	10	US-09-908-975-8908			Sequence 8908, Ap
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56.4	24	14	US-10-145-128A-111	Sequence 111, App	185	12.2	55.5	29	14	US-10-159-006-70	Sequence
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56.4	25	14	US-10-098-263B-30812	Sequence 30812, A	217	12.2	54.5	23	9	US-09-989-722-323	Sequence
56.4	25	14	US-10-098-263B-31196	Sequence 31196, A	218	12.2	54.5	23	9	US-09-989-723-323	Sequence
56.4	25	14	US-10-098-263B-46888	Sequence 46888, A	219	12.2	54.5	23	9	US-09-989-727-323	Sequence
56.4	25	14	US-10-098-263B-75692	Sequence 75692, A	220	12.2	54.5	23	9	US-09-989-727-323	Sequence
56.4	25	14	US-10-098-263B-83493	Sequence 83493, A	221	12.2	54.5	23	9	US-09-989-731-323	Sequence
56.4	25	14	US-10-098-263B-83494	Sequence 83494, A	222	12.2	54.5	23	9	US-09-989-732-323	Sequence
56.4	25	14	US-10-098-263B-84586	Sequence 84586, A	223	12.2	54.5	23	9	US-09-991-073-323	Sequence
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56.4	28	14	US-10-098-263B-101733	Sequence 101733, A	225	12.2	54.5	23	9	US-09-991-163-323	Sequence
56.4	28	9	US-09-895-141-49	Sequence 49, Appl	226	12.2	54.5	23	9	US-09-991-163-323	Sequence
56.4	29	9	US-09-879-919-8	Sequence 8, Appl	227	12.2	54.5	23	9	US-09-993-604-323	Sequence
56.4	29	9	US-09-879-919-10	Sequence 10, Appl	228	12.2	54.5	23	9	US-09-990-456-323	Sequence
56.4	29	13	US-10-082-260-8	Sequence 8, Appl	229	12.2	54.5	23	9	US-09-989-721-323	Sequence
56.4	29	13	US-10-082-260-10	Sequence 10, Appl	230	12.2	54.5	23	9	US-09-992-598-323	Sequence
56.4	29	14	US-10-268-951-8	Sequence 8, Appl	231	12.2	54.5	23	9	US-09-989-293A-323	Sequence
56.4	30	14	US-10-268-951-10	Sequence 10, Appl	232	12.2	54.5	23	9	US-09-989-735-323	Sequence
56.4	30	14	US-10-056-794-6	Sequence 6, Appl	233	12.2	54.5	23	9	US-09-990-444-323	Sequence
56.4	30	14	US-10-296-995-5	Sequence 5, Appl	234	12.2	54.5	23	9	US-09-991-181-323	Sequence
56.4	47	15	US-10-349-143-2788	Sequence 2788, Ap	234	12	54.5	23	9	US-09-989-730-323	Sequence

54.5	23	9	US-09-990-436-323	Sequence 323, App	c 308	12	54.5	52	14	US-10-090-827-21	Sequence
54.5	23	9	US-09-993-687-323	Sequence 323, App	309	12	54.5	59	14	US-10-222-654-46	Sequence
54.5	23	10	US-09-989-734-323	Sequence 323, App	310	12	54.5	60	9	US-09-735-705-375	Sequence
54.5	23	10	US-09-997-653-323	Sequence 323, App	311	12	54.5	60	9	US-09-850-716A-375	Sequence
54.5	23	10	US-09-993-667-323	Sequence 323, App	312	12	54.5	60	9	US-09-897-778-375	Sequence
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54.5	23	10	US-09-990-711-323	Sequence 323, App	c 317	12	54.5	60	10	US-09-908-975-15194	Sequence
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54.5	23	10	US-09-997-573-323	Sequence 323, App	322	11.8	53.6	20	10	US-09-770-107-31	Sequence
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54.5	23	10	US-09-990-726-323	Sequence 323, App	c 324	11.8	53.6	20	15	US-10-159-856-17	Sequence
54.5	23	10	US-09-997-559-323	Sequence 323, App	c 325	11.8	53.6	20	15	US-10-159-856-94	Sequence
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54.5	23	10	US-09-990-443-323	Sequence 323, App	c 327	11.8	53.6	20	15	US-10-289-762-2265	Sequence
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54.5	23	10	US-09-997-628-323	Sequence 323, App	c 329	11.8	53.6	24	9	US-09-730-018-8	Sequence
54.5	23	10	US-09-997-683-323	Sequence 323, App	c 330	11.8	53.6	24	10	US-09-382-860-180	Sequence
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54.5	23	10	US-09-997-440-323	Sequence 323, App	333	11.8	53.6	25	14	US-10-215-112-6585	Sequence
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54.5	23	10	US-09-993-463-323	Sequence 323, App	c 336	11.8	53.6	25	14	US-10-098-263B-18761	Sequence
54.5	23	10	US-09-997-542-323	Sequence 323, App	c 337	11.8	53.6	25	14	US-10-098-263B-24491	Sequence
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54.5	23	10	US-09-990-439-323	Sequence 323, App	c 339	11.8	53.6	25	14	US-10-098-263B-26510	Sequence
54.5	23	10	US-09-990-427-323	Sequence 323, App	c 340	11.8	53.6	25	14	US-10-098-263B-26963	Sequence
54.5	23	10	US-09-989-328-323	Sequence 323, App	c 341	11.8	53.6	25	14	US-10-098-263B-26964	Sequence
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54.5	23	10	US-09-992-521-323	Sequence 323, App	c 344	11.8	53.6	25	14	US-10-098-263B-35624	Sequence
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54.5	23	11	US-09-992-643-323	Sequence 323, App	c 355	11.8	53.6	30	14	US-10-182-018-8	Sequence
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54.5	25	14	US-10-215-112-2650	Sequence 2650, Ap	359	11.8	53.6	31	14	US-10-195-752-12	Sequence
54.5	25	14	US-10-215-112-3113	Sequence 3113, Ap	360	11.8	53.6	31	14	US-10-300-215-189	Sequence
54.5	25	14	US-10-098-263B-7214	Sequence 7214, Ap	361	11.8	53.6	31	14	US-10-300-215-212	Sequence
54.5	25	14	US-10-098-263B-12733	Sequence 12733, A	362	11.8	53.6	31	14	US-10-300-215-225	Sequence
54.5	25	14	US-10-098-263B-22557	Sequence 22557, A	363	11.8	53.6	31	14	US-10-300-215-242	Sequence
54.5	25	14	US-10-098-263B-22792	Sequence 22792, A	c 364	11.8	53.6	32	9	US-09-965-099-107	Sequence
54.5	25	14	US-10-098-263B-29311	Sequence 29311, A	c 365	11.8	53.6	32	10	US-09-947-839-8	Sequence
54.5	25	14	US-10-098-263B-61699	Sequence 61699, A	c 366	11.8	53.6	32	13	US-10-051-852-107	Sequence
54.5	25	14	US-10-098-263B-66399	Sequence 66399, A	c 367	11.8	53.6	32	15	US-10-430-176-107	Sequence
54.5	25	14	US-10-098-263B-95422	Sequence 95422, A	c 368	11.8	53.6	33	9	US-09-874-547-14	Sequence
54.5	25	14	US-10-098-263B-97119	Sequence 97119, A	c 369	11.8	53.6	34	9	US-09-333-527-13	Sequence
54.5	25	14	US-10-098-263B-126082	Sequence 126082,	c 370	11.8	53.6	34	15	US-10-127-427-13	Sequence
54.5	26	10	US-09-468-147-157	Sequence 157, App	c 371	11.8	53.6	34	15	US-10-374-531-66	Sequence
54.5	32	9	US-09-993-164-17	Sequence 17, Appl	c 372	11.8	53.6	35	9	US-09-893-615-75	Sequence
54.5	34	10	US-09-215-163-38	Sequence 38, Appl	c 373	11.8	53.6	35	15	US-09-215-163-30	Sequence
54.5	36	10	US-09-215-163-15	Sequence 15, Appl	c 374	11.8	53.6	35	15	US-10-601-171-75	Sequence
54.5	39	9	US-09-974-973-15	Sequence 15, Appl	c 375	11.8	53.6	36	14	US-10-222-028A-11	Sequence
54.5	39	15	US-10-273-973-57	Sequence 57, Appl	c 376	11.8	53.6	37	9	US-09-855-271-2	Sequence
54.5	43	10	US-09-990-586-32	Sequence 32, Appl	c 377	11.8	53.6	37	9	US-09-730-857-33	Sequence
54.5	43	14	US-10-310-113-28	Sequence 38, Appl	c 378	11.8	53.6	37	9	US-09-949-559-53	Sequence
54.5	43	14	US-10-230-880-32	Sequence 32, Appl	c 379	11.8	53.6	37	10	US-09-875-221A-53	Sequence
54.5	50	15	US-10-131-827-3629	Sequence 3629, Ap	c 380	11.8	53.6	38	9	US-09-874-547-65	Sequence



53.6	38	9	US-09-874-547-75	Sequence 75, Appl	454	11.6	52.7	50	14	US-10-012-121A-192	Sequenc
53.6	38	10	US-09-898-121A-2	Sequence 2, Appl	455	11.6	52.7	50	14	US-10-006-116A-192	Sequenc
53.6	39	14	US-10-231-452-66	Sequence 66, Appl	456	11.6	52.7	50	14	US-10-006-117A-192	Sequenc
53.6	41	9	US-09-988-899-61	Sequence 61, Appl	457	11.6	52.7	50	14	US-10-017-527A-192	Sequenc
53.6	41	14	US-10-160-232-22	Sequence 22, Appl	458	11.6	52.7	50	14	US-10-013-913A-192	Sequenc
53.6	42	9	US-09-874-547-15	Sequence 15, Appl	459	11.6	52.7	50	14	US-10-007-194A-192	Sequenc
53.6	43	9	US-09-924-099-30	Sequence 30, Appl	460	11.6	52.7	50	14	US-10-013-430A-192	Sequenc
53.6	44	15	US-10-412-703A-40	Sequence 40, Appl	461	11.6	52.7	50	14	US-10-011-671A-192	Sequenc
53.6	45	14	US-10-160-232-21	Sequence 21, Appl	462	11.6	52.7	50	14	US-10-012-755A-192	Sequenc
53.6	47	8	US-08-936-140-29	Sequence 29, Appl	463	11.6	52.7	50	14	US-10-015-386A-192	Sequenc
53.6	47	8	US-08-936-140-29	Sequence 29, Appl	464	11.6	52.7	50	14	US-10-011-692A-192	Sequenc
53.6	51	8	US-08-781-986A-2800	Sequence 2800, Ap	465	11.6	52.7	50	14	US-10-006-768A-192	Sequenc
53.6	51	9	US-09-147-142-25	Sequence 25, Appl	466	11.6	52.7	50	14	US-10-017-610A-192	Sequenc
53.6	60	10	US-09-908-975-6607	Sequence 6607, Ap	467	11.6	52.7	50	14	US-10-006-063A-192	Sequenc
53.6	60	10	US-09-908-975-8296	Sequence 8296, Ap	468	11.6	52.7	50	14	US-10-020-063A-192	Sequenc
53.6	60	10	US-09-908-975-15786	Sequence 15786, A	469	11.6	52.7	50	14	US-10-015-391A-192	Sequenc
53.6	60	10	US-09-908-975-19875	Sequence 19875, A	470	11.6	52.7	50	14	US-10-017-407A-192	Sequenc
53.6	60	10	US-09-908-975-20491	Sequence 20491, A	471	11.6	52.7	50	14	US-10-011-833A-192	Sequenc
53.6	60	10	US-09-908-975-22383	Sequence 22383, A	472	11.6	52.7	50	14	US-10-006-041A-192	Sequenc
53.6	60	10	US-09-908-975-23324	Sequence 23324, A	473	11.6	52.7	50	14	US-10-015-822A-192	Sequenc
53.6	60	10	US-09-908-975-31593	Sequence 31593, A	474	11.6	52.7	50	14	US-10-015-387A-192	Sequenc
53.6	18	9	US-09-969-373-4506	Sequence 4506, Ap	475	11.6	52.7	50	14	US-10-006-130A-192	Sequenc
52.7	18	9	US-09-969-373-4510	Sequence 4510, Ap	476	11.6	52.7	50	14	US-10-017-253A-192	Sequenc
52.7	18	15	US-10-349-143-4682	Sequence 4682, Ap	477	11.6	52.7	50	14	US-10-015-392A-192	Sequenc
52.7	19	14	US-10-005-356-140	Sequence 140, App	478	11.6	52.7	50	14	US-10-017-306A-192	Sequenc
52.7	20	9	US-09-734-847A-21	Sequence 21, Appl	479	11.6	52.7	50	14	US-10-017-867A-192	Sequenc
52.7	20	9	US-09-800-629A-157	Sequence 157, App	480	11.6	52.7	50	14	US-10-012-064A-192	Sequenc
52.7	20	14	US-10-126-355-18	Sequence 18, Appl	481	11.6	52.7	50	14	US-10-013-909A-192	Sequenc
52.7	20	15	US-10-349-143-10661	Sequence 10661, A	482	11.6	52.7	50	14	US-10-015-671A-192	Sequenc
52.7	21	9	US-09-835-232-14	Sequence 14, Appl	483	11.6	52.7	50	14	US-10-015-610A-192	Sequenc
52.7	21	14	US-10-308-485-14	Sequence 14, Appl	484	11.6	52.7	50	14	US-10-012-137A-192	Sequenc
52.7	22	8	US-08-731-499-30	Sequence 30, Appl	485	11.6	52.7	50	14	US-10-012-752A-192	Sequenc
52.7	24	10	US-09-940-185-2443	Sequence 2443, Ap	486	11.6	52.7	50	14	US-10-012-754A-192	Sequenc
52.7	25	14	US-10-098-263B-47935	Sequence 47935, A	487	11.6	52.7	50	14	US-10-013-910A-192	Sequenc
52.7	25	14	US-10-098-263B-53096	Sequence 53096, A	488	11.6	52.7	50	14	US-10-013-912A-192	Sequenc
52.7	25	14	US-10-098-263B-57005	Sequence 57005, A	489	11.6	52.7	50	14	US-10-015-653A-192	Sequenc
52.7	25	14	US-10-098-263B-57770	Sequence 57770, A	490	11.6	52.7	50	14	US-10-012-101B-192	Sequenc
52.7	25	14	US-10-098-263B-77075	Sequence 77075, A	491	11.6	52.7	50	14	US-10-015-480A-192	Sequenc
52.7	25	14	US-10-098-263B-78116	Sequence 78116, A	492	11.6	52.7	50	14	US-10-012-237A-192	Sequenc
52.7	25	14	US-10-098-263B-84685	Sequence 84685, A	493	11.6	52.7	50	14	US-10-015-715A-192	Sequenc
52.7	25	14	US-10-098-263B-89176	Sequence 89176, A	494	11.6	52.7	50	14	US-10-012-237A-192	Sequenc
52.7	25	14	US-10-098-263B-90102	Sequence 90102, A	495	11.6	52.7	50	14	US-10-013-906A-192	Sequenc
52.7	25	14	US-10-098-263B-113911	Sequence 113911, A	496	11.6	52.7	50	14	US-10-015-388A-192	Sequenc
52.7	25	14	US-10-098-263B-115692	Sequence 115692, A	497	11.6	52.7	50	14	US-10-012-753A-192	Sequenc
52.7	25	14	US-10-098-263B-116850	Sequence 116850, A	498	11.6	52.7	50	14	US-10-015-385A-192	Sequenc
52.7	25	14	US-10-098-263B-117292	Sequence 117292, A	499	11.6	52.7	50	14	US-10-007-236A-192	Sequenc
52.7	25	14	US-10-098-263B-118592	Sequence 118592, A	500	11.6	52.7	50	14	US-10-015-389A-192	Sequenc
52.7	25	14	US-10-098-263B-123311	Sequence 123311, A	501	11.6	52.7	50	14	US-10-015-519A-192	Sequenc
52.7	26	14	US-10-213-288-7	Sequence 7, Appl	502	11.6	52.7	50	15	US-10-013-915A-192	Sequenc
52.7	31	9	US-09-845-160-10	Sequence 10, Appl	503	11.6	52.7	50	15	US-10-015-394A-192	Sequenc
52.7	31	9	US-09-845-160-11	Sequence 11, Appl	504	11.6	52.7	50	15	US-10-015-390A-192	Sequenc
52.7	38	10	US-09-825-805-1365	Sequence 1365, Ap	505	11.6	52.7	50	15	US-10-011-795A-192	Sequenc
52.7	38	10	US-09-877-478-4504	Sequence 4504, Ap	506	11.6	52.7	50	15	US-10-131-827-1603	Sequenc
52.7	39	9	US-09-263-959-167	Sequence 167, App	507	11.6	52.7	50	15	US-10-131-827-7437	Sequenc
52.7	41	14	US-10-005-956-203	Sequence 203, App	508	11.6	52.7	50	15	US-10-131-827-7516	Sequenc
52.7	42	9	US-09-735-787-25	Sequence 25, Appl	509	11.6	52.7	50	15	US-10-012-231A-192	Sequenc
52.7	42	9	US-09-735-787-29	Sequence 29, Appl	510	11.6	52.7	50	15	US-09-908-975-5800	Sequenc
52.7	42	14	US-10-138-870-25	Sequence 25, Appl	511	11.6	52.7	50	15	US-09-908-975-6300	Sequenc
52.7	42	14	US-10-138-870-29	Sequence 29, Appl	512	11.6	52.7	50	15	US-09-908-975-6473	Sequenc
52.7	43	14	US-10-037-986-246	Sequence 246, App	513	11.6	52.7	50	15	US-09-908-975-7710	Sequenc
52.7	43	14	US-10-408-085-246	Sequence 246, App	514	11.6	52.7	50	15	US-09-908-975-10650	Sequenc
52.7	45	10	US-09-860-474-229	Sequence 229, App	515	11.6	52.7	50	15	US-09-908-975-10936	Sequenc
52.7	45	14	US-10-409-565-229	Sequence 229, App	516	11.6	52.7	50	15	US-09-908-975-12204	Sequenc
52.7	46	9	US-09-263-959-130	Sequence 130, App	517	11.6	52.7	50	15	US-09-908-975-12204	Sequenc
52.7	47	14	US-10-121-746-61	Sequence 61, Appl	518	11.6	52.7	50	15	US-10-012-231A-192	Sequenc
52.7	47	15	US-10-349-143-1483	Sequence 1483, Ap	519	11.6	52.7	50	15	US-09-908-975-5800	Sequenc
52.7	48	10	US-09-918-156-2	Sequence 2, Appl	520	11.6	52.7	50	15	US-09-908-975-6300	Sequenc
52.7	48	10	US-09-158-106-35	Sequence 35, Appl	521	11.6	52.7	50	15	US-09-908-975-7710	Sequenc
52.7	48	14	US-10-023-888-29	Sequence 29, Appl	522	11.6	52.7	50	15	US-09-908-975-10650	Sequenc
52.7	50	10	US-09-946-374-192	Sequence 192, App	523	11.6	52.7	50	15	US-09-908-975-10936	Sequenc
52.7	50	14	US-10-006-856A-192	Sequence 192, App	524	11.6	52.7	50	15	US-09-908-975-10936	Sequenc
52.7	50	14	US-10-006-818A-192	Sequence 192, App	525	11.6	52.7	50	15	US-09-908-975-12204	Sequenc
52.7	50	14	US-10-015-393A-192	Sequence 192, App	526	11.6	52.7	50	15	US-09-908-975-12204	Sequenc
52.7	50	14	US-10-015-393A-192	Sequence 192, App	527	11.6	52.7	50	15	US-09-908-975-12204	Sequenc
52.7	50	14	US-10-015-393A-192	Sequence 192, App	528	11.6	52.7	50	15	US-09-908-975-12204	Sequenc

32.7	60	10	US-09-908-975-13340	Sequence 13340, A	600	11.4	51.8	41	9	US-09-988-899-62	Sequence
32.7	60	10	US-09-908-975-13617	Sequence 13617, A	c 601	11.4	51.8	41	10	US-09-892-949-71	Sequence
32.7	60	10	US-09-908-975-14381	Sequence 14381, A	c 602	11.4	51.8	41	15	US-10-351-157-41	Sequence
32.7	60	10	US-09-908-975-15216	Sequence 15216, A	c 603	11.4	51.8	42	9	US-09-817-487A-5	Sequence
32.7	60	10	US-09-908-975-15441	Sequence 15441, A	c 604	11.4	51.8	42	14	US-10-300-215-174	Sequence
32.7	60	10	US-09-908-975-16790	Sequence 16790, A	c 605	11.4	51.8	42	15	US-10-417-476-19	Sequence
32.7	60	10	US-09-908-975-18148	Sequence 18148, A	c 606	11.4	51.8	45	9	US-09-859-053-1	Sequence
32.7	60	10	US-09-908-975-18153	Sequence 18153, A	c 607	11.4	51.8	46	9	US-09-263-959-124	Sequence
32.7	60	10	US-09-908-975-18931	Sequence 18931, A	c 608	11.4	51.8	47	9	US-09-780-929-121	Sequence
32.7	60	10	US-09-908-975-18998	Sequence 18998, A	c 609	11.4	51.8	47	15	US-10-349-143-2109	Sequence
32.7	60	10	US-09-908-975-19495	Sequence 19495, A	c 610	11.4	51.8	47	15	US-10-349-143-3741	Sequence
32.7	60	10	US-09-908-975-19638	Sequence 19638, A	c 611	11.4	51.8	47	15	US-10-349-143-3852	Sequence
32.7	60	10	US-09-908-975-19938	Sequence 19938, A	c 612	11.4	51.8	48	8	US-08-779-784-15	Sequence
32.7	60	10	US-09-908-975-20360	Sequence 20360, A	c 613	11.4	51.8	50	10	US-09-950-442-40	Sequence
32.7	60	10	US-09-908-975-22707	Sequence 22707, A	c 614	11.4	51.8	50	15	US-10-238-695-40	Sequence
32.7	60	10	US-09-908-975-31650	Sequence 31650, A	c 615	11.4	51.8	50	15	US-10-131-827-3901	Sequence
32.7	60	10	US-10-156-306-4366	Sequence 4366, Ap	c 616	11.4	51.8	50	15	US-10-131-827-5633	Sequence
32.7	60	10	US-10-300-215-183	Sequence 183, App	c 617	11.4	51.8	50	15	US-10-131-827-6737	Sequence
32.7	60	10	US-10-300-215-236	Sequence 236, App	c 618	11.4	51.8	50	15	US-10-131-827-7127	Sequence
32.7	60	10	US-09-956-712-88	Sequence 88, Appl	c 619	11.4	51.8	50	15	US-10-131-827-7421	Sequence
32.7	60	10	US-10-633-913-88	Sequence 88, Appl	c 620	11.4	51.8	50	15	US-10-131-827-7500	Sequence
32.7	60	10	US-10-281-479A-13	Sequence 13, Appl	c 621	11.4	51.8	51	10	US-09-977-797A-93	Sequence
32.7	60	10	US-10-275-180A-13	Sequence 13, Appl	c 622	11.4	51.8	51	10	US-09-155-106-36	Sequence
32.7	60	10	US-10-286-132A-13	Sequence 13, Appl	c 623	11.4	51.8	56	14	US-10-222-654-28	Sequence
32.7	60	10	US-10-289-762-1520	Sequence 1520, Ap	c 624	11.4	51.8	57	9	US-09-845-899A-21	Sequence
32.7	60	10	US-10-289-762-1525	Sequence 1525, Ap	c 625	11.4	51.8	60	10	US-09-908-975-5035	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 144, App	c 626	11.4	51.8	60	10	US-09-908-975-5554	Sequence
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32.7	60	10	US-09-981-566A-144	Sequence 253, App	c 628	11.4	51.8	60	10	US-09-908-975-8504	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 29, Appl	c 629	11.4	51.8	60	10	US-09-908-975-8612	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 118, App	c 630	11.4	51.8	60	10	US-09-908-975-10411	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 313, App	c 631	11.4	51.8	60	10	US-09-908-975-11950	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 4298, Ap	c 632	11.4	51.8	60	10	US-09-908-975-13477	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 10915, A	c 633	11.4	51.8	60	10	US-09-908-975-14337	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 14341, A	c 634	11.4	51.8	60	10	US-09-908-975-15010	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 28798, A	c 635	11.4	51.8	60	10	US-09-908-975-16613	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 33617, A	c 636	11.4	51.8	60	10	US-09-908-975-17703	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 33710, A	c 637	11.4	51.8	60	10	US-09-908-975-17867	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 41681, A	c 638	11.4	51.8	60	10	US-09-908-975-18115	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 41682, A	c 639	11.4	51.8	60	10	US-09-908-975-18157	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 52656, A	c 640	11.4	51.8	60	10	US-09-908-975-18623	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 54534, A	c 641	11.4	51.8	60	10	US-09-908-975-20961	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 60930, A	c 642	11.4	51.8	60	10	US-09-908-975-21870	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 64943, A	c 643	11.4	51.8	60	10	US-09-908-975-23372	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 65782, A	c 644	11.4	51.8	60	10	US-10-047-403-44	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 72646, A	c 645	11.2	50.9	17	10	US-09-818-875-4062	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 75025, A	c 646	11.2	50.9	17	10	US-09-818-875-4063	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 77024, A	c 647	11.2	50.9	17	14	US-10-238-700-426	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 93222, A	c 648	11.2	50.9	17	14	US-10-238-700-1205	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 99368, A	c 649	11.2	50.9	17	15	US-10-209-787-4062	Sequence
32.7	60	10	US-09-981-566A-144	Sequence 102403, A	c 650	11.2	50.9	17	15	US-10-209-787-4063	Sequence
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00.9	25	14	US-10-098-263B-23500	Sequence 23500, A	11	50.0	39	9	US-09-794-748-37	Sequence
00.9	25	14	US-10-098-263B-30435	Sequence 30435, A	11	50.0	39	9	US-09-794-925-38	Sequence
00.9	25	14	US-10-098-263B-30436	Sequence 30436, A	11	50.0	39	9	US-09-794-925-38	Sequence
00.9	25	14	US-10-098-263B-39611	Sequence 39611, A	11	50.0	39	9	US-09-681-442-37	Sequence
00.9	25	14	US-10-098-263B-40852	Sequence 40852, A	11	50.0	39	9	US-09-263-959-220	Sequence
00.9	25	14	US-10-098-263B-47959	Sequence 47959, A	11	50.0	39	10	US-09-869-414-37	Sequence
00.9	25	14	US-10-098-263B-54424	Sequence 54424, A	11	50.0	39	10	US-09-869-414-38	Sequence
00.9	25	14	US-10-098-263B-55309	Sequence 55309, A	11	50.0	39	10	US-09-548-366-37	Sequence
00.9	25	14	US-10-098-263B-57831	Sequence 57831, A	11	50.0	39	10	US-09-548-366-37	Sequence
00.9	25	14	US-10-098-263B-58267	Sequence 58267, A	11	50.0	39	10	US-09-548-366-37	Sequence
00.9	25	14	US-10-098-263B-66895	Sequence 66895, A	11	50.0	39	10	US-09-548-366-37	Sequence

39 14 US-10-283-349-52  
50.0 39 15 US-10-417-820A-109  
50.0 40 10 US-09-995-973-29  
50.0 40 10 US-09-995-484-29  
50.0 42 9 US-09-874-547-17  
50.0 43 14 US-10-156-604-4  
50.0 46 14 US-10-062-809-65  
50.0 47 14 US-10-076-802-67  
50.0 47 14 US-10-010-729-54  
50.0 47 15 US-10-367-169-67  
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50.0 50 15 US-10-131-827-2550  
50.0 50 15 US-10-131-827-3323  
50.0 50 15 US-10-131-827-5584  
50.0 50 15 US-10-131-827-6421  
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50.0 50 15 US-10-131-827-7273  
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50.0 51 9 US-09-795-847-41  
50.0 51 9 US-09-795-847-42  
50.0 51 9 US-09-794-743-41  
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50.0 51 9 US-09-794-748-42  
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50.0 51 9 US-09-794-925-42  
50.0 51 9 US-09-874-923-27  
50.0 51 9 US-09-881-442-41

## ALIGNMENTS

/c  
plication US/09931375A  
US20030027151A1  
TION:  
MAN, Matthew L.  
NG, Yacqin  
SEN, Bjorn R.  
WADI, Georges  
MAN-ROMAN, Sergio  
TION: REGULATOR GENE AND SYSTEM USEFUL FOR THE DIAGNOSIS AND THERAPY OF  
TION: OSTEOPOROSIS  
: 38464-0004  
ATION NUMBER: US/09/931,375A  
: DATE: 2001-08-17  
ION NUMBER: US 60/304,851  
ATE: 2001-07-13  
ION NUMBER: US 60/234,337  
ATE: 2000-09-22  
ION NUMBER: US 60/226,119  
ATE: 2000-08-18  
ID NOS: 89  
ntIn version 3.0

Official Sequence  
TION: Primer

64.5%; Score 14.2; DB 10; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0;  
QY 3 ACAATCACAGTCTCTGCGG 21  
Db 20 AAAATCACAGTCTCTGCGG 2  
RESULT 2  
US-09-908-975-15980/C  
; Sequence 15980, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: GHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15980  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-15980  
Query Match 64.5%; Score 14.2; DB 10; Length 60;  
Best Local Similarity 84.2%; Pred. No. 1.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0;  
QY 1 AGACAATCACAGTCTCTGC 19  
Db 60 AGACAATCACAGTCTCTGC 42  
RESULT 3  
US-10-098-263B-53982  
; Sequence 53982, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 53982  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-53982  
Query Match 62.7%; Score 13.8; DB 14; Length 25;  
Best Local Similarity 88.2%; Pred. No. 2.1e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0;  
QY 1 AGACAATCACAGTCTCT 17  
Db 6 ATACAATCACAGTCTCT 22



1/c  
Application US/09908975  
US20030165843A1  
TION:  
SHAN, Avi  
SSERMAN, Alon  
NTZ, Eli  
NTZ, Liat  
IGLER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
TION: THAT POPULATE A TRANSCRIPTOME  
FILE REFERENCE: 36688-0005  
TION NUMBER: US/09/908,975  
DATE: 2001-07-20  
TION NUMBER: US 60/287,724  
DATE: 2001-05-02  
TION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
ntIn version 3.0

no sapiens

11

61.8%; Score 13.6; DB 10; Length 60;  
ilarity 80.0%; Pred. No. 3e+03; 4; Indels 0; Gaps 0;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCACAGTCTCTGCGGA 22  
|||  
ATACCACTCTCTGGAA 7

366/c

Application US/09908975  
US20030165843A1  
TION:  
SHAN, Avi  
SSERMAN, Alon  
NTZ, Eli  
NTZ, Liat  
IGLER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
TION: THAT POPULATE A TRANSCRIPTOME  
FILE REFERENCE: 36688-0005  
TION NUMBER: US/09/908,975  
DATE: 2001-07-20  
TION NUMBER: US 60/287,724  
DATE: 2001-05-02  
TION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
ntIn version 3.0

no sapiens

366

61.8%; Score 13.6; DB 10; Length 60;  
ilarity 80.0%; Pred. No. 3e+03; 4; Indels 0; Gaps 0;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CAATCACAGTCTCTGCGG 21  
|||  
CAATCACTCTCTATACAG 37

RESULT 11  
US-09-908-975-14283/c  
; Sequence 14283, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRAN  
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14283  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-14283

Query Match 61.8%; Score 13.6; DB 10; Length 60;  
Best Local Similarity 80.0%; Pred. No. 3e+03; 4; Indels 0;  
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACAATCACAGTCTCTGCGGA 22  
|||  
Db 60 ACATTGACAGTCTCTGCGGA 41

RESULT 12

US-09-908-975-8908/c  
; Sequence 8908, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRAN  
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8908  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-8908

Query Match 60.9%; Score 13.4; DB 10; Length 60;  
Best Local Similarity 93.3%; Pred. No. 3.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 8 CACAGTCTCTGCGGA 22  
|||  
Db 16 CACAGTCTCTGAGGA 2

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us-10-090-326-6.max.rnpb

Publication US/10189256  
US20040005569A1  
TION: Antisense Oligonucleotide  
ada F. Baker  
san M. Freier  
meth W. Dobie  
TION: ANTISENSE MODULATION OF NF-KAPPA-B P50 SUBUNIT EXPRESSION  
PTS-0050  
TION NUMBER: US/10/189,256  
DATE: 2002-07-02  
ID NOS: 143

Official Sequence

TION: Antisense Oligonucleotide

60.0%; Score 13.2; DB 15; Length 20;  
larity 83.3%; Pred. No. 4.3e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ATCAGAGTCTCTGCGG 20  
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GTGACAGTCTCTGCGG 3

Publication US/10190366

US20040006031A1

TION:

holas M. Dean

san M. Freier

meth W. Dobie

TION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION

PTS-0023

TION NUMBER: US/10/190,366

DATE: 2002-07-02

ID NOS: 409

Official Sequence

TION: Antisense Oligonucleotide

60.0%; Score 13.2; DB 15; Length 20;  
larity 83.3%; Pred. No. 4.3e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCACAGTCTCTGCGG 21  
|||||  
TCATAGCCTCTGTGG 20

/c

Publication US/10190366

US20040006031A1

TION:

holas M. Dean

san M. Freier

meth W. Dobie

TION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION

PTS-0023

TION NUMBER: US/10/190,366

DATE: 2002-07-02

ID NOS: 409

SEQ ID NO 332  
LENGTH: 20  
TYPE: DNA  
ORGANISM: H. sapiens  
FEATURE:  
US-10-190-366-332

Query Match 60.0%; Score 13.2; DB 15; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 4 CAATCAGAGTCTCTGCGG 21

|||||

Db 18 CAATCATAGCCTCTGTGG 1

RESULT 16

US-09-840-743-77/c

Sequence 77, Application US/09840743

Publication No. US20030135890A1

GENERAL INFORMATION:

APPLICANT: Fischer, Robert L.

APPLICANT: Choi, Yeonhee

APPLICANT: Hannon, Mike

APPLICANT: Okamura, Jack Kishiro

APPLICANT: Tatarinova, Tatiana Valerievna

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Nucleic Acids That Control Plant Development

FILE REFERENCE: 023070-099910US

CURRENT APPLICATION NUMBER: US/09/840,743

CURRENT FILING DATE: 2001-04-23

PRIOR APPLICATION NUMBER: US 09/553,690

PRIOR FILING DATE: 2000-04-21

NUMBER OF SEQ ID NOS: 119

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 77

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: primer SKB-

US-09-840-743-77

Query Match 60.0%; Score 13.2; DB 10; Length 22;  
Best Local Similarity 83.3%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 GACAATCAGAGTCTCTGC 19

|||||

Db 18 GACAATAACCGTCTCTCC 1

RESULT 17

US-10-098-263B-65769

Sequence 65769, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 65769

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-65769

Query Match 60.0%; Score 13.2; DB 14; Length 25;



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ilarity 83.3%; Pred. No. 4.4e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

PCACAGTCTCTCGGGA 22
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TAAATGCTCTCTCGGGA 23

13912/c
2, Application US/10098263B
. US20030104410A1
ATION:
ttman, Michael
TION: Human Microarray
E: 3118.1
CATION NUMBER: US/10/098,263B
3 DATE: 2003-01-08
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
roarray Probe Sequence Listing Generator V 1.1
12

no sapien
13912
60.0%; Score 13.2; DB 14; Length 25;
ilarity 83.3%; Pred. No. 4.4e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AATCAGTCTCTCGG 20
|||||
AAACTCACTCTCTCGG 1

15691
1, Application US/10098263B
. US20030104410A1
ATION:
ttman, Michael
TION: Human Microarray
E: 3118.1
CATION NUMBER: US/10/098,263B
3 DATE: 2003-01-08
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
roarray Probe Sequence Listing Generator V 1.1
91

no sapien
15691
60.0%; Score 13.2; DB 14; Length 25;
ilarity 83.3%; Pred. No. 4.4e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ATCAGTCTCTCGG 21
|||||
ATCATATCTCTCGG 19

23312/c
2, Application US/10098263B
. US20030104410A1
ATION:
ttman, Michael
TION: Human Microarray
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FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 123312
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-123312

Query Match 60.0%; Score 13.2; DB 14; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 3 ACAATCACAGTCTCTCGG 20
Db 18 ACAACTCACTCTCTCGG 1

RESULT 21
US-09-893-615-73/c
Sequence 73, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTE
POSITIVE BACTERIA
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-893-615-73

Query Match 60.0%; Score 13.2; DB 9; Length 35;
Best Local Similarity 72.2%; Pred. No. 4.6e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0;
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lication US/09215163  
US20030170248A1  
TION: HUMANIZED MONOCLONAL ANTIBODIES THAT PROTECT AGAINST  
SON, Jeffrey R.  
3, Hing  
TION: SHIGA TOXIN INDUCED DISEASE  
TION: CELSA, Angela  
ATT, Clare K.  
TION: HUMANIZED MONOCLONAL ANTIBODIES THAT PROTECT AGAINST  
TION: SHIGA TOXIN INDUCED DISEASE  
: 04995.0032-00000  
TION NUMBER: US/09/215,163  
DATE: 1998-12-18  
ID NOS: 44  
tIn Ver. 2.0

Official Sequence

TION: Description of Artificial Sequence: Synthetic  
TION: Oligonucleotide

60.0%; Score 13.2; DB 10; Length 35;  
larity 72.2%; Pred. No. 4.6e+03;  
Conservative 3; Mismatches 2; Indels 0; Gaps 0;

TCACAGTCTCTGCGG 21  
||:||||:|  
TCACGTCTCYKAG 15

plication US/10601171  
US20040013673A1  
T: Fischer, Gerald W.  
Schuman, Richard F.  
Wong, Hing  
Stinson, Jeffrey L.  
INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND  
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM  
POSITIVE BACTERIA

F SEQUENCES: 89  
NDENCE ADDRESS:  
RESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &  
DUNNER, LLP  
BET: 1300 I Street, NW  
Y: Washington

NTY: USA  
: 20005-3315  
READABLE FORM:  
IUM TYPE: Floppy disk  
PUTER: IBM PC compatible  
RATING SYSTEM: PC-DOS/MS-DOS  
TWARE: PatentIn Release #1.0, Version #1.30  
APPLICATION DATA:  
PLICATION NUMBER: US/10/601,171  
ING DATE: 23-Jun-2003  
/AGENT INFORMATION:  
IE: Einaudi, Carol P.  
ISTRATION NUMBER: 32,220  
ERENCE/DOCKET NUMBER: 04995.0041-00000

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-10-601-171-73

Query Match 60.0%; Score 13.2; DB 15; Length 35;  
Best Local Similarity 72.2%; Pred. No. 4.6e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0;

QY 4 CAATCACAGTCTCTGCGG 21  
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Db 32 CACTCAGTCTCYKAG 15

RESULT 24  
US-10-349-143-1473  
; Sequence 1473, Application US/10349143  
; Publication No. US2004000584A1  
GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a hi  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,85  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,73  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,61  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 1473  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 99-25379-389 : polymorphic base C or T  
US-10-349-143-1473

Query Match 60.0%; Score 13.2; DB 15; Length 47;  
Best Local Similarity 75.0%; Pred. No. 4.8e+03;  
Matches 15; Conservative 1; Mismatches 4; Indels 0;

QY 2 GACATCACAGTCTCTGCGG 21  
||:||||:|  
Db 19 GAGCAYCACACTCTGCGG 38

RESULT 25  
US-10-131-827-852/c  
; Sequence 852, Application US/10131827  
; Publication No. US20040009479A1  
GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MC

09:38:24 2004

us-10-090-326-6.max.rnpb

UTION: CHRONIC INFLAMMATORY DISEASES  
: 506612000120  
ATION NUMBER: US/10/131,827  
DATE: 2002-09-06  
ION NUMBER: US 10/006,290  
ATE: 2001-10-22  
ION NUMBER: US 60/296,764  
ATE: 2001-06-08  
ID NOS: 9090  
ntIn version 3.1

io sapiens

50.0%; Score 13.2; DB 15; Length 50;  
larity 83.3%; Pred. No. 4.8e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

\*CAGAGTCTCTGCGGA 22  
||| ||||| |||  
\*CATAGTCTCTGGGTA 4

.46/c  
Application US/09908975  
US20030165843A1

ATION: SHAN, Avi  
SSERMAN, Alon  
NTZ, Eli  
NTZ, Liat  
HIGER, Simchon

UTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
TION: THAT POPULATE A TRANSCRIPTOME

3: 36688-0005  
ATION NUMBER: US/09/908,975  
DATE: 2001-07-20  
ION NUMBER: US 60/287,724  
DATE: 2001-05-02  
ION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
ntIn version 3.0

io sapiens  
146

60.0%; Score 13.2; DB 10; Length 60;  
larity 83.3%; Pred. No. 4.9e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

\*TCAGAGTCTCTGCGG 21  
||| ||||| |||  
\*TCATAGTCTCTGCTG 24

5781/c  
Application US/10098263B  
US20030104410A1

ATION: tman, Michael  
TION: Human Microarray  
3: 3118.1  
ATION NUMBER: US/10/098,263B  
DATE: 2003-01-08  
ION NUMBER: 60/276,759  
DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 65781  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-65781

Query Match 59.1%; Score 13; DB 14; Length 25;  
Best Local Similarity 76.2%; Pred. No. 5.6e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGG 21  
||| ||||| |||  
Db 25 AGAGCCTCAGAGTCTCTGTGG 5

RESULT 28

US-10-098-263B-113313/c  
; Sequence 113313, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 113313  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-113313

Query Match 59.1%; Score 13; DB 14; Length 25;  
Best Local Similarity 76.2%; Pred. No. 5.6e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGG 21  
||| ||||| |||  
Db 22 AGACTCTCGAGTCACTGCGG 2

RESULT 29

US-10-098-263B-113314/c  
; Sequence 113314, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 113314  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-113314

Query Match 59.1%; Score 13; DB 14; Length 25;  
Best Local Similarity 76.2%; Pred. No. 5.6e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGG 21  
||| ||||| |||  
Db 22 AGACTCTCGTGTACTGCGG 2

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RESULT 32
US-09-795-006A-40/c
; Sequence 40, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: oligonucleotide sequence derived from multiple
; OTHER INFORMATION: endothelial growth factor
US-09-795-006A-40

Query Match          59.1%; Score 13; DB 9; Length 60;
Best Local Similarity 76.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 2 GACAAATCACAGTCTCTCGCGA 22
   ||||| ||||| |||||
Db 54 GCCAATCACACTTCTCTCGCGA 34

RESULT 33
US-09-908-975-19195
; Sequence 19195, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRAN
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19195
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-19195

Query Match          59.1%; Score 13; DB 10; Length 60;
Best Local Similarity 76.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 2 GACAAATCACAGTCTCTCGCGA 22
   ||||| ||||| |||||
Db 10 GCCCATGACTGTCTCTCGAGA 30

RESULT 34
US-09-908-975-19195
; Sequence 19195, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRAN
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19195
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-19195

Query Match          59.1%; Score 13; DB 15; Length 50;
Best Local Similarity 76.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 2 GACAAATCACAGTCTCTCGCG 21
   ||||| ||||| |||||
Db 10 GCCCATGACTGTCTCTCAGG 4
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408/c
; Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, AVI
; APPLICANT: WASSERMAN, ALON
; APPLICANT: MINTZ, ELI
; APPLICANT: MINTZ, LIAT
; APPLICANT: FAIGLER, SIMCHON
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRA
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 23253
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-23253

Query Match          59.1%; Score 13; DB 10; Length 60;
Best Local Similarity 76.2%; Pred. No. 6.2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGAATCACAGTCTCTGCGG 21
    |||||
DB 14 ACATTCAGTCTCAGCTG 34
    |||||

RESULT 37
US-10-156-306-4767
; Sequence 4767, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases
; FILE REFERENCE: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MEHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4767
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-4767

Query Match          58.2%; Score 12.8; DB 14; Length 17;
Best Local Similarity 62.5%; Pred. No. 6.7e+03;
Matches 10; Conservative 4; Mismatches 2; Indels 0;

QY 4 CAATCACAGTCTCTGC 19
    |||||
DB 2 CAAUCCAGUCUCUUC 17
    |||||

RESULT 38
US-10-156-306-5763
; Sequence 5763, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases
; FILE REFERENCE: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MEHB01-664-A (400/050)

```

ATION NUMBER: US/10/156,306  
DATE: 2002-05-28  
ID NOS: 8013  
ntin version 3.0

o sapiens  
3

58.2%; Score 12.8; DB 14; Length 17;  
larity 62.5%; Pred. No. 6.7e+03;  
Conservative 4; Mismatches 2; Indels 0; Gaps 0;

TCACAGTCTCTGC 19  
: |||||:|:  
UCCAGUCUCUUC 16

Publication US/09833067  
02005488A1

TION:

ANLEY, PETER

NICH, KENNETH

TION: DISSOCIATED PILLI, THEIR PRODUCTION AND USE

: 050939/0102

ATION NUMBER: US/09/833,067

DATE: 2001-04-12

ION NUMBER: 60/196,493

ATE: 2000-04-12

ID NOS: 26

ntin Ver. 2.1

ificial Sequence

TION: Description of Artificial Sequence: Primer

58.2%; Score 12.8; DB 9; Length 20;  
larity 87.5%; Pred. No. 6.9e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CAATCAGTCTC 16  
: |||||:  
3AATCGCAGTCTC 3

Publication US/09833079  
020142008A1

TION:

ANLEY, PETER

NICH, KENNETH

AMIDT, M. ALEXANDER

TION: IMMUNOGENIC PILLI PRESENTING FOREIGN PEPTIDES, THEIR

TION: PRODUCTION AND USE

: 050939/0104

ATION NUMBER: US/09/833,079

DATE: 2001-04-12

ID NOS: 39

ntin Ver. 2.1

ificial Sequence

TION: Description of Artificial Sequence: Primer

Query Match 58.2%; Score 12.8; DB 9; Length 20;  
Best Local Similarity 87.5%; Pred. No. 6.9e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 AGACAATCAGTCTC 16  
DB 18 AGAGAATCGCAGTCTC 3

RESULT 41

US-09-797-207-16

; Sequence 16, Application US/09797207

; Patent No. US20020098563A1

; GENERAL INFORMATION:

; APPLICANT: KORCZAK, BOZENA

; TITLE OF INVENTION: NOVEL CORE 2 BETA-1, 6-N-ACETYLGLYCOSAMINYLT

; FILE REFERENCE: GLYCO-7P1

; CURRENT APPLICATION NUMBER: US/09/797,207

; CURRENT FILING DATE: 2001-03-02

; EARLIER APPLICATION NUMBER: 09/495,913

; EARLIER FILING DATE: 2000-02-02

; EARLIER APPLICATION NUMBER: 60/118,674

; EARLIER FILING DATE: 1999-02-03

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 16

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-797-207-16

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Best Local Similarity 87.5%; Pred. No. 7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 7 TCACAGTCTCTGCGGA 22  
DB 2 TCACAGTCTCTGTTGA 17

RESULT 42

US-10-445-318-16

; Sequence 16, Application US/10445318

; Publication No. US20040033521A1

; GENERAL INFORMATION:

; APPLICANT: KORCZAK, BOZENA

; TITLE OF INVENTION: NOVEL CORE 2 BETA-1, 6-N-ACETYLGLYCOSAMINYLT

; FILE REFERENCE: GLYCO-7P1

; CURRENT APPLICATION NUMBER: US/10/445,318

; CURRENT FILING DATE: 2003-05-27

; PRIOR APPLICATION NUMBER: US/09/797,207

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 09/495,913

; PRIOR FILING DATE: 2000-02-02

; PRIOR APPLICATION NUMBER: 60/118,674

; PRIOR FILING DATE: 1999-02-03

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 16

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer

US-10-445-318-16

Query Match 58.2%; Score 12.8; DB 12; Length 22;  
Best Local Similarity 87.5%; Pred. No. 7e+03;

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us-10-090-326-6.max.rnpb

Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
ACAGTCTCTGGCGA 22  
|||||  
ACAGTCTCTGGTGA 17

2151/c  
Application US/10098263B  
US20030104410A1  
tman, Michael  
TION: Human Microarray  
3: 3118.1  
ATION NUMBER: US/10/098,263B  
3 DATE: 2003-01-08  
TION NUMBER: 60/276,759  
DATE: 2001-03-16  
ID NOS: 131066  
array Probe Sequence Listing Generator V 1.1

no sapien  
2151

58.2%; Score 12.8; DB 14; Length 25;  
larity 87.5%; Pred. No. 7.1e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AAATCACAGTCTCT 17  
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AAATCACGGTCACT 1

1483  
Application US/10098263B  
US20030104410A1  
TION:  
tman, Michael  
TION: Human Microarray  
3: 3118.1  
ATION NUMBER: US/10/098,263B  
3 DATE: 2003-01-08  
TION NUMBER: 60/276,759  
DATE: 2001-03-16  
ID NOS: 131066  
array Probe Sequence Listing Generator V 1.1

no sapien  
1483

58.2%; Score 12.8; DB 14; Length 25;  
larity 87.5%; Pred. No. 7.1e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ACAGTCTCTGGCGA 22  
|||||  
ACAGTCTCTGGGAA 21

1605  
Application US/10098263B  
US20030104410A1  
TION:  
tman, Michael  
TION: Human Microarray  
3: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 86605  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-86605  
  
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Best Local Similarity 87.5%; Pred. No. 7.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;  
  
QY 2 GACAATCACAGTCTCT 17  
|||||  
Db 8 GACAATCACAGTCTCT 23  
  
Search completed: February 29, 2004, 13:42:33  
Job time : 149.143 secs

09:38:25 2004

us-10-090-326-6.max.rst

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
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February 29, 2004, 08:43:19 ; Search time 1651.43 Seconds  
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JS-10-090-326-6  
22  
l agacaatcacagtctctgogga 22  
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Japop 10.0 , Gapext 1.0  
37513289 seqs, 14931090276 residues  
hits satisfying chosen parameters: 203984  
length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

EST: \*  
: em estba: \*  
: em esthum: \*  
: em estin: \*  
: em estnu: \*  
: em estov: \*  
: em estpl: \*  
: em estro: \*  
: em htc: \*  
: gb est1: \*  
: gb est2: \*  
: gb htc: \*  
: gb est3: \*  
: gb est4: \*  
: gb est5: \*  
: em estfun: \*  
: em estom: \*  
: em gss hum: \*  
: em gss inv: \*  
: em gss pln: \*  
: em gss vrt: \*  
: em gss fun: \*  
: em gss man: \*  
: em gss mus: \*  
: em gss pro: \*  
: em gss rod: \*  
: em gss phg: \*  
: em gss vrl: \*  
: gb gss1: \*  
: gb gss2: \*

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er than or equal to the score of the result being printed,  
ved by analysis of the total score distribution.

SUMMARIES

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61.8	58	9	AA211707			AA211707 ZQ84f11.r

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13.2	60.0	52	BM448549			BM448549
13.2	60.0	59	BG527761			BG527761
13.2	60.0	60	BI908468			BI908468
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12.6	57.3	43	AZ833640			AZ833640
12.6	57.3	45	AZ955701			AZ955701
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12.6	57.3	50	AU105958			AU105958
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12.4	56.4	43	BH902203			BH902203
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11.8	53.6	55	AI154882			AI154882
11.6	52.7	29	AZ760190			AZ760190
11.6	52.7	32	BH792384			BH792384
11.6	52.7	33	AU256484			AU256484
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11.6	52.7	58	AA107040			AA107040
11.6	52.7	60	BQ454632			BQ454632
11.6	52.7	60	BQ454764			BQ454764
11.6	52.7	60	CD962191			CD962191
11.6	52.7	60	BH863067			BH863067



51.8	20	28	AZ412898	11	50.0	47	14	T25588	T25588
51.8	29	14	CF861062	11	50.0	48	28	BH840707	BH840707
51.8	30	14	CF860995	11	50.0	50	9	AI127829	AI127829
51.8	31	9	AA863835	11	50.0	50	9	AI102391	AI102391
51.8	31	28	AZ437063	11	50.0	50	9	AI102391	AI102391
51.8	31	28	BH851766	11	50.0	50	29	TA208F04Q	TA208F04Q
51.8	31	28	BZ353562	11	50.0	51	10	AA461289	AA461289
51.8	34	28	AZ785142	11	50.0	51	28	B04190	B04190
51.8	37	9	AA444863	11	50.0	51	29	CG802231	CG802231
51.8	39	12	BJ075771	11	50.0	52	9	AA967363	AA967363
51.8	45	28	AZ502422	11	50.0	52	14	AI214100	AI214100
51.8	46	9	AA607492	11	50.0	52	14	CA795142	CA795142
51.8	47	14	AI2643	11	50.0	52	14	CB22147	CB22147
51.8	48	28	AZ603153	11	50.0	52	28	AZ773269	AZ773269
51.8	49	28	AZ603153	11	50.0	52	28	BH862019	BH862019
51.8	49	28	AZ768953	11	50.0	53	28	BH852239	BH852239
51.8	50	9	AI106551	11	50.0	53	28	BH850069	BH850069
51.8	50	9	AI106829	11	50.0	55	29	AB081958	AB081958
51.8	50	9	AI106909	11	50.0	56	28	AZ630437	AZ630437
51.8	50	9	AI108071	11	50.0	56	29	AL762888	AL762888
51.8	50	29	AI940148	11	50.0	57	9	AA790616	AA790616
51.8	52	10	BF641940	11	50.0	57	9	AA798465	AA798465
51.8	52	14	CF300173	11	50.0	57	14	CB913876	CB913876
51.8	53	14	CF291012	11	50.0	58	9	BH909214	BH909214
51.8	54	28	CC326783	11	50.0	58	10	BE057307	BE057307
51.8	57	28	AZ482281	11	50.0	58	28	BH912876	BH912876
51.8	58	14	CB548541	11	50.0	58	28	CC053444	CC053444
51.8	60	9	AL850332	11	50.0	60	28	EZ378400	EZ378400
50.9	29	28	AZ424753	11	50.0	60	28	EZ378520	EZ378520
50.9	31	10	BF666846	11	50.0	60	28	AZ790062	AZ790062
50.9	31	28	AZ810463	11	50.0	60	28	AZ861517	AZ861517
50.9	36	28	AZ800134	11	50.0	60	28	BZ592652	BZ592652
50.9	37	28	AZ827785	11	50.0	60	28	AZ837449	AZ837449
50.9	37	28	DR32X10S	11	50.0	60	28	BQ587774	BQ587774
50.9	42	28	AZ511989	11	50.0	60	28	BQ587775	BQ587775
50.9	43	14	H41669	11	50.0	60	28	AL485920	AL485920
50.9	43	28	AZ795373	11	50.0	60	28	AL462387	AL462387
50.9	47	28	BH633020	11	50.0	60	28	AA108667	AA108667
50.9	49	9	AA693305	11	50.0	60	28	BI832750	BI832750
50.9	50	9	AI103545	11	50.0	60	28	AZ658401	AZ658401
50.9	50	9	AI107254	11	50.0	60	28	AL454924	AL454924
50.9	51	14	N99012	11	50.0	60	28	AL452314	AL452314
50.9	53	14	CB922548	11	50.0	60	28	AL473134	AL473134
50.9	53	14	CD023923	11	50.0	60	28	AL459084	AL459084
50.9	54	28	BZ382315	11	50.0	60	28	AZ806846	AZ806846
50.9	55	9	AI625660	11	50.0	60	28	AL486044	AL486044
50.9	55	10	BE374434	11	50.0	60	28	AZ324505	AZ324505
50.9	55	28	BH861943	11	50.0	60	28	BH846254	BH846254
50.9	56	10	BF013330	11	50.0	60	28	BH909818	BH909818
50.9	56	12	BZ058421	11	50.0	60	28	AG218427	AG218427
50.9	56	28	AZ603330	11	50.0	60	28	BX187126	BX187126
50.9	57	12	BG152248	11	50.0	60	28	AZ771653	AZ771653
50.9	58	9	AI963579	11	50.0	60	28	BH810095	BH810095
50.9	58	9	AU009179	11	50.0	60	28	BH909806	BH909806
50.9	58	28	AZ818314	11	50.0	60	28	AA763910	AA763910
50.9	60	9	AZ572707	11	50.0	60	28	R93342	R93342
50.9	60	28	CC456672	11	50.0	60	28	BH863323	BH863323
50.0	25	28	BZ352906	11	50.0	60	28	AL456734	AL456734
50.0	28	9	AA138008	11	50.0	60	28	H21630	H21630
50.0	29	28	AZ658502	11	50.0	60	28	AZ833880	AZ833880
50.0	34	9	AI116347	11	50.0	60	28	AB082470	AB082470
50.0	34	13	CO1088	11	50.0	60	28	AL769815	AL769815
50.0	34	29	AI943585	11	50.0	60	28	AL769815	AL769815
50.0	37	28	AZ662395	11	50.0	60	28	BX203428	BX203428
50.0	38	28	AZ410352	11	50.0	60	28	AA402658	AA402658
50.0	42	14	D67715	11	50.0	60	28	AZ634499	AZ634499
50.0	42	28	AZ579512	11	50.0	60	28	AI093925	AI093925
50.0	44	28	AZ825920	11	50.0	60	28	AZ659694	AZ659694
50.0	44	29	CG892045	11	50.0	60	28	AZ807976	AZ807976
50.0	44	29	AB082470	11	50.0	60	28	AL787018	AL787018
50.0	45	28	AZ439466	11	50.0	60	28	AU103208	AU103208
50.0	45	28	BZ357956	11	50.0	60	28		

49.1	50	9	AU105007	AU105007	AU105007	10.6	48.2	52	10	BE321854
49.1	50	9	AU105007	AU105007	AU105007	10.6	48.2	52	14	CB226148
49.1	50	9	AU105008	AU105008	AU105008	10.6	48.2	52	28	BZ768479
49.1	50	9	AU105008	AU105008	AU105008	10.6	48.2	53	29	CC516008
49.1	50	9	AU105010	AU105010	AU105010	10.6	48.2	53	29	CG892142
49.1	50	9	AU105010	AU105010	AU105010	10.6	48.2	53	29	AV689957
49.1	50	14	CF291606	CF291606	1400T--0	10.6	48.2	54	12	BJ062424
49.1	50	28	AZ351661	AZ351661	IM0089M17	10.6	48.2	54	28	AZ776469
49.1	50	29	TA330E01Q	TA330E01Q	TA330E01Q	10.6	48.2	55	9	AA886912
49.1	51	13	BQ548575	BQ548575	rd33e09.y	10.6	48.2	55	9	AV619150
49.1	52	9	AA903054	AA903054	ck51e07.s	10.6	48.2	55	10	BE057857
49.1	52	9	AI431224	AI431224	sa22c10.y	10.6	48.2	55	14	CB357612
49.1	52	14	CB056129	CB056129	NISC_jj13	10.6	48.2	55	28	BZ377638
49.1	52	29	BX555460	BX555460	Arabidops	10.6	48.2	55	29	CG719978
49.1	54	9	AA916665	AA916665	oh85g02.s	10.6	48.2	55	29	TA373B02Q
49.1	54	9	AI926524	AI926524	wo46a08.x	10.6	48.2	56	9	AA654695
49.1	54	28	BH811867	BH811867	SALK_0602	10.6	48.2	56	9	AA487913
49.1	54	28	BZ594263	BZ594263	SALK_0837	10.6	48.2	56	9	AA582069
49.1	54	29	AI938861	AI938861	Arabidops	10.6	48.2	57	9	AI582069
49.1	55	9	AI091130	AI091130	qa46e02.s	10.6	48.2	57	14	CF864827
49.1	55	9	AI241482	AI241482	qr69c04.x	10.6	48.2	57	28	CC060282
49.1	55	14	H84389	H84389	YV85G10.r1	10.6	48.2	57	29	BX661466
49.1	55	28	AZ325145	AZ325145	IM0047J23	10.6	48.2	58	9	AA711331
49.1	55	28	CC035254	CC035254	3591_1_74	10.6	48.2	58	12	BJ035240
49.1	57	10	BF507211	BF507211	359P-24a	10.6	48.2	58	28	AZ371514
49.1	57	13	BQ625664	BQ625664	ph9h005.y	10.6	48.2	59	28	AZ402760
49.1	57	28	AZ481308	AZ481308	IM0303P24	10.6	48.2	59	28	AZ848297
49.1	57	29	AI938862	AI938862	Arabidops	10.6	48.2	59	29	BX894663
49.1	57	29	BX547649	BX547649	Arabidops	10.6	48.2	60	10	BE023743
49.1	58	9	AA769106	AA769106	oa74g08.s	10.6	48.2	60	12	BG315430
49.1	58	9	AI324804	AI324804	mc33c06.x	10.6	48.2	60	28	AZ758212
49.1	58	9	AA260418	AA260418	vb06a04.r	10.6	48.2	60	28	BH789942
49.1	58	29	BX657531	BX657531	Arabidops	10.6	48.2	60	29	CNS06E2T
49.1	59	28	AZ371127	AZ371127	IM0122L06	10.6	48.2	60	29	DME545946
49.1	60	28	AZ774911	AZ774911	2M0004F13	10.4	47.3	21	9	AB088506
49.1	60	29	AI951291	AI951291	Arabidops	10.4	47.3	27	28	AZ780337
49.1	62	28	AZ419130	AZ419130	IM0195D03	10.4	47.3	27	28	AZ812632
49.1	62	28	AZ604981	AZ604981	IM0425M22	10.4	47.3	28	28	AZ310671
49.1	62	28	BH861186	BH861186	SALK_0346	10.4	47.3	29	14	CF317180
49.1	62	29	BX533801	BX533801	Arabidops	10.4	47.3	31	9	AU257331
49.1	62	32	AZ780813	AZ780813	2M0018I20	10.4	47.3	31	12	BI768049
49.1	62	34	AA108667	AA108667	mp30h11.r	10.4	47.3	32	28	AZ657691
49.1	62	35	AU244000	AU244000	AU244000	10.4	47.3	32	28	AZ635323
49.1	62	37	BX285618	BX285618	Arabidops	10.4	47.3	32	29	BX894321
49.1	62	38	AI45802	AI45802	HUMG03019	10.4	47.3	33	28	AZ828702
49.1	62	38	AI753738	AI753738	Arabidops	10.4	47.3	34	9	AA101200
49.1	62	39	BE388093	BE388093	601284409	10.4	47.3	35	28	AZ664145
49.1	62	39	TA135601Q	TA135601Q	Arabidops	10.4	47.3	35	29	TA83DC02P
49.1	62	39	TA150B10P	TA150B10P	Arabidops	10.4	47.3	36	28	AZ307723
49.1	62	40	AA226145	AA226145	nc09f09.r	10.4	47.3	37	28	AZ596892
49.1	62	40	AZ422365	AZ422365	IM0201H03	10.4	47.3	37	29	CC798598
49.1	62	40	AZ591528	AZ591528	IM0401K11	10.4	47.3	37	29	CG712147
49.1	62	40	AI949623	AI949623	Arabidops	10.4	47.3	37	29	CG712147
49.1	62	41	AZ776402	AZ776402	2M0010B05	10.4	47.3	37	29	CG712147
49.1	62	41	BZ595938	BZ595938	SALK_0904	10.4	47.3	38	29	AZ597945
49.1	62	43	CC940781	CC940781	01S0591-0	10.4	47.3	38	29	BX660257
49.1	62	43	CL002012	CL002012	01S0614-0	10.4	47.3	38	29	BX660257
49.1	62	45	AZ320120	AZ320120	IM0404F02	10.4	47.3	40	9	AA338064
49.1	62	45	AI764340	AI764340	Arabidops	10.4	47.3	42	29	TA115G05P
49.1	62	46	AI242223	AI242223	qb87d04.x	10.4	47.3	42	29	TA232A04Q
49.1	62	47	BX002665	BX002665	Arabidops	10.4	47.3	43	9	AI079098
49.1	62	47	BZ763638	BZ763638	SALK_1200	10.4	47.3	43	14	W95731
49.1	62	50	AI661103	AI661103	AL661103	10.4	47.3	43	28	BH810212
49.1	62	50	AI03880	AI03880	Arabidops	10.4	47.3	44	9	AI153789
49.1	62	50	AI03931	AI03931	Arabidops	10.4	47.3	45	28	AZ809363
49.1	62	50	AI05229	AI05229	Arabidops	10.4	47.3	46	28	AZ501490
49.1	62	50	AI06245	AI06245	Arabidops	10.4	47.3	47	28	AZ795054
49.1	62	50	AI06829	AI06829	Arabidops	10.4	47.3	47	28	BH904732
49.1	62	50	CD028816	CD028816	mgc5010x0	10.4	47.3	47	29	BX201354
49.1	62	50	AZ841710	AZ841710	2M0139C22	10.4	47.3	48	14	CF298019
49.1	62	50	CG800335	CG800335	1118010B1	10.4	47.3	49	9	AV960480
49.1	62	51	AV838411	AV838411	Arabidops	10.4	47.3	49	28	BH608677
49.1	62	52	BF631987	BF631987	NF025C05D	10.4	47.3	49	28	BZ384969
49.1	62	52	10	BF631987	NF025C05D	10.4	47.3	49	29	BX531144

47.3	50	9	AU105499	AU105499	AU105499	C	443	10.2	46.4	38	28	AZ439902	AZ439990
47.3	50	9	AU105500	AU105500	AU105500	444	10.2	46.4	38	28	AZ791447	AZ791444	
47.3	50	9	AU105502	AU105502	AU105502	445	10.2	46.4	38	29	AG239701	AG239701	
47.3	50	9	AU105569	AU105569	AU105569	446	10.2	46.4	39	29	CG719218	CG719218	
47.3	50	9	AU105744	AU105744	AU105744	447	10.2	46.4	40	14	H43763	H43763	
47.3	50	9	AU106167	AU106167	AU106167	448	10.2	46.4	40	14	R50450	R50450	
47.3	50	9	AU107197	AU107197	AU107197	449	10.2	46.4	40	28	AZ975594	AZ975594	
47.3	50	9	AU107893	AU107893	AU107893	C 450	10.2	46.4	41	28	BH893295	BH893295	
47.3	50	9	AU107901	AU107901	AU107901	C 451	10.2	46.4	41	29	CG708849	CG708849	
47.3	50	9	AA591203	AA591203	AA591203	C 452	10.2	46.4	41	14	H21630	H21630	
47.3	50	13	C00960	C00960	HUMG500331	C 453	10.2	46.4	44	28	CC457233	CC457233	
47.3	50	28	AZ329369	AZ329369	LM0053002	454	10.2	46.4	45	12	BH118003	BH118003	
47.3	51	14	N99012	N99012	za67a06.r1	C 455	10.2	46.4	45	28	BH811345	BH811345	
47.3	51	28	AZ314162	AZ314162	LM0030014	C 456	10.2	46.4	45	29	BX167809	BX167809	
47.3	51	28	AL764952	AL764952	Arabidops	C 457	10.2	46.4	45	29	BX562880	BX562880	
47.3	51	29	BX662168	BX662168	Arabidops	C 458	10.2	46.4	46	9	AI153463	AI153463	
47.3	52	9	AA579113	AA579113	nf35c08.s	C 459	10.2	46.4	48	9	AI069651	AI069651	
47.3	52	10	BF098948	BF098948	601750445	C 460	10.2	46.4	48	14	CB210335	CB210335	
47.3	52	29	BX895866	BX895866	Arabidops	461	10.2	46.4	48	28	AZ843479	AZ843479	
47.3	53	9	AV679304	AV679304	AV679304	462	10.2	46.4	49	9	AA878633	AA878633	
47.3	53	13	BQ253288	BQ253288	san65b11.	463	10.2	46.4	49	9	AA154640	AA154640	
47.3	53	28	BH810529	BH810529	SALK 0497	464	10.2	46.4	49	10	BF722018	BF722018	
47.3	53	28	BH810530	BH810530	SALK 0497	C 465	10.2	46.4	49	28	AZ425231	AZ425231	
47.3	53	28	BH905779	BH905779	SALK 1077	C 466	10.2	46.4	49	28	AZ487167	AZ487167	
47.3	53	28	BZ662063	BZ662063	SALK 0255	C 467	10.2	46.4	50	9	AI581704	AI581704	
47.3	53	28	AZ679570	AZ679570	LM0367M02	468	10.2	46.4	50	9	AI02525	AI02525	
47.3	54	28	AZ617117	AZ617117	LM0448C17	C 469	10.2	46.4	50	9	AI05219	AI05219	
47.3	54	28	B01570	B01570	CSRL-13396-	C 470	10.2	46.4	50	9	AI05221	AI05221	
47.3	54	28	BH905359	BH905359	SALK 1059	C 471	10.2	46.4	50	9	AI05222	AI05222	
47.3	54	28	TA288F01Q	TA288F01Q	AL486059	C 472	10.2	46.4	50	9	AI05223	AI05223	
47.3	54	28	BH848589	BH848589	SALK 0685	C 473	10.2	46.4	50	9	AI05226	AI05226	
47.3	55	29	CG727990	CG727990	LM0080C20	C 474	10.2	46.4	50	9	AI05228	AI05228	
47.3	56	28	AZ345891	AZ345891	SALK 0960	C 475	10.2						

46.4	57	28	AZ606962	AZ606962	1M0423I08	C 589	10	45.5	49	9	AA588107	AA588107
46.4	57	28	AZ799654	AZ799654	2M0057C14	590	10	45.5	49	12	BJ034094	BJ034094
46.4	57	28	BZ770470	BZ770470	SALK_1434	C 591	10	45.5	49	28	AZ788840	AZ788840
46.4	58	9	AL887120	AL887120	AL887120	592	10	45.5	49	28	AZ852964	AZ852964
46.4	58	13	BX622133	BX622133	BX622133	593	10	45.5	50	9	AU102591	AU102591
46.4	58	14	CF117521	CF117521	fp620_41	C 594	10	45.5	50	9	AU103250	AU103250
46.4	58	28	AZ820315	AZ820315	2M009XK22	C 595	10	45.5	50	9	AU103496	AU103496
46.4	58	28	BH911876	BH911876	SALK_0726	C 596	10	45.5	50	9	AU103942	AU103942
46.4	58	28	BZ664694	BZ664694	SALK_1099	C 597	10	45.5	50	9	AU103944	AU103944
46.4	59	9	AI246105	AI246105	q128g05.x	598	10	45.5	50	9	AU104460	AU104460
46.4	59	9	AI902424	AI902424	CM-BT006-	599	10	45.5	50	9	AU1044751	AU1044751
46.4	59	28	AZ799451	AZ799451	2M0056N19	600	10	45.5	50	9	AU104921	AU104921
46.4	59	28	BH790579	BH790579	SALK_0573	601	10	45.5	50	9	AU104999	AU104999
46.4	59	28	BZ53776	BZ53776	BZ53776	602	10	45.5	50	9	AU105100	AU105100
46.4	60	9	AU255711	AU255711	AU255711	603	10	45.5	50	9	AU105503	AU105503
46.4	60	10	BF638152	BF638152	NF032F02P	604	10	45.5	50	9	AU106131	AU106131
46.4	60	14	CD963913	CD963913	SDY_213_G	605	10	45.5	50	9	AU106243	AU106243
46.4	60	29	AL752218	AL752218	Arabidops	606	10	45.5	50	9	AU106245	AU106245
46.4	60	29	AL752219	AL752219	Arabidops	C 607	10	45.5	50	9	AU108034	AU108034
46.4	60	29	AZ514533	AZ514533	1M0361H08	C 608	10	45.5	50	14	T11356	T11356
46.4	60	29	AG261847	AG261847	Lotus cor	C 609	10	45.5	51	9	AA989603	AA989603
46.4	60	29	AZ957070	AZ957070	2M0223M14	C 610	10	45.5	51	9	AL887036	AL887036
46.4	60	29	BZ593155	BZ593155	SALK_0622	C 611	10	45.5	51	28	AZ768265	AZ768265
46.4	60	29	TA184H01P	TA184H01P	AL474762	C 612	10	45.5	51	28	AZ917839	AZ917839
46.4	60	29	AZ52971	AZ52971	LM0254A10	C 613	10	45.5	51	28	AZ917868	AZ917868
46.4	60	29	BH792448	BH792448	SALK_0642	C 614	10	45.5	51	28	AZ990935	AZ990935
46.4	60	29	BJ041432	BJ041432	BJ041432	C 615	10	45.5	51	28	BZ766946	BZ766946
46.4	60	29	AZ863661	AZ863661	2M0171E24	C 616	10	45.5	51	28	CC040051	CC040051
46.4	60	29	BH862997	BH862997	SALK_0929	617	10	45.5	52	9	AA068274	AA068274
46.4	60	29	BI330146	BI330146	602983757	618	10	45.5	52	9	AA627779	AA627779
46.4	60	29	BH904984	BH904984	SALK_1054	619	10	45.5	52	10	AW697135	AW697135
46.4	60	29	AZ821716	AZ821716	2M0039A10	620	10	45.5	52	12	BI858951	BI858951
46.4	60	29	AZ465734	AZ465734	LM0275A22	C 621	10	45.5	52	12	BM076700	BM076700
46.4	60	29	AA866679	AA866679	ud07b12.x	622	10	45.5	52	14	H28465	H28465
46.4	60	29	AI188273	AI188273	qd11g10.x	623	10	45.5	52	14	UI7529	UI7529
46.4	60	29	AI856794	AI856794	sb78a12.y	624	10	45.5	52	28	AZ356499	AZ356499
46.4	60	29	H98928	H98928	yx11c11.r1	625	10	45.5	52	28	B03518	B03518
46.4	60	29	CC456051	CC456051	SALK_0933	C 626	10	45.5	52	28	B33728	B33728
46.4	60	29	AG262121	AG262121	Lotus cor	C 627	10	45.5	52	28	BZ769458	BZ769458
46.4	60	29	AZ379756	AZ379756	LM0135C12	C 628	10	45.5	53	9	AA716037	AA716037
46.4	60	29	BZ291626	BZ291626	SALK_1214	C 629	10	45.5	53	29	AL946415	AL946415
46.4	60	29	AA258320	AA258320	z559f02.s	C 630	10	45.5	53	29	TA300807P	TA300807P
46.4	60	29	BI159059	BI159059	602922811	C 631	10	45.5	54	12	BJ001183	BJ001183
46.4	60	29	N95034	N95034	zb32b05.s1	632	10	45.5	54	14	CA898530	CA898530
46.4	60	29	CC792827	CC792827	SALK_0020	C 633	10	45.5	54	28	CC033971	CC033971
46.4	60	29	BH856001	BH856001	SALK_0838	C 634	10	45.5	54	29	CG426277	CG426277
46.4	60	29	AI553941	AI553941	ts54c02.x	C 635	10	45.5	55	9	AA673303	AA673303
46.4	60	29	AI972751	AI972751	w43a08.x	C 636	10	45.5	55	9	AA736635	AA736635
46.4	60	29	AU260188	AU260188	AU260188	C 637	10	45.5	55	9	AA513533	AA513533
46.4	60	29	R79446	R79446	y187f11.s1	C 638	10	45.5	55	14	CA868924	CA868924
46.4	60	29	AZ798954	AZ798954	2M0056J06	639	10	45.5	55	14	CA905572	CA905572
46.4	60	29	AZ959428	AZ959428	2M0227P05	640	10	45.5	55	28	AZ93821	AZ93821
46.4	60	29	CC180911	CC180911	01S0568-0	641	10	45.5	55	28	BH790250	BH790250
46.4	60	29	CG883145	CG883145	02S2018-0	C 642	10	45.5	55	29	TA381A03P	TA381A03P
46.4	60	29	CG895231	CG895231	03S4735-0	643	10	45.5	56	9	AI920126	AI920126
46.4	60	29	AG216656	AG216656	Drosophila	644	10	45.5	56	9	AW100567	AW100567
46.4	60	29	CF216400	CF216400	PT1195 Hy	C 645	10	45.5	56	14	CB275121	CB275121
46.4	60	29	CG705556	CG705556	01S0583-0	C 646	10	45.5	56	14	D21636	D21636
46.4	60	29	AZ366200	AZ366200	1M015N23	C 647	10	45.5	56	28	AZ23243	AZ23243
46.4	60	29	CG727673	CG727673	1119095H0	648	10	45.5	56	28	BH641779	BH641779
46.4	60	29	AA705006	AA705006	z195e12.s	C 649	10	45.5	56	29	CC882862	CC882862
46.4	60	29	AI130438	AI130438	SMOVL3CAN	C 650	10	45.5	56	29	CG710793	CG710793
46.4	60	29	AI182737	AI182737	ub80a05.x	C 651	10	45.5	56	29	CG785744	CG785744
46.4	60	29	AL585781	AL585781	AL585781	C 652	10	45.5	56	29	BX203710	BX203710
46.4	60	29	TS0449	TS0449	yb76qd09.s1	653	10	45.5	57	28	AZ378584	AZ378584
46.4	60	29	BH909212	BH909212	SALK_0524	654	10	45.5	57	28	AZ591159	AZ591159
46.4	60	29	AZ815318	AZ815318	2M0083A03	655	10	45.5	57	28	AZ629479	AZ629479
46.4	60	29	BZ379658	BZ379658	SALK_1136	656	10	45.5	57	28	BH849364	BH849364
46.4	60	29	CG427103	CG427103	01S0723-0	657	10	45.5	57	28	BH850801	BH850801
46.4	60	29	AA724196	AA724196	ai09a11.s	658	10	45.5	57	29	CC940871	CC940871
46.4	60	29	AI219230	AI219230	gg13c09.x	659	10	45.5	57	29	CC940927	CC940927
46.4	60	29				660	10	45.5	57	29	CG427634	CG427634
46.4	60	29				661	10	45.5	57	29	BX659862	BX659862

45.5	57	29	TA32A09P	AL454444 T. brucei	735	9.8	44.5	40	28	BH792128	BH792121
45.5	58	13	BQ626004	BQ626004 ph8a04.y	c 736	9.8	44.5	40	28	BH905777	BH905777
45.5	58	14	R29183	R29183 F1-292D 22	c 737	9.8	44.5	40	28	BZ662351	BZ662351
45.5	58	14	AZ797403	AZ797403 2M0053C12	c 738	9.8	44.5	41	14	CF329037	CF329037
45.5	58	28	BH635408	BH635408 1008004F0	c 739	9.8	44.5	41	28	AZ598104	AZ598104
45.5	58	28	BZ291526	BZ291526 SALK 1208	c 740	9.8	44.5	41	28	BZ353306	BZ353306
45.5	58	28	BZ766732	BZ766732 SALK 1377	741	9.8	44.5	41	29	BX229919	BX229919
45.5	58	28	BZ766894	BZ766894 SALK 1380	742	9.8	44.5	41	29	BX290940	BX290940
45.5	58	29	CG732759	CG732759 1119150H0	c 743	9.8	44.5	41	29	BX659231	BX659231
45.5	59	9	AW059770	AW059770 LE4e07.YG	c 744	9.8	44.5	42	9	AJ878619	AJ878619
45.5	59	12	BP134619	BP134619 BP134619	c 745	9.8	44.5	42	28	AZ388234	AZ388234
45.5	59	14	CB356900	CB356900 ZF001-F00	746	9.8	44.5	42	28	AZ785487	AZ785487
45.5	59	14	R12254	R12254 YF33F12.r1	747	9.8	44.5	42	28	AZ988113	AZ988113
45.5	59	28	AZ810237	AZ810237 2M0074I08	748	9.8	44.5	42	29	BX004505	BX004505
45.5	59	28	AZ962219	AZ962219 2M0230P19	c 749	9.8	44.5	42	29	BX157375	BX157375
45.5	59	28	AZ997591	AZ997591 2M0284L07	750	9.8	44.5	42	29	BX246612	BX246612
45.5	59	28	BH791228	BH791228 SALK 0592	751	9.8	44.5	42	29	TA275804Q	TA275804Q
45.5	59	29	CG986132	CG986132 CH240.156	c 752	9.8	44.5	43	28	AZ444259	AZ444259
45.5	60	12	BG742961	BG742961 602632063	753	9.8	44.5	43	28	AZ647300	AZ647300
45.5	60	13	BQ565015	BQ565015 gi29a01.Y	c 754	9.8	44.5	43	29	CC886686	CC886686
45.5	60	14	CD954417	CD954417 SBO 245 G	c 755	9.8	44.5	43	29	CG726304	CG726304
45.5	60	14	H55216	H55216 CHR220155 C	c 756	9.8	44.5	44	9	AJ509940	AJ509940
45.5	60	28	BH866411	BH866411 SALK 1012	757	9.8	44.5	44	14	CF301381	CF301381
45.5	60	28	CC179537	CC179537 SALK 0708	758	9.8	44.5	44	28	AZ502054	AZ502054
45.5	60	29	CG933318	CG933318 CH240.327	c 759	9.8	44.5	44	28	AZ509981	AZ509981
45.5	60	29	CG715527	CG715527 1119042B0	760	9.8	44.5	44	28	AZ661695	AZ661695
45.5	60	29	BX893293	BX893293 Arabidops	761	9.8	44.5	45	9	AV958176	AV958176
45.5	19	9	AA912825	AA912825 ol143d11.s	762	9.8	44.5	45	10	BE267956	BE267956
44.5	22	29	TA147806Q	TA147806 T. brucei	763	9.8	44.5	45	10	BE513871	BE513871
44.5	22	29	TA20A05P	TA20A05 T. brucei	764	9.8	44.5	45	10	BE560611	BE560611
44.5	23	9	AU256868	AU256868 AU256868	c 765	9.8	44.5	45	28	AZ590180	AZ590180
44.5	23	12	AZ389515	AZ389515 1M0150110	c 766	9.8	44.5	45	28	BH847646	BH847646
44.5	24	12	BM397400	BM397400 5009-0-32	c 767	9.8	44.5	45	29	EX133661	EX133661
44.5	26	28	AZ579595	AZ579595 1M0367012	c 768	9.8	44.5	46	9	AA780164	AA780164
44.5	28	14	CF319548	CF319548 HD--10-B1	769	9.8	44.5	46	10	BE267872	BE267872
44.5	28	28	AZ781011	AZ781011 2M0018D21	c 770	9.8	44.5	46	28	AZ437798	AZ437798
44.5	29	28	AZ441837	AZ441837 1M0234007	771	9.8	44.5	46	28	AZ833146	AZ833146
44.5	29	28	AZ654172	AZ654172 1M0528007	c 772	9.8	44.5	46	28	CC455214	CC455214
44.5	29	28	BH609778	BH609778 HIV09D10	773	9.8	44.5	47	10	BE267896	BE267896
44.5	31	12	BI768049	BI768049 603056352	774	9.8	44.5	47	10	BE270087	BE270087
44.5	32	10	BF120744	BF120744 601758133	775	9.8	44.5	47	10	BE295974	BE295974
44.5	32	28	AZ579540	AZ579540 1M0367107	776	9.8	44.5	47	10	BE513247	BE513247
44.5	32	28	AZ607412	AZ607412 1M0429A24	777	9.8	44.5	47	10	BE561502	BE561502
44.5	34	28	AZ647310	AZ647310 1M0513D15	c 778	9.8	44.5	47	28	AZ474499	AZ474499
44.5	35	28	AZ345535	AZ345535 1M0080005	c 779	9.8	44.5	47	28	AZ760561	AZ760561
44.5	35	28	AZ598147	AZ598147 1M0412J16	780	9.8	44.5	47	29	DR46K23S	DR46K23S
44.5	35	28	AZ950698	AZ950698 2M0214F19	781	9.8	44.5	48	9	A1008951	A1008951
44.5	36	9	AU2990339	AU2990339 2M0274G01	c 782	9.8	44.5	48	12	EG430009	EG430009
44.5	36	28	AZ335390	AZ335390 1M0065M16	c 783	9.8	44.5	48	28	BH914173	BH914173
44.5	36	28	AZ454226	AZ454226 1M0256P04	784	9.8	44.5	48	28	BZ763133	BZ763133
44.5	36	28	BH850482	BH850482 SALK 0713	c 785	9.8	44.5	49	9	AA872957	AA872957
44.5	36	28	BH850482	BH850482 SALK 0713	c 786	9.8	44.5	49	9	AA935229	AA935229
44.5	36	29	BX653401	BX653401 Arabidops	c 787	9.8	44.5	49	9	AJ019278	AJ019278
44.5	36	29	BX895439	BX895439 Arabidops	788	9.8	44.5	49	9	AS872540	AS872540
44.5	37	9	AA657467	AA657467 tt66c03.s	789	9.8	44.5	49	10	BE397307	BE397307
44.5	37	9	AA994662	AA994662 ou46g09.s	790	9.8	44.5	49	14	W65956	W65956
44.5	37	14	H28311	H28311 Y160d11.s1	c 791	9.8	44.5	49	28	AZ802864	AZ802864
44.5	37	28	AZ430297	AZ430297 1M0214A15	c 792	9.8	44.5	49	29	AJ752367	AJ752367
44.5	37	28	BH855008	BH855008 SALK 0867	c 793	9.8	44.5	50	9	AU103551	AU103551
44.5	37	29	TA282E05P	TA282E05 T. brucei	c 794	9.8	44.5	50	9	AU103911	AU103911
44.5	38	9	AL643708	AL643708 AL643708	796	9.8	44.5	50	9	AU104014	AU104014
44.5	38	28	AQ025540	AQ025540 EP(X)1614	797	9.8	44.5	50	9	AU104523	AU104523
44.5	38	29	TA241B11Q	TA241B11 T. brucei	798	9.8	44.5	50	9	AU104524	AU104524
44.5	39	10	BE512831	BE512831 601171854	799	9.8	44.5	50	9	AU104526	AU104526
44.5	39	10	BE544028	BE544028 601069976	800	9.8	44.5	50	9	AU104529	AU104529
44.5	40	9	AI154170	AI154170 ud78h11.r	801	9.8	44.5	50	9	AU104530	AU104530
44.5	40	9	AI424339	AI424339 te95el2.x	802	9.8	44.5	50	9	AU104531	AU104531
44.5	40	9	AA437989	AA437989 vd21b08.s	803	9.8	44.5	50	9	AU104532	AU104532
44.5	40	14	H43763	H43763 YD21b05.r1	804	9.8	44.5	50	9	AU104534	AU104534
44.5	40	28	AZ322671	AZ322671 1M0043N11	805	9.8	44.5	50	9	AU104535	AU104535
44.5	40	28	BH642154	BH642154 1080858G1	806	9.8	44.5	50	9	AU104536	AU104536
44.5	40	28			807	9.8	44.5	50	9	AU104537	AU104537

44.5	50	9	AUI04542	AUI04542	AUI04542	881	9.8	44.5	54	29	CC796046	CC796046
44.5	50	9	AUI04545	AUI04545	AUI04545	882	9.8	44.5	54	29	AL758438	AL758438
44.5	50	9	AUI04546	AUI04546	AUI04546	C 883	9.8	44.5	54	29	AX893257	AX893257
44.5	50	9	AUI04548	AUI04548	AUI04548	C 884	9.8	44.5	54	29	TA358C03P	TA358C03P
44.5	50	9	AUI04551	AUI04551	AUI04551	885	9.8	44.5	55	9	AA058459	AA058459
44.5	50	9	AUI04561	AUI04561	AUI04561	886	9.8	44.5	55	9	AA711965	AA711965
44.5	50	9	AUI04565	AUI04565	AUI04565	887	9.8	44.5	55	9	AA922594	AA922594
44.5	50	9	AUI04566	AUI04566	AUI04566	C 888	9.8	44.5	55	9	AI021508	AI021508
44.5	50	9	AUI04568	AUI04568	AUI04568	C 889	9.8	44.5	55	9	AA627357	AA627357
44.5	50	9	AUI04569	AUI04569	AUI04569	C 890	9.8	44.5	55	14	CB369327	CB369327
44.5	50	9	AUI04570	AUI04570	AUI04570	891	9.8	44.5	55	14	CF327435	CF327435
44.5	50	9	AUI04576	AUI04576	AUI04576	892	9.8	44.5	55	28	AZ309353	AZ309353
44.5	50	9	AUI04577	AUI04577	AUI04577	C 893	9.8	44.5	55	28	AZ958077	AZ958077
44.5	50	9	AUI04578	AUI04578	AUI04578	894	9.8	44.5	55	29	DME546724	DME546724
44.5	50	9	AUI04581	AUI04581	AUI04581	C 895	9.8	44.5	56	9	AA650287	AA650287
44.5	50	9	AUI04583	AUI04583	AUI04583	896	9.8	44.5	56	12	BG315269	BG315269
44.5	50	9	AUI04873	AUI04873	AUI04873	C 897	9.8	44.5	56	12	BG694574	BG694574
44.5	50	9	AUI04880	AUI04880	AUI04880	898	9.8	44.5	56	14	CF300304	CF300304
44.5	50	9	AUI04904	AUI04904	AUI04904	899	9.8	44.5	56	28	AZ419420	AZ419420
44.5	50	9	AUI04916	AUI04916	AUI04916	900	9.8	44.5	56	28	BH849530	BH849530
44.5	50	9	AUI05371	AUI05371	AUI05371	C 901	9.8	44.5	56	28	BH849530	BH849530
44.5	50	9	AUI05594	AUI05594	AUI05594	902	9.8	44.5	56	29	AL761721	AL761721
44.5	50	9	AUI06515	AUI06515	AUI06515	903	9.8	44.5	57	9	AA899441	AA899441
44.5	50	12	BE373543	BE373543	BE373543	904	9.8	44.5	57	10	BF636979	BF636979
44.5	50	12	BI331898	BI331898	BI331898	905	9.8	44.5	57	10	BF643402	BF643402
44.5	50	14	CB369340	CB369340	CB369340	C 906	9.8	44.5	57	14	CA794226	CA794226
44.5	50	14	CB753410	CB753410	CB753410	907	9.8	44.5	57	28	AZ311594	AZ311594
44.5	50	14	D19973	D19973	D19973	C 908	9.8	44.5	57	28	AZ508051	AZ508051
44.5	50	14	H55222	H55222	H55222	909	9.8	44.5	57	28	AZ792680	AZ792680
44.5	50	14	CH220161	CH220161	CH220161	910	9.8	44.5	57	28	BH900967	BH900967
44.5	50	29	CS651133	CS651133	CS651133	C 911	9.8	44.5	57	28	CC248731	CC248731
44.5	50	29	EX651733	EX651733	EX651733	C 912	9.8	44.5	57	29	DRIM24T	DRIM24T
44.5	51	10	AW247867	AW247867	AW247867	C 913	9.8	44.5	57	29	TA288H09Q	TA288H09Q
44.5	51	14	CA911579	CA911579	CA911579	C 914	9.8	44.5	58	9	AA669819	AA669819
44.5	51	14	CB368388	CB368388	CB368388	C 915	9.8	44.5	58	9	AI960912	AI960912
44.5	51	14	CB369278	CB369278	CB369278	916	9.8	44.5	58	9	AA260418	AA260418
44.5	51	14	CB383647	CB383647	CB383647	917	9.8	44.5	58	9	AA527714	AA527714
44.5	51	14	R87253	R87253	R87253	918	9.8	44.5	58	9	AA595844	AA595844
44.5	51	28	AZ592484	AZ592484	AZ592484	C 919	9.8	44.5	58	12	BI327689	BI327689
44.5	51	28	AZ830258	AZ830258	AZ830258	C 920	9.8	44.5	58	12	BI903269	BI903269
44.5	51	28	BH792413	BH792413	BH792413	C 921	9.8	44.5	58	12	BI903329	BI903329
44.5	51	29	CL002800	CL002800	CL002800	C 922	9.8	44.5	58	12	BI966898	BI966898
44.5	52	9	AL961397	AL961397	AL961397	C 923	9.8	44.5	58	14	CB752435	CB752435
44.5	52	9	AA545281	AA545281	AA545281	C 924	9.8	44.5	58	14	R60614	R60614
44.5	52	10	AW781349	AW781349	AW781349	C 925	9.8	44.5	58	14	W84003	W84003
44.5	52	10	BE248274	BE248274	BE248274	C 926	9.8	44.5	58	28	AZ784257	AZ784257
44.5	52	12	BI418262	BI418262	BI418262	C 927	9.8	44.5	58	28	AZ785541	AZ785541
44.5	52	12	BJ035097	BJ035097	BJ035097	C 928	9.8	44.5	58	28	BH863476	BH863476
44.5	52	14	CF327377	CF327377	CF327377	C 929	9.8	44.5	58	28	BZ596071	BZ596071
44.5	52	28	AZ784267	AZ784267	AZ784267	C 930	9.8	44.5	58	29	CG777339	CG777339
44.5	52	28	B02129	B02129	B02129	C 931	9.8	44.5	58	29	CG777339	CG777339
44.5	52	28	CC042729	CC042729	CC042729	C 932	9.8	44.5	59	9	AA207740	AA207740
44.5	52	29	CG784934	CG784934	CG784934	933	9.8	44.5	59	10	AW516149	AW516149
44.5	53	9	AI865237	AI865237	AI865237	934	9.8	44.5	59	14	CB373617	CB373617
44.5	53	9	AU076690	AU076690	AU076690	C 935	9.8	44.5	59	14	CB751654	CB751654
44.5	53	10	BE386052	BE386052	BE386052	936	9.8	44.5	59	14	D21021	D21021
44.5	53	12	BI735167	BI735167	BI735167	C 937	9.8	44.5	59	28	AZ800944	AZ800944
44.5	53	14	CF290833	CF290833	CF290833	938	9.8	44.5	59	28	AZ812360	AZ812360
44.5	53	14	CF291470	CF291470	CF291470	939	9.8	44.5	59	28	BZ384935	BZ384935
44.5	53	14	CF291480	CF291480	CF291480	C 940	9.8	44.5	60	9	AI202808	AI202808
44.5	53	14	CF300766	CF300766	CF300766	941	9.8	44.5	60	9	AV949826	AV949826
44.5	53	14	CF319067	CF319067	CF319067	942	9.8	44.5	60	12	BM176063	BM176063
44.5	53	28	AZ806537	AZ806537	AZ806537	C 943	9.8	44.5	60	14	CB006939	CB006939
44.5	53	28	AZ806855	AZ806855	AZ806855	944	9.8	44.5	60	14	CB019945	CB019945
44.5	53	28	B46648	B46648	B46648	945	9.8	44.5	60	14	CD288877	CD288877
44.5	53	28	BH852213	BH852213	BH852213	C 946	9.8	44.5	60	14	CD711104	CD711104
44.5	53	29	TA254C04Q	TA254C04Q	TA254C04Q	947	9.8	44.5	60	14	H55414	H55414
44.5	53	29	TA278G01Q	TA278G01Q	TA278G01Q	C 948	9.8	44.5	60	28	AZ389209	AZ389209
44.5	54	13	BQ835161	BQ835161	BQ835161	949	9.8	44.5	60	28	AZ433302	AZ433302
44.5	54	14	CF291727	CF291727	CF291727	C 950	9.8	44.5	60	28	BH797925	BH797925
44.5	54	14	CF310715	CF310715	CF310715	C 951	9.8	44.5	60	28	BH865646	BH865646
44.5	54	14	CF328491	CF328491	CF328491	952	9.8	44.5	60	28	BZ661548	BZ661548
44.5	54	14	D38714	D38714	D38714	953	9.8	44.5	60	29	BX293141	BX293141

43.6 22 29 TXA13C09P  
 43.6 22 29 TXA4R06P  
 43.6 24 28 A2480758  
 43.6 24 28 A2612609  
 43.6 25 28 A2368070  
 43.6 25 28 A2368070  
 43.6 27 29 A2348F09Q  
 43.6 28 28 A2633750  
 43.6 28 28 A2381403  
 43.6 28 28 A2650845  
 43.6 29 28 A2306174  
 43.6 29 28 A2391934  
 43.6 29 28 A2493781  
 43.6 29 28 A2514176  
 43.6 29 28 A2618807  
 43.6 29 28 A2458683  
 43.6 30 28 A2458683  
 43.6 30 28 A2471850  
 43.6 30 28 A2179D12P  
 43.6 31 28 A2587885  
 43.6 31 28 BH848251  
 43.6 32 28 BH903706  
 43.6 32 28 BH903708  
 43.6 32 28 BH903709  
 43.6 32 28 CC456593  
 43.6 32 29 AG217358  
 43.6 33 9 AV957181  
 43.6 33 9 AW059779  
 43.6 33 28 A2796922  
 43.6 33 28 A2867886  
 43.6 34 9 A259780  
 43.6 34 9 AV955108  
 43.6 34 10 BE257894  
 43.6 34 28 A2589160  
 43.6 35 9 AV950287  
 43.6 35 28 B2382809  
 43.6 36 13 C21469  
 43.6 36 28 BH856945  
 43.6 36 28 BH856991  
 43.6 36 28 B2382634  
 43.6 36 28 B2383354  
 43.6 37 9 AA931624  
 43.6 37 9 AA933761  
 43.6 37 9 AI720133  
 43.6 37 14 T52826  
 43.6 37 28 A2304994  
 43.6 37 28 A2815710  
 43.6 37 28 B2382743

## ALIGNMENTS

\*4296 39 bp mRNA linear EST 14-MAR-2002  
 \*4296 Nori Satoh unpublished cDNA library, cleavage stage embryo  
 \*4296 intestinalis cDNA clone c106b12 5', mRNA sequence.

\*4296.1 GI:19442595

intestinalis  
 intestinalis  
 uryzoa; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 obobranchia; Clonidae; Ciona.  
 (bases 1 to 39)  
 h.N., Satou, Y., Kohara, Y. and Shin-i, T.  
 essed genes in Ciona intestinalis  
 ublished (2000)  
 .act: Nori Satoh  
 irtment of Zoology  
 o University  
 o-Ku, Kyoto, Kyoto 606-8502, Japan  
 81-75-753-4081

AL490298 T. brucei  
 AL455010 T. brucei  
 A2480758 IM0302604  
 A2612609 IM0439P23  
 A2368070 IM0118A01  
 A496196 T. brucei  
 A2633750 IM0489I09  
 A2381403 IM0138A04  
 A2650845 IM0521B13  
 A2306174 IM0070G07  
 A2391934 IM0154N14  
 A2493781 IM0328F09  
 A2514176 IM0360K14  
 A2618807 IM0450N11  
 CC458683 IM0263D03  
 A2471850 IM0286M08  
 AL474655 T. brucei  
 A2587885 IM0395C23  
 BH848251 SALK\_0677  
 BH903706 SALK\_1031  
 BH903708 SALK\_1031  
 BH903709 SALK\_1031  
 CC456593 SALK\_0994  
 AG217358 Drosophila  
 AV957181 AV957181  
 AW059779 LE5602.Y9  
 A2796922 2M0052D21  
 A2867886 2M0178H22  
 A259780 Y87b10.x  
 AV955108 AV955108  
 BE257894 601109491  
 A2589160 IM0397021  
 AV950287 AV950287  
 B2382809 SALK\_1189  
 C21469 HUMG001046  
 BH856945 SALK\_0775  
 BH856991 SALK\_0775  
 B2382634 SALK\_1185  
 B2383354 SALK\_1338  
 AA931624 o035b08.s  
 AA933761 om59g06.s  
 AI720133 as78a11.x  
 T52826 Y81b02.s1  
 A2304994 IM0005E09  
 A2815710 2M0084E16  
 B2382743 SALK\_1187

FEATURES  
 source  
 Location/Qualifiers  
 1..39  
 /organism="Ciona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="c106b12"  
 /tissue\_type="whole animal"  
 /dev\_stage="cleavage stage embryo"  
 /clone\_lib="Nori Satoh unpublished cDNA library"  
 stage\_embryo"

## ORIGIN

Query Match 67.3%; Score 14.8; DB 9; Length 39;  
 Best Local Similarity 72.7%; Pred. No. 8.5e+03;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0;  
 QY 1 AGACAATCACAGTCTCTCGGA 22  
 38 ANANNATCCAGTCCCTGNGGA 17  
 |||||  
 |||||

## RESULT 2

AZ612511/c 41 bp DNA linear GSS  
 LOCUS  
 DEFINITION  
 IM04390C6R Mouse 10kb plasmid UUGC1M library Mus musculi  
 clone UUGC1M0439006 R, genomic survey sequence.

ACCESSION AZ612511  
 VERSION AZ612511.1 GI:11734797

KEYWORDS  
 GSS.

SOURCE  
 Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu  
 1 (bases 1 to 41)

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ha  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, J  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads fr  
 plasmid inserts  
 Unpublished (2000)

## JOURNAL

COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030  
 84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0439 row: 0 column: 06

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 41.

Location/Qualifiers

## FEATURES

## source

1..41  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0439006"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resista  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA fr  
 musculus C57BL/6J (male) was obtained from the  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/  
 was hydrodynamically sheared by repeated passag  
 0.005 inch orifice at constant velocity. The st  
 was blunt end-repaired with T4 DNA polymerase a

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

64.5%; Score 14.2; DB 28; Length 41;  
 Similarity 84.2%; Pred. No. 1.7e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 ACAATCAGTCTCTGC 19  
 ||||| ||||| |||||  
 ACAATCTCAGTCACTGC 22

3576 59 bp DNA linear GSS 29-SEP-2000  
 10K16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 3 UUGC1M0080K16 F, genomic survey sequence.  
 3576

3576.1 GI:10424813

musculus (house mouse)  
 musculus  
 Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 59)  
 D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Y., M., Rose, R., Stokes, R., Tingey, A., von  
 Hauser, A., and Wright, D., Weiss, R.  
 whole genome scaffolding with paired end reads from 10kb  
 mid inserts  
 lished (2000)  
 ct: Robert B. Weiss  
 rsity of Utah Genome Center  
 rsity of Utah  
 08, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 , USA  
 801 585 5606  
 801 585 7177  
 : ddunn@genetics.utah.edu  
 t Length: 10000 Std Error: 0.00  
 : 0080 row: K column: 16  
 primer: CGTTGTAACAGCGCCAGT  
 : Plasmid ends  
 quality sequence stop: 59.  
 Location/Qualifiers  
 1. .59  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0080K16"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: pWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 63.6%; Score 14; DB 28; Length 59;  
 Best Local Similarity 77.3%; Pred. No. 2.4e+04;  
 Matches 17; Conservative 0; Mismatches 5; Indels 0;  
 QY 1 AGACAATCAGTCTCTGCGGA 22  
 ||||| ||||| |||||  
 Db 37 AGAAATCAGCTCTCAGGA 16

## RESULT 4

AA211707  
 LOCUS  
 DEFINITION  
 2984F11.r1 Stratagene hNT neuron (#937233) Homo sapiens  
 IMAGE:648333 5' similar to TR:G1322042 GOK ; m  
 sequence.

ACCESSION  
 AA211707

VERSION  
 AA211707.1

KEYWORDS  
 EST.

SOURCE  
 Homo sapiens (human)

ORGANISM  
 Homo sapiens

REFERENCE  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

AUTHORS  
 1 (bases 1 to 58)

Hillier, L., Allen, M., Bowles, L., Dubucque, T., Geisler, G., Kitzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, J., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, WashU-NCI human EST Project  
 Unpublished (1997)

TITLE  
 JOURNAL

COMMENT  
 Contact: Wilson RK

Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; cont

IMAGE Consortium (info@image.lnl.gov) for further inform

Trace considered overall poor quality

Possible reversed clone: Similarity on wrong strand

Insert Length: 1561 Std Error: 0.00

Seq primer: -28m3 rev1 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

1. .58  
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 /mol\_type="mRNA"  
 /db\_xref="GDB:5277996"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:648333"  
 /dev\_stage="hNT neurons"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /clone\_lib="Stratagene hNT neuron (#937233)"  
 /note="Vector: pBluescript SK+ Site 1: EcoRI, S  
 xhoI; Cloned unidirectionally. Primer: Oligo dI  
 Differentiated, post mitotic hNT neurons. Avera  
 size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor seq  
 GAATTCGACGACGAG 3' -3' adaptor sequence: 5'  
 CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN



61.8%; Score 13.6; DB 9; Length 58;  
 ilarity 80.0%; Pred. No. 3.7e+04;  
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;

AACATCAGCTCTCTGGG 20  
 |||||  
 AGAAGCACAGCTCTTGGG 31

6301 28 bp DNA linear GSS 15-OCT-2002  
 1386-5prime Drosophila melanogaster P{SUPor-P} P element  
 15' end of P element, genomic survey sequence.

6301  
 6301.1 GI:24018037

ophila melanogaster (fruit fly)  
 yota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 tera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 droidea; Drosophilidae; Drosophila.  
 bases 1 to 28)  
 s, R., Hoskins, R., Liao, G., Mozen, N., Teang, G., He, Y.,  
 en, G., Bellen, H., Rubin, G. and Spradling, A.  
 Berkeley Drosophila Genome Project Gene Disruption Project  
 ublished (2001)  
 act: Gerald Rubin  
 eley Drosophila Genome Project  
 ersity of California, Berkeley  
 Building, Berkeley, CA 94720-3200, USA  
 5106439947  
 1: gerry@fruitfly.berkeley.edu  
 ence recovery method was inverse PCR.  
 nent  
 : P element insertion position is base 21 in the 28 bases. This  
 ortion position refers to the first base of the 8 base target  
 gnition sequence.  
 is: transposon-tagged  
 Location/Qualifiers  
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 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone\_lib="Drosophila melanogaster P{SUPor-P} P element  
 insertion lines"  
 /note="Inverse PCR was performed on Drosophila  
 melanogaster strains each of which contains one or more  
 P{SUPor-P} P-element transposon insertion. The resultant  
 fragment for each strain was directly sequenced to  
 determine the genomic sequence at the site of insertion.  
 Details of the protocols used can be found at  
 http://www.fruitfly.org/about/methods/inverse.pcr.html."

60.0%; Score 13.2; DB 28; Length 28;  
 ilarity 83.3%; Pred. No. 4.2e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AATCAGCTCTCTGGG 21  
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 AGTCACAGCTCTCGCGG 2

13611 49 bp mRNA linear EST 27-APR-1998  
 el2.s1 NCI CGAP Co8 Homo sapiens cDNA clone IMAGE1474030 3'  
 lar to TR:Q17564 Q17564 C01F6.8 ; mRNA sequence.  
 13611

AA93361.1.1 GI:3089879  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Hom  
 1 (bases 1 to 49)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., P  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Cloning by: Washington University Genome Sequenc  
 Clone distribution: NCI-CGAP clone distribution inform  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seg primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1474030"  
 /tissue\_type="adenocarcinoma"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Co8"  
 /note="Organ: colon; Vector: p7T3D-Pac (Pharma  
 modified polylinker; 1st strand cDNA was prepar  
 colon adenocarcinoma, and was then primed with  
 oligo(dT) primer. Double-stranded cDNA was lig  
 RI adaptors (Pharmacia), digested with Not I ar  
 into the Not I and Eco RI sites of the modifier  
 vector. Library is normalized. Library was coi  
 Bento Soares and M. Fatima Bonaldo."

Query Match 60.0%; Score 13.2; DB 9; Length 49;  
 Best Local Similarity 83.3%; Pred. No. 5.3e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;  
 QY 5 AATCAGCTCTCTCGGA 22  
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 Db 30 AATTTCAGTCTCTGCAGA 13

RESULT 7  
 BM307546/c  
 LOCUS BM307546.1  
 DEFINITION sak30f06.y1 Gm-cl075 Glycine max cDNA clone SOYBEAN CLON  
 Gm-cl075-4500 5', mRNA sequence.  
 ACCESSION BM307546  
 VERSION BM307546.1 GI:18039252  
 KEYWORDS EST.  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; F  
 Glycine.  
 1 (bases 1 to 49)  
 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell,  
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Ma  
 Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B.  
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., F  
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Card  
 McCann, R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project

published (1999)  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 : 314 286 1800  
 : 314 286 1810  
 e-mail: est@watson.wustl.edu  
 This clone is available through: ResGen, Invitrogen Corp. 2130  
 North Memorial Parkway Huntsville, AL 35801 For further information  
 1: (800)-533-4363 or contact: ccu@resgen.com web site:  
 resgen.com

active full length read  
 prior to vector length is 50  
 primer: -40RP from Gibco.

Location/Qualifiers  
 1. .49  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl075-4500"  
 /tissue\_type="differentiating somatic embryos cultured on  
 MSM6AC"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl075"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
 XhoI; The cDNA library was constructed from mRNA isolated  
 from differentiating somatic embryos cultured on MSM6AC.  
 The library was prepared using the Stratagene pBluescript  
 II SK(+) library construction kit. Complementary DNA was  
 synthesized from mRNA using a primer consisting of a  
 poly(dT) sequence with an XhoI restriction site. EcoRI  
 adaptors were ligated to the blunt-ended cDNA fragments  
 followed by XhoI digestion. The cDNA fragments were  
 directionally cloned into the EcoRI-XhoI restriction site  
 of the pBluescript vector. The ligated cDNA fragments  
 were transformed into E. coli ElectroMax DH10B host cells.  
 Tissue culture and library construction were performed by  
 Françoise Thibaud-Nissen and Anu Khana (Lila Vodkin lab,  
 University of Illinois)."

60.0%; Score 13.2; DB 12; Length 49;  
 milarity 83.3%; Pred. No. 5.3e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GACATTCACAGTCTCTG 18  
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 GACATTCATAGTATTG 2

48549 52 bp mRNA linear EST 01-APR-2002  
 025D03 59719 An expressed sequence tag database for the  
 olerant green alga, Dunaliella salina Dunaliella salina cDNA  
 ne DSA025D03 5, mRNA sequence.

48549  
 48549.1 GI:19854121

aliella salina  
 aliella salina  
 aryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 aliellaceae; Dunaliella.  
 (bases 1 to 52)  
 hman,J.C.

expressed sequence tag database for the halotolerant green alga,  
 aliella salina  
 ublished (2002)  
 tact: Cushman JC  
 artment of Biochemistry  
 versity of Nevada  
 00, Reno, NV 89557-0014, USA

Tel: 775-784-1918  
 Fax: 775-784-1650  
 Email: jcushman@unr.edu  
 PCR Primers  
 FORWARD: T3 20mer  
 BACKWARD: T7 21mer  
 Plate: 025 row: D column: 03  
 Seq primer: T3 20mer  
 High quality sequence stop: 52.  
 Location/Qualifiers  
 1. .52  
 /organism="Dunaliella salina"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3046"  
 /clone="DSA025D03"  
 /tissue\_type="Cells, which was adapted in 2.5M  
 incremental series from 1.7 to 2.0 to 2.25 to  
 were exposed to 3.4 M NaCl for 5 hours"  
 /cell\_type="Green"  
 /clone\_lib="An expressed sequence tag database  
 halotolerant green alga, Dunaliella salina"  
 /note="Vector: Lambda Uni-Zap XR, Bluescript i  
 EcoRI; Site 2: XhoI; Library construction was  
 according to Stratagene's recommended protocol  
 Lambda UniZapXR vector and cDNA synthesis kit.

Query Match 60.0%; Score 13.2; DB 12; Length 52;  
 Best Local Similarity 83.3%; Pred. No. 5.4e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 2 GACATTCACAGTCTCTGC 19  
 |||||  
 Db 18 GAAAGTCACAGTCTTGC 1

RESULT 9  
 BG527761/c  
 LOCUS  
 DEFINITION  
 BG527761 59 bp mRNA linear EST  
 602556705F1 NIH\_MGC\_59 Homo sapiens cDNA clone IMAGE:46  
 mRNA sequence.

ACCESSION  
 BG527761  
 BG527761.1 GI:13519298  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 1 (bases 1 to 59)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collectio  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: ARCC

cDNA Library Preparation: CLONETECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LNCMI495 row: i column: 02  
 High quality sequence stop: 59.  
 Location/Qualifiers  
 1. .59  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4685641"  
 /tissue\_type="mucocpidermoid carcinoma"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_59"  
 /note="Organ: lung; Vector: pDNR-LIB (Clontech

FEATURES  
 source

SfilI (ggcgcctcgcc); Site 2: SfilI (ggccattatggcc);  
Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGAGCGCGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

60.0%; Score 13.2; DB 12; Length 59;  
similarity 83.3%; Pred. No. 5.7e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
ATCACAGTCTCTGCGGA 22  
|||||  
ATCCCGTCTGCGGA 39  
|||||

8468 60 bp mRNA linear EST 16-OCT-2001  
8468 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5218207 5',  
a sequence.

8468.1 GI:16171424

sapiens (human)  
sapiens  
tryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Malia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
(bases 1 to 60)  
MGC http://mgi.nci.nih.gov/  
onal Institutes of Health, Mammalian Gene Collection (MGC)  
blished (1999)  
act: Robert Strausberg, Ph.D.  
l: cgabs@mail.nih.gov  
ue Procurement: Life Technologies, Inc.  
A Library Preparation: Life Technologies, Inc.  
A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
Sequencing by: Incyte Genomics, Inc.  
ne distribution: MGC clone distribution information can be  
d through the I.M.A.G.E. Consortium/LLNL at:  
://image.llnl.gov  
e: L16M11548 row: g column: 08  
quality sequence stop: 60.  
Location/Qualifiers  
1. 60

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5218207"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_118"  
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dt primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."

60.0%; Score 13.2; DB 12; Length 60;  
similarity 83.3%; Pred. No. 5.8e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGACAATCACACTCTCTG 18  
|||  
Db 38 AGGAATCACACTCTCAG 55  
|||

RESULT 11  
AZ313241/c

LOCUS  
DEFINITION  
AZ313241 35 bp DNA linear GSS  
1M0029H13R Mouse 10kb plasmid UUGCLM library Mus muscul  
clone UUGCLM0029H13 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AZ313241.1 GI:10357975  
GSS.  
Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS  
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mu  
1 (bases 1 to 35)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ha  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads fr  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0029 row: H column: 13  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 35.  
Location/Qualifiers  
1. 35

FEATURES  
source

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCLM0029H13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resista  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/note="Vector: PWD42nv; Purified genomic DNA fr  
musculus C57BL/6J (male) was obtained from the  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/  
was hydrodynamically sheared by repeated passag  
0.005 inch orifice at constant velocity. The si  
was blunt end-repaired with T4 DNA polymerase a  
polynucleotide kinase. Adaptor oligonucleotides  
ligated to the blunt ends in high molar excess  
adaptor DNA was purified and size-selected fr  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-num  
inducible derivative of plasmid R1. The vector  
with adaptors complementary to the insert adapt  
purified. The sheared, adaptor mouse DNA was  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Strata  
and selected for ampicillin resistance."

ORIGIN

Query Match 59.1%; Score 13; DB 28; Length 35;  
Best Local Similarity 76.2%; Pred. No. 5.7e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;

ACAATCACAGTCTCTGCGG 21  
|||||  
ACTATCACAGGCAGTGTGG 3

6366 40 bp DNA linear GSS 14-NOV-2003  
044 pig genomic DNA Sus scrofa genomic, genomic survey  
ence,  
6366  
6366.1 GI:38323955

scrofa (pig)  
scrofa  
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
bases 1 to 40)  
itakis,E.T., Raymond,A., Scamuffa,N., Ucla,C., Kirkness,E.,  
ier,C. and Antonarakis,S.E.  
utionary discrimination of mammalian conserved non-genic  
ences (CNGs)  
nce 302 (5647), 1033-1035 (2003)  
.7884  
act: Dermitzakis ET  
sion of Medical Genetics  
eristy of Geneva Medical School  
e Michel Servet, 1211 Geneva, Switzerland  
0041 22 3795719  
0041 22 3795706  
l: emanouil.dermitzakis@medecine.unige.ch  
is: PCR product.  
Location/Qualifiers

1..40  
/organism="Sus scrofa"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9823"  
/clone\_lib="pig genomic DNA"  
/note="direct sequencing of PCR product; sequences  
orthologous to human chromosome 21 conserved sequences or  
non-coding RNAs from the whole genome"

59.1%; Score 13; DB 29; Length 40;  
ilarity 76.2%; Pred. No. 6e+04;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ACAATCACAGTCTCTGCGG 21  
|||||  
CAATTCACAGTCTCAGCTG 18

2233 58 bp mRNA linear EST 11-APR-2003  
TYzh8ig11.y1 TgME49 3 day invitro bradyzoite Toxoplasma gondii  
\ clone TgESTyh8ig11.y1 5', mRNA sequence.

2233.1 GI:29819525  
plasma gondii  
plasma gondii  
ryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
ocystidae; Toxoplasma.  
(bases 1 to 58)

J.K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,  
ton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,  
ier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,  
er E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,  
edy,S., Maguire,L., Waterston,R. and Wilson,R.  
plasma EST Project  
ublished (2001)  
:act: Clifton, S.

Toxoplasma EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: toxo@watson.wustl.edu  
Contact David Sibley (toxoes@borcim.wustl.edu) for fur  
information relating to organism, libraries, or clone a  
Seq primer: -40RP from Gibco.

FEATURES  
Location/Qualifiers  
source

1..58  
/organism="Toxoplasma gondii"  
/mol\_type="mRNA"  
/db\_xref="taxon:5811"  
/clone="TgESTyh8ig11.y1"  
/dev\_stage="3 day"  
/lab\_host="ElectronTen Blue cells"  
/clone\_lib="TgME49 3 day invitro bradyzoite"  
/note="Vector: pBluescript SK; Site 1: NotI; S;  
cDNA was reverse transcribed using Superscript  
anchored (7wobble') oligo dt primer, containing  
restriction site, according to standard proto  
second strand cDNA was digested with NOTI rest:  
endonuclease, purified and size fractionated w  
SizeSep 400 spun column (Amersham) and directl  
cloned into the SmaI and NotI sites of pBluesc  
Following electroporation into ElectronTen Blu  
(Stratagene), 5 x 106 primary CFU were bottle  
semisolid culture media [2xLB+15% SeaPrep agar  
After 48 hrs at 30 degrees Celcius, cells were  
pooled and stored in 2xLB + 15% glycerol."

## ORIGIN

Query Match 59.1%; Score 13; DB 14; Length 58;  
Best Local Similarity 76.2%; Pred. No. 7.1e+04;  
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCGG 21  
|||||  
Db 45 AGAAAAACAGAGGCTCCGCGG 25

RESULT 14  
AG255919/c  
LOCUS  
DEFINITION  
Lotus corniculatus var. japonicus DNA, clone:LjT40i08\_s  
survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AG255919  
AG255919.1 GI:26655756  
GSS.  
Lotus corniculatus var. japonicus (Lotus japonicus)  
Lotus corniculatus var. japonicus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; L  
Lotus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
1  
Sato,S., Nakamura,Y. and Tabata,S.  
Lotus japonicus TAC End sequences  
Published Only in Database (2002)  
Sato,S.  
Direct Submission  
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Researc  
The First Laboratory for Plant Gene Research; 2-6-7  
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan  
(E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/  
Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)  
Location/Qualifiers

## FEATURES

## source

1..36  
/organism="Lotus corniculatus var. japonicus"  
/mol\_type="genomic DNA"  
/strain="Miyakojima MG-20"

```

/variety="japonicus"
/db_xref="taxon:34305"
/clone="LjT40108_sfi"
/clone_lib="genomic_TAC library"
/note="VECTOR:pYLFAC7-synonym: Lotus japonicus"

58.2%; Score 12.8; DB 29; Length 36;
ilarity 87.5%; Pred. No. 7.2e+04;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ATCACAGTCTCTGC 19
|||||
ATCAAGTCTCTGC 18

4053 44 bp DNA linear GSS 13-JUN-2002
078674.42.00.x Arabidopsis thaliana TDNA insertion lines
idopsis thaliana genomic clone SALK_078674.42.00.x, genomic
ey sequence.
4053
4053.1 GI:21424924

idopsis thaliana (thale cress)
idopsis thaliana
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; eudicotyledons; core eudicots;
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
(bases 1 to 44)
iso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
inab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
n,P., Zimmerman,J. and Ecker,J.R.
quence-Indexed Library of Insertion Mutations in the
idopsis Genome
blished (2001)
act: Joseph R. Ecker
stitute Genomic Analysis Laboratory (SIGNAL)
alk Institute for Biological Studies
0 N. Torrey Pines Road, La Jolla, CA 92037, USA
: 858 453 4100 x1752
: 858 558 6379
l: ecker@alk.edu
s: This sequence recovered from the left border of
a. This sequence lies within 300 bases of the 5' end of
328715.
ss: TDNA tagged.
Location/Qualifiers
1..44
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_078674.42.00.x"
/note="SALK_078674.42.00.x"
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

58.2%; Score 12.8; DB 28; Length 44;
milarity 87.5%; Pred. No. 7.8e+04;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AATCACAGTCTCTGC 19
|||||
GATCACATCTCTGC 17

```

```

RESULT 16
BH861326/c
LOCUS
DEFINITION
SALK_067995 Arabidopsis thaliana TDNA insertion lines Ar
thaliana genomic clone SALK_067995, genomic survey seque
BH861326
BH861326.1 GI:22096652
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
rosids; eurosids II; Brassicales; Brassicaceae; Arabido
1 (bases 1 to 45)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., I
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left bo
TDNA. This sequence lies within an annotated exon of At:
Class: TDNA tagged.
Location/Qualifiers
1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_067995"
/clone_lib="Arabidopsis thaliana TDNA insertion
/note="PCR was performed on Arabidopsis thalia
each of which contains one or more TDNA inser
elements. The resultant fragment for each lin
directly sequenced to determine the genomic se
the site of insertion. Details of the protoc
be found at http://signal.salk.edu/tdna_protoc

58.2%; Score 12.8; DB 28; Length 45;
Best Local Similarity 87.5%; Pred. No. 7.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 4 CAATCACAGTCTCTGC 19
|||||
Db 18 CAATCACAGCTCTTAC 3

RESULT 17
BF643352/c
LOCUS
DEFINITION
NF004A05EC1F1034 Elicited cell culture Medicago truncat
clone NF004A05EC 5', mRNA sequence.
BF643352
BF643352.1 GI:11908477
EST.
SOURCE
Medicago truncatula (barrel medic)
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Medicago.
1 (bases 1 to 52)
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A.
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble F

```

09:38:25 2004

us-10-090-326-6.max.rst

```
pr for Medicago Genomics Research
published (2000)
act: Dixon RA
: Biology Division
Samuel Roberts Noble Foundation
Sam Noble Parkway, Ardmore, OK 73402, USA
580 221 7302
580 221 7380
l: radixon@noble.org
t length: 52 Std Error: 0.00
s: 004 row: A column: 05
primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
1. .52
/mol_type="mRNA"
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clones="NF004A05EC"
/tissue type="Cell cultures derived from root tissues"
/dev stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/clone_lib="Elicited cell culture"
/notes="vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
```

```
58.2%; Score 12.8; DB 10; Length 52;
ilarity 87.5%; Pred. No. 8.4e+04;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CAATCAGCTCTCT 17
|||||
CAACACACTCTCT 29

3382 60 bp DNA linear GSS 05-AUG-2002
093779 Arabidopsis thaliana TDNA insertion lines Arabidopsis
iana genomic clone SALK_093779, genomic survey sequence.
3382
3382.1 GI:22098936
idopsis thaliana (thale cress)
idopsis thaliana
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; eudicotyledons; core eudicots;
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
bases 1 to 60)
so,J.M., Leisner,T.J.; Barajas,P.; Chen,H.; Cheuk,R.;
inab,C.; Jeske,A.; Karnes,M.; Kim,C.J.; Parker,H.; Prednis,L.;
n.P.; Zimmerman,J. and Ecker,J.R.
quence-Indexed Library of Insertion Mutations in the
idopsis Genome
blished (2001)
act: Joseph R. Ecker
: Institute Genomic Analysis Laboratory (SIGAL)
Salk Institute for Biological Studies
.O N. Torrey Pines Road, La Jolla, CA 92037, USA
858 453 4100 x1752
858 558 6379
l: ecker@salk.edu
is single pass sequence recovered from the left border of
A. This sequence lies within 300 bases of the 5' end of
#28715.
ss: TDNA tagged.
Location/Qualifiers
1. .60
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
```

```
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_093779"
/notes="PCR was performed on Arabidopsis thaliana TDNA insertion
each of which contains one or more TDNA insert
elements. The resultant fragment for each line
directly sequenced to determine the genomic seq
the site of insertion. Details of the protocol
be found at http://signal.salk.edu/tdna_protoo

Query Match 58.2%; Score 12.8; DB 28; Length 60;
Best Local Similarity 87.5%; Pred. No. 8.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 4 CAATCAGCTCTCTGC 19
|||||
Db 23 CGATCAACTCTCTGC 38

RESULT 19
AI958680 34 bp mRNA linear EST
LOCUS IC95B01.y1 Zebrafish WashU WPMG EST Danio rerio cDNA cl
DEFINITION IMAGE:3729097 5', similar to SW:PUS1_MOUSE P50580
PROLIFERATION-ASSOCIATED PROTEIN 1 ;, mRNA sequence.
ACCESSION AI958680
VERSION AI958680.1 GI:5751393
KEYWORDS EST
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 34)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra
Rddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyl
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., S
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., Mc
Waterston,R. and Wilson,R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Other ESTs: fc95b01.xl
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@wustl.wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Ar
Matthew Clark. DNA Sequencing by: Washington University
Sequencing Center Clone Distribution: Genome Systems, St
Missouri (web address: www.genomesystems.com) (email cor
info@genomesystems.com) and Research Genetics, Huntsvill
(web address: www.resgen.com) (email contact: info@resge
ResourcenzentrumPrimarDatenbank, Berlin, Germany (web e
www.rzpd.de)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T3 Er from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .34
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3729097"
/sex="mixed"
/tissue type="26 somite embryos, adult livers,
stage embryos"
/lab_host="XLI-blue MRF"
```

/clone lib="Zebrafish WashU MPIMG EST"  
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st  
 strand cDNA was primed with a Not I - oligo(dT)15 primer  
 [5'-pGACTAGTCACGACGCGCGCGCCCTTTTCTTTT3'];  
 double-stranded cDNA was ligated to Sal I adaptors (BRL),  
 digested with Not I and cloned into the Not I and Sal I  
 sites of the pSPORT1 vector (BRL). Library was constructed  
 by Matthew Clark (Lehrach lab; ICRF, London and Max Planck  
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST  
 analysis were selected following oligonucleotide  
 hybridization fingerprinting of arrayed clones from  
 zebrafish late somitogenesis (26 ss), adult liver or  
 embryonic shield stage (5.6 h) libraries. Fingerprint  
 data were used to computationally cluster cDNAs, and a  
 single cDNA from each cluster was chosen for sequencing.  
 In some cases multiple members of the same cluster were  
 sequenced to assess clustering parameters, or single clones  
 were sequenced additional times to assess quality  
 control."

57.3%; Score 12.6; DB 9; Length 34;  
 ilarity 78.9%; Pred. No. 8.7e+04; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 4;

HACAAATCACAGTCTCTGCG 19

TTCAATAACTGTCGTCG 28

7818 37 bp mRNA linear EST 15-FEB-1999  
 g12.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:1980166 3'  
 lar to TR:Q01943 Q01943 EXTENSIN ; contains element TAR1  
 ititive element ; , mRNA sequence.

7818 GI:4109439

sapiens (human)

sapiens

aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 (bases 1 to 37)

-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

ional Cancer Institute, Cancer Genome Anatomy Project (CGAP),

or Gene Index

ublished (1997)

tact: Robert Strausberg, Ph.D.

il: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)

sue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

ert-Buck, M.D., Ph.D.

NA Library Preparation: Life Technologies, Inc.

NA Library Arrayed by: Greg Lennon, Ph.D.

A sequencing by: Washington University Genome Sequencing Center

one distribution: NCI-CGAP clone distribution information can be

nd through the I.M.A.G.E. Consortium/LLNL at:

-bio.llnl.gov/bbrp/image/image.html

ce considered overall poor quality

ert length: 1039 Std Error: 0.00

primer: -40UP from Gibco

h quality sequence stop: 1.

Location/Qualifiers

1. .37

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1980166"

/tissue type="poorly differentiated adenocarcinoma with

signed ring cell features"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Gas4"

# ORIGIN

Query Match 57.3%; Score 12.6; DB 9; Length 37;  
 Best Local Similarity 78.9%; Pred. No. 9e+04;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACAATCACAGTCTCTGCGG 21

DB 19 ACAATGAAAGACTGCGCG 37

# RESULT 21

AZ782132

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

/note="Organ: stomach; Vector: PCMV-SPORT6; Sit  
 Site 2: NotI; Cloned unidirectionally. Primer:  
 Average insert size 1.69 kb. Life Technologies  
 11549-011"

37 bp DNA linear GSS  
 2M0022D08F Mouse 10kb plasmid UUGCLM library Mus musculi  
 clone UUGC2M0022D08 F, genomic survey sequence.

AZ782132

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads fr  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah  
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0022 row: D column: 08  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 37.

# FEATURES

source

1. .37  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0022D08"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, TI-resist  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /note="Vector: PWD42nv; Purified genomic DNA f  
 musculus C57BL/6J (male) was obtained from th  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares>  
 was hydrodynamically sheared by repeated passa  
 0.005 inch orifice at constant velocity. The s  
 was blunt end-repaired with T4 DNA polymerase  
 polynucleotide kinase. Adaptor oligonucleotide  
 ligated to the blunt ends in high molar exces  
 adapted DNA was purified and size-selected f  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from  
 of PWD42 (GI4732114|gb|AF129072.1), a copy-nu  
 inducible derivative of plasmid R1. The vector  
 with adaptors complementary to the insert adap

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

57.3%; Score 12.6; DB 28; Length 37;  
ilarity 78.9%; Pred. No. 9e+04;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACAATCACAGTCTCTGC 19

|||||  
CTAAACTCAGTCTCTGC 33

3640 43 bp DNA linear GSS 20-FEB-2001  
15B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
e UUGC2M0115B23 R, genomic survey sequence.

3640

3640.1 GI:13003548

musculus (house mouse)

musculus  
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
bases 1 to 43)

D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
M.H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
ly, M., Rose, R., Stokes, R., Tingley, A., von  
exhauser, A. and Wright, D., Weiss, R.

e whole genome scaffolding with paired end reads from 10kb  
mid inserts

blished (2000)

act: Robert B. Weiss

ersity of Utah Genome Center

308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

2, USA

801 585 5606

801 585 7177

l: ddunn@genetics.utah.edu

rt Length: 10000 Std Error: 0.00

e: 0115 row: B column: 23

primer: CACACAGGAAACAGCTATGACC

s: plasmid ends

quality sequence stop: 43.

Location/Qualifiers

1. .43

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clones="UUGC2M0115B23"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

# ORIGIN

Query Match 57.3%; Score 12.6; DB 28; Length 43;  
Best Local Similarity 78.9%; Pred. No. 9.6e+04;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;

Qy 1 AGACAATCACAGTCTCTGC 19

|||||  
Db 24 AGACACAGCAGGCTCTCTC 6

# RESULT 23

AZ955701/c

LOCUS

DEFINITION 2M0221H21R Mouse 10kb plasmid UUGC2M library Mus musculus  
Clone UUGC2M0221H21 R, genomic survey sequence.

ACCESSION AZ955701

VERSION AZ955701.1 GI:13826928

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur  
1 (bases 1 to 45)

# REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ham  
Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T  
Reilly, M., Rose, R., Stokes, R., Tingley, A., von  
Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads fro  
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0221 row: H column: 21

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 45.

Location/Qualifiers

1. .45

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clones="UUGC2M0221H21"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, Tl-resistant  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA fr  
musculus C57BL/6J (female) was obtained from t

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/  
was hydrodynamically sheared by repeated passag  
0.005 inch orifice at constant velocity. The sh  
was blunt end-repaired with T4 DNA polymerase a  
polynucleotide kinase. Adaptor oligonucleotides

ligated to the blunt ends in high molar excess  
adapted DNA was purified and size-selected fo  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-num

inducible derivative of plasmid R1. The vector  
with adaptors complementary to the insert adapt

purified. The sheared, adapted mouse DNA was  
adapted vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratag  
and selected for ampicillin resistance."



purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

57.3%; Score 12.6; DB 28; Length 45;

ilarity 78.9%; Pred. No. 9.8e+04;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

GACAAATCACAGTCTCTGC 19

|||||

SACACTCACAGTTTTC 24

35957 50 bp mRNA linear EST 30-AUG-2001  
35957 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
35957 1324, mRNA sequence.

35957.1 GI:13555478

; sapiens (human)

; sapiens

aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 50)

aki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

aki, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,

aki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

erse transcriptional initiation revealed by fine, large-scale

ping of mRNA start sites

3 Rep. 2 (5), 388-393 (2001)

70072

75929

tact: Yutaka Suzuki

artment of Virology

titute of Medical Science, University of Tokyo

-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

il: yusuzuki@ims.u-tokyo.ac.jp

uki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

ano, S. Construction and characterization of a full

gth-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CAS01324"

/clone\_lib="Sugano Homo sapiens cDNA library"

57.3%; Score 12.6; DB 9; Length 50;

ilarity 78.9%; Pred. No. 1e+05;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

GACAAATCACAGTCTCTGC 19

|||||

GACGACACACAGCTGTGC 26

05958 50 bp mRNA linear EST 30-AUG-2001

05958 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

05753, mRNA sequence.

05958

05958.1 GI:13555479

; sapiens (human)

to sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho  
1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., S

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Ok

Sasaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, la

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gen

149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="HS105753"

/clone\_lib="Sugano Homo sapiens cDNA library"

#### ORIGIN

Query Match 57.3%; Score 12.6; DB 9; Length 50;

Best Local Similarity 78.9%; Pred. No. 1e+05; 4; Indels 0;

Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 1 AGACAATCACAGTCTCTGC 19

|||||

38 AGACGACACACAGCTGTGC 20

#### RESULT 26

AU105959/c

LOCUS

AU105959 Sugano Homo sapiens cDNA library Homo sapiens

INCE0044, mRNA sequence.

ACCESSION

AU105959

VERSION

AU105959.1 GI:13555480

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., S

Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Ok

Sasaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, la

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gen

149-156 (1997).

Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

09:38:25 2004

us-10-090-326-6.max.rst

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/clone="INEC0044"
/clone_lib="Sugano Homo sapiens cDNA library"

57.3%; Score 12.6; DB 9; Length 50;
larity 78.9%; Pred. No. 1e+05; 4; Indels 0; Gaps 0;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACAATCACAGTCTGTC 19
|||||
CGACCACAGCCTGTC 26

1754 51 bp mRNA linear EST 09-OCT-1997
05.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
3:976641 5', mRNA sequence.
1754
1754.1 GI:2523630
musculus (house mouse)
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ases 1 to 51)
t,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
l,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
lenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
ing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
ston,R.
Yashu-HHMI Mouse EST Project
lished (1996)
ct: Maria M/Mouse EST Project
J-HHMI Mouse EST Project
ington University School of MedicineP
Forest Park Parkway, Box 8501, St. Louis, MO 63108
314 286 1800
314 286 1810
l: mouseest@watson.wustl.edu
clone is available royalty-free through LLNL ; contact the
3 Consortium (info@image.llnl.gov) for further information.
357369.

Location/Qualifiers
1. .51
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:976641"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
/clone_lib="Knowles Solter mouse 2 cell"
/note="Organ: embryo; Vector: pBluescribe (modified);
Site 1: MluI; Site 2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
SalI(dT): 5'-CGGTGACCGTCGACCGTGTGTTTGT-3'. cDNAs
were cloned into the MluI/SalI sites of a modified
pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."

57.3%; Score 12.6; DB 9; Length 51;
ilarity 78.9%; Pred. No. 1e+05; 4; Indels 0; Gaps 0;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ACAATCACAGTCTGTC 19
|||||
TCATCCACAGCCTGTC 21
```

```
CK225144/c
LOCUS
DEFINITION
mRNA sequence.
51 bp mRNA linear EST
700324494H1 RAHINOT01 Rattus norvegicus cDNA clone 70032
mRNA sequence.
CK225144
CK225144.1 GI:39631248
EST.
KEYWORDS
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
Rattus.
REFERENCE
1 (bases 1 to 51)
AUTHORS
Vitt,U., Gietzen,D., Stevens,K., Wingrove,J., Becha,S.,
Burrill,J., Chawla,N., Chien,J., Crawford,M., Ison,C., K
Kwong,M., Park,J., Policky,J., Weiler,M., White,R., Xu,Y
Daniels,S., Jacob,H., Jensen-Seaman,M.I., Lazar,J., Stuv
Schmidt,J.
TITLE
Identification of candidate disease genes by EST alignme
synteny and expression and verification of Ensembl genes
chromosome 1q43-54
Genome Res. (2004) In press
COMMENT
Contact: Vitt U
Incyte Genomics, Inc.
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 849 8840
Fax: 650 845 5495
Email: uvitt@incyte.com.
FEATURES
Location/Qualifiers
1. .51
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="700324484"
/tissue_type="Hippocampus"
/clone_lib="RAHINOT01"
/note="Rat, Hippocampus, SD, M, Pool"
ORIGIN
Query Match 57.3%; Score 12.6; DB 14; Length 51;
Best Local Similarity 78.9%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0;

Qy 3 ACAATCACAGTCTGTCGG 21
|||||
Db 25 ACACCTACAGGCTCTCGG 7

RESULT 29
BG386881/c
LOCUS
DEFINITION
mRNA sequence.
57 bp mRNA linear EST
602454676F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:458
mRNA sequence.
BG386881
BG386881.1 GI:13280430
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
REFERENCE
1 (bases 1 to 57)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: sgabs-i@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
```

```

e: LNCM1306 row: 9 column: 19
! quality sequence stop: 57.
! Location/Qualifiers
1. .57
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4583082"
/tissue_type="adenocarcinoma cell line"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH MSC 15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
57.3%; Score 12.6; DB 12; Length 57;
ularity 78.9%; Pred. No. 1.1e+05;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;
ATCACAGTCTCTGCGGA 22
|||||
|CTCACAGTCATCGCGGA 9

37
c12.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone
E:76150 5', mRNA sequence.
37.1 GI:661574
sapiens (human)
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
bases 1 to 58)
ier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
soe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W.,
ins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
lis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
fing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
askis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
Marra, M.
ration and analysis of 280,000 human expressed sequence tags
me Res. 6 (9), 807-828 (1996)
4478
549
act: Wilson RK
ington University School of Medicine
Forest Park Parkway, Box 8501, St. Louis, MO 63108
314 286 1800
314 286 1810
l: est@watson.wustl.edu
rt Size: 126
ce: IMAGE Consortium, LNL This clone is available royalty-free
ugh LNL; contact the IMAGE Consortium (info@image.llnl.gov)
further information.
rt Length: 126 Std Error: 0.00
primer: M13RPI
! quality sequence stop: 282.
! Location/Qualifiers
1. .58
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:505879"
/db_xref="taxon:9606"

/clone="IMAGE:76150"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/note="Organ: ovary; Vector: Bluescript SK; Site 1:
XhoI; Site 2: XhoI; Cloned unidirectionally. Primer
Total ovary tissue, normal, caucasian. Average
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor s:
GAATTCGCGACGAG 3' ~3' adaptor sequence: 5'
CTCAGATTTTTCCTTTTTCCTTTT 3'"

ORIGIN
Query Match 57.3%; Score 12.6; DB 14; Length 58;
Best Local Similarity 78.9%; Pred. No. 1.1e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 3 ACATCACAGTCTCTGCGG 21
|||||
|CTCACAGTCTCTGCGG 28

DB 46 ACAAGTCAGTCTCTGCGG 28

RESULT 31
AA111557/c
LOCUS
DEFINITION
mp33e05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone 1
5' similar to TR:G688443 G688443 ALL-1 PROTEIN ;, MRNA E
AA111557
ACCESSION
AA111557.1 GI:1663509
VERSION
EST.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
1 (bases 1 to 43)
REFERENCE
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R.,
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine#
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 3-4 286 1800
Fax: 3-4 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; cont
IMAGE Consortium (info@image.llnl.gov) for further infor
MGI:347608
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .43
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:572960"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_thymus_2NbMT"
/note="Vector: p7T3D-Pac (Pharmacia) with a mc
polylinker; Site 1: Not I; Site 2: Eco RI; 1st
was primed with a Not I - oligo(dT) primer [5',
TGTACCAACTGAGTGGGAGCGCGCGTTCCTTTTTCCTTTT
3']; double-stranded cDNA was ligated to Eco RI

```

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Donaldo."

ilarity 56.4%; Score 12.4; DB 9; Length 43;

Conservative 72.7%; Pred. No. 1.2e+05; Mismatches 6; Indels 0; Gaps 0;

ACATCAGCTCTCTCGGA 22

|||||

ATCCCACTGCTCTGTGGA 5

2203 43 bp DNA linear GSS 04-SEP-2002  
091457.21.55.x Arabidopsis thaliana TDNA insertion lines  
idopsis thaliana genomic clone SALK\_091457.21.55.x, genomic  
ev sequence.

2203.1 GI:22713084

idopsis thaliana (thale cress)

idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
bases 1 to 43)

so, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
inab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
n, P., Zimmermann, J. and Ecker, J.R.

quence-Indexed Library of Insertion Mutations in the

idopsis genome

blished (2001)

act: Joseph R. Ecker

Institute Genomic Analysis Laboratory (SIGnAL)

Salk Institute for Biological Studies

0 N. Torrey Pines Road, La Jolla, CA 92037, USA

858 453 4100 x1752

858 558 6379

l: ecker@salk.edu

is single pass sequence recovered from the left border of  
. This sequence lies within an annotated exon of At4g37610.

s: TDNA tagged.

Location/Qualifiers

1. .43

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_091457.21.55.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ilarity 56.4%; Score 12.4; DB 28; Length 43;

Conservative 72.7%; Pred. No. 1.2e+05; Mismatches 1; Indels 0; Gaps 0;

ATCAGCTCTCT 17

|||||

ATCAGCTCTCT 18

CC886732/c  
LOCUS

DEFINITION SALK\_148961.18.00.n Arabidopsis thaliana TDNA insertion  
Arabidopsis thaliana genomic clone SALK\_148961.18.00.n,  
survey sequence.

ACCESSION

VERSION CC886732.1 GI:33363088

KEYWORDS GSS.

SOURCE

ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
sematophyta; Magnoliophyta; eudicotyledons; core eudic  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidof  
1 (bases 1 to 51)

REFERENCE

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., F  
Shinn, P., Zimmermann, J. and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

COMMENT

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGnAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left bor  
TDNA. This sequence lies within an annotated exon of At1  
Class: TDNA tagged.

FEATURES

source

1. .51

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_148961.18.00.n"

/clone\_lib="Arabidopsis thaliana TDNA insertion  
note="PCR was performed on Arabidopsis thalian  
each of which contains one or more TDNA insert  
elements. The resultant fragment for each line  
directly sequenced to determine the genomic seq  
the site of insertion. Details of the protocol  
be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

ORIGIN

Query Match 56.4%; Score 12.4; DB 29; Length 51;

Best Local Similarity 92.9%; Pred. No. 1.3e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0;

Oy 1 AGACAATCACAGTC 14

|||||

Db 26 AGACAATCACAGTC 13

RESULT 34

AZ849766/c

LOCUS

DEFINITION 2M0151P13F Mouse 10kb plasmid UGCLM library Mus musculus  
clone UUC2M0151P13 F, genomic survey sequence.

ACCESSION

VERSION AZ849766.1 GI:13034106

KEYWORDS GSS.

SOURCE

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur  
1 (bases 1 to 55)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ham  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T  
Reilly, M., Rose, M., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads fro

mid inserts  
 blished (2000)  
 act: Robert B. Weiss  
 ersity of Utah Genome Center  
 ersity of Utah  
 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 2, USA  
 801 585 5606  
 801 585 7177  
 l: ddunne@genetics.utah.edu  
 rt Length: 10000 Std Error: 0.00  
 e: 0151 row: P column: 13  
 primer: CGTTGTAACAGCGCCAGT  
 is: plasmid ends  
 quality sequence stop: 55.  
 Location/Qualifiers  
 1..55  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0151P13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10Kb plasmid UUGC1M library"  
 /note="Vector: PWB42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (GI:4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

56.4%; Score 12.4; DB 28; Length 55;  
 ilarity 72.7%; Pred. No. 1.3e+05;  
 Conservativity 0; Mismatches 6; Indels 0; Gaps 0;  
 18163  
 ACACATCACAGTCTCTGCGGA 22  
 |||||  
 ACAGGCCAGGCTCTGCAGA 14

18163  
 067586.49.45.x Arabidopsis thaliana TDNA insertion lines  
 idopsis thaliana genomic clone SALK\_067586.49.45.x, genomic  
 ey sequence.  
 18163  
 18163.1 GI:21419034

idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 amatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 [bases 1 to 57]  
 iso J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 zinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 nt, P., Zimmerman, J. and Ecker, J.R.

TITLE  
 JOURNAL  
 COMMENT

A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@alk.edu  
 This is single pass sequence recovered from the left bot  
 TDNA. This sequence lies within an annotated exon of AC1  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..57  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_067586.49.45.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /note="PCR was performed on Arabidopsis thaliana  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic sec  
 the site of insertion. Details of the protocol  
 be found at http://signal.salk.edu/tdna\_protoc

Query Match 56.4%; Score 12.4; DB 28; Length 57;  
 Best Local Similarity 92.9%; Pred. No. 1.3e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;  
 QY 5 AATCACAGTCTCTG 18  
 |||||  
 Db 10 AATCATAGTCTCTG 23

RESULT 36  
 AW059588/c  
 LOCUS  
 AW059588 60 bp mRNA linear EST  
 HuH.best.dncl5.final.cluster\_78 (3) DNCL5 Homo sapiens  
 similar to glutathione peroxidase, mRNA sequence.  
 ACCESSION  
 AW059588  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hom  
 1 (bases 1 to 60)  
 Brenner, S., Williams, S.R., Vermaas, E.H., Storck, T., Moor  
 McCollum, C., Mao, J.I., Kirchner, J.J., Eletter, S., DuBridge  
 Burcham, T. and Albrecht, G.  
 In vitro cloning of complex mixtures of DNA on microbeac  
 separation of differentially expressed cDNAs  
 Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)  
 20144098  
 10677516  
 Contact: Burcham TS  
 LYNX Therapeutics, Inc.  
 25861 Industrial Blvd., Hayward, CA 94545, USA  
 Tel: 510 670 9338  
 Fax: 510 670 9302  
 Email: timb@lynxgen.com  
 Sequence obtained from LYNX Therapeutics Megasort techn  
 Collected from the down-regulated gate. Consensus sequen  
 cences in cluster.  
 High quality sequence stop: 60.  
 Location/Qualifiers  
 1..60  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

FEATURES  
 source

```

/db xref="taxon:9606"
/cell_type="monocytic leukemia"
/cell_line="THP-1 (TIB-202)"
/clone_lib="DNC15"
/notes="Vector: pCR2.1; Cloning of PCR products from
micro-beads carrying 3' end of down-regulated cDNA. THP-1
cells non-induced (treated with DMSO only). "
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56.4%; Score 12.4; DB 9; Length 60;  
 ilarity 92.9%; Pred. No. 1.4e+05;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TACAGTCTCTGC 19  
 |||||  
 TCCAGTCTCTGC 46

3761 60 bp mRNA linear EST 23-AUG-2000  
 3761 DNC15 Homo sapiens cDNA similar to GLUTATHIONE  
 KIDASE, mRNA sequence.  
 3761.1 GI:6652083

sapiens (human)  
 sapiens  
 cyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 bases 1 to 60)  
 ler,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,  
 llum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,  
 am,T. and Albrecht,G.  
 itro cloning of complex mixtures of DNA on microbeads: Physical  
 ration of differentially expressed cDNAs  
 . Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)  
 1098  
 7516  
 act: Burcham TS  
 Therapeutics, Inc.  
 . Industrial Blvd., Hayward, CA 94545, USA  
 510 670 9338  
 510 670 9302  
 t: timbelynxgen.com  
 nce obtained from LVMX Therapeutics Megasort technology.  
 acted from the down-regulated gate.  
 quality sequence stop: 60.  
 Location/Qualifiers  
 1. .60  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_type="monocytic leukemia"  
 /cell\_line="THP-1 (TIB-202)"  
 /clone\_lib="DNC15"  
 /notes="Vector: pCR2.1; Cloning of PCR products from  
 micro-beads carrying 3' end of down-regulated cDNA. THP-1  
 cells non-induced (treated with DMSO only). "

56.4%; Score 12.4; DB 9; Length 60;  
 ilarity 92.9%; Pred. No. 1.4e+05;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TACAGTCTCTGC 19  
 |||||  
 TCCAGTCTCTGC 46

33 37 bp mRNA linear EST 30-JUL-1996

DEFINITION HUMG01659 Human promyelocyte Homo sapiens cDNA clone pm  
 mRNA sequence.

ACCESSION D20683  
 VERSION D20683.1 GI:501779  
 KEYWORDS E8f.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 37)  
 AUTHORS Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y.  
 Yoshinari,H., Arimoto,J. and Matsubara,K.  
 TITLE Gene expression of human promyelocytic cell line HL60 be  
 after induction of differentiation. A new application of  
 cDNA sequencing  
 JOURNAL Unpublished (1993)  
 COMMENT Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T.,  
 Yoshinari,H., Arimoto,J. and Matsubara,K.  
 Institute for Molecular and Cellular Biology  
 Osaka University  
 3-1 Yamada-oka,Suita,Osaka 565,Japan.

FEATURES  
 source  
 1. .37  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="pm2073"  
 /clone\_lib="Human promyelocyte"  
 /note="Female, adult, cell\_line = HL60, cell\_ty  
 promyelocyte. "

ORIGIN  
 Query Match 55.5%; Score 12.2; DB 14; Length 37;  
 Best Local Similarity 82.4%; Pred. No. 1.4e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 6 ATCACAGTCTCTCGGA 22  
 |||||  
 Db 2 ATCCAGTCTCTGAGA 18

RESULT 39  
 BX289471/c  
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-426G01-0  
 DEFINITION genomic survey sequence.

ACCESSION BX289471  
 VERSION BX289471.1 GI:28888467  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., S.  
 and Weisshaar,B.  
 A pipeline for automated high-throughput generation of F  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines  
 Unpublished

REFERENCE 2  
 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and We:  
 A new Arabidopsis thaliana T-DNA mutagenised population  
 for flanking sequence tag based reverse genetics  
 Unpublished  
 3 (bases 1 to 47)  
 Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.  
 Direct Submission  
 Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institut  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829  
 This sequence is recovered from the left border of the T  
 indicats an insertion within the locus defined by clone

ences are generated at the MPI for Plant Breeding Research in context of the GABI-Kat project. GABI-Kat is part of the German Genomics program designated 'GABI'. Information on line availability can be found at:  
 p://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers  
 1. .47  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="CK-426G01-018075"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

55.5%; Score 12.2; DB 29; Length 47;  
 alarity 82.4%; Pred. No. 1.5e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACATCATCAGTCTCT 17  
 |||||  
 ACATCATAGCCTCT 8

18085 53 bp mRNA linear EST 18-AUG-2003  
 --08-M20\_b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 ary (JMT) Oryza sativa cDNA clone JMT--08-M20, mRNA sequence.  
 18085  
 18085.1 GI:33824545

a sativa  
 a sativa  
 rycoya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 artoidae; Oryzeae; Oryza.  
 bases 1 to 53)  
 J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 I.S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 re-scale Sequencing Analysis of Rice ESTs  
 ublished (2003)  
 act: Nahm B.H.  
 mics and Genetics Institute, GreenGene Biotech Inc.; Division  
 ioscience and Bioinformatics, Myongji University  
 in, Kyeonggi, Korea  
 82 31 330 6193  
 82 31 321 6355  
 1: bhnamgbbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1. .53  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="JMT--08-M20"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="AtJMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis Jasmonate Carboxyl

methytransferase overexpression line."

ORIGIN  
 Query Match 55.5%; Score 12.2; DB 14; Length 53;  
 Best Local Similarity 82.4%; Pred. No. 1.6e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGACAATCACAGTCTCT 17  
 |||||  
 Db 36 AGAAATTCACAGTCTCT 52

RESULT 41  
 AZ463714 28 bp DNA linear GSS  
 AZ463714/c  
 LOCUS  
 DEFINITION  
 1M0272C15R Mouse 10kb plasmid UUC1M library Mus musculi  
 clone JUC1M0272C15 R, genomic survey sequence.

ACCESSION  
 AZ463714  
 VERSION  
 AZ463714.1 GI:10621839  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu;  
 1 (bases 1 to 28)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ha;  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen,  
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
 Niedernauser, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads fr

plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 303, Biomedical Polymers Research Bldg., 20 S. 2030  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0272 row: C column: 15  
 Seq primer: CACACGAGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 28.

Location/Qualifiers  
 1. .28  
 /organism="Mus musculus"  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resiste  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA fr  
 musculus C57BL/6J (male) was obtained from the  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/  
 was hydrodynamically sheared by repeated passag  
 0.005 inch orifice at constant velocity. The si  
 was blunt end-repaired with T4 DNA polymerase a  
 polynucleotide kinase. Adaptor oligonucleotides  
 ligated to the blunt ends in high molar excess  
 adapted DNA was purified and size-selected fr  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a  
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-num  
 inducible derivative of plasmid R1. The vector  
 with adaptors complementary to the insert adapt  
 purified. The sheared, adapted mouse DNA was  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Strata

FEATURES  
 Source

and selected for ampicillin resistance."

54.5%; Score 12; DB 28; Length 28;  
 100.0%; Pred. No. 1.5e+05;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATCACAGTCT 15  
 |||||  
 ATCACAGTCT 14

1793 36 bp DNA linear GSS 13-DEC-2000  
 70E18R Mouse 10kb plasmid UGCM library Mus musculus genomic  
 1 UGCM1M0370E18 R, genomic survey sequence.

1793.1 GI:11697160

musculus (house mouse)

musculus  
 Cyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 bases 1 to 36)  
 .D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 ly, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 rhauser, A., and Wright, D., Stokes, R., Tingey, A., von  
 a whole genome scaffolding with paired end reads from 10kb  
 mid inserts

ished (2000)

ict: Robert B. Weiss  
 rsity of Utah Genome Center

rsity of Utah

108. Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 , USA

801 585 5606

801 585 7177

ddunn@genetics.utah.edu

t Length: 10000 Std Error: 0.00

0370 row: E column: 18

primer: CACACGGAACACCTAAGACC

plasmid ends

quality sequence stop: 36.

Location/Qualifiers

1. .36

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGCM1M0370E18"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCM library"

/notes="Vector: FWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWB42 (G1/4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

# ORIGIN

Query Match 54.5%; Score 12; DB 28; Length 36;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGACAATCACAGTCTCTGCG 20  
 |||||  
 Db 15 AGCCATTACAGTGTCTGTG 34

RESULT 43  
 AL947932/c

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-308D12-0  
 genomic survey sequence.

ACCESSION AL947932

VERSION AL947932.1 GI:24404554

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., S.  
 and Weisshaar, B.

A pipeline for automated high-throughput generation of F.  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines  
 Unpublished

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

3 (bases 1 to 41)  
 Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and We  
 A new Arabidopsis thaliana T-DNA mutagenesis population  
 for flanking sequence tag based reverse genetics  
 Unpublished  
 Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829  
 This sequence is recovered from the left border of the T  
 indicates an insertion within the locus defined by clone  
 The sequences are generated at the MPI for Plant Breeding  
 in the context of the GABI-Kat project. GABI-Kat is part  
 German Plant Genomics program designated 'GABI'. Informa  
 line availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES

source

1. .41

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-308D12-015815"

/note="PCR was performed on DNA from Arabidopsis  
 plants (T1) which were transformed with the T-DNA  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from t  
 were directly sequenced to determine the genomic  
 flanking the insertion. Sequences displaying sig  
 similarity to the A. thaliana nuclear genome seq  
 processed for submission. T-DNA derived sequence  
 removed"

# ORIGIN

Query Match 54.5%; Score 12; DB 29; Length 41;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 3 ACAATCACAGTCTCTGCGGA 22



||||| ||| |||  
AGTCACAGATCTCTCGGA 1

4299 45 bp mRNA linear EST 08-SEP-1999  
56940 A. thaliana, Columbia Col-0, rosette-3 Arabidopsis  
iana cDNA clone 701556940, mRNA sequence.  
4299  
4299.1 GI:5851328

idopsis thaliana (thale cress)

idopsis thaliana  
xyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

bases 1 to 45)  
, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,  
, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,  
one, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D.,  
R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C.,  
io, T., Policky, J., Suzuki, G., Argentine, C., Shah, S.,  
iga, A., Murry, L., Turner, C., Krikorian, S., Elder, D. and  
on, D.

idopsis thaliana Gene Expression MicroArray

ublished (1999)  
act: David Smoller, Ph.D.  
me Systems, Inc., a wholly owned subsidiary of Incyte  
maceticals, Inc.  
. World Parkway Circle, St. Louis, MO 63134, USA  
877-577-2733  
314-427-3324

1: service@genomesystems.com.

Location/Qualifiers

1. .45  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/cultivar="Columbia Col-0"  
/db\_xref="taxon:3702"  
/clone="701556940"  
/tissue\_type="rosette"  
/dev\_stages="4 - 7 weeks"  
/clone\_lib="A. thaliana, Columbia Col-0, rosette-3"  
/note="Vector: pSPORT; Site 1: NotI; Site 2: SalI; cDNA  
library was derived from untreated rosette tissue from  
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.  
Plants were grown in 1:1:1 peat moss/vermiculite/perlite  
soil at 22 deg. C +/- 3 deg. C under constant light, and  
watered with fertilizer. cDNA synthesis was initiated  
using a NotI-oligo(dT) primer. Double-stranded cDNA was  
blunted, ligated to SalI adaptors, digested with NotI,  
size-selected, and cloned into the NotI and SalI sites of  
the pSPORT vector."

54.5%; Score 12; DB 9; Length 45;

ilarity 75.0%; Pred. No. 1.9e+05;  
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

TAATCAGATCTCTCTCGGA 22

|||||

CAACACTCTCTCTTTCGGA 38

57345 50 bp DNA linear GSS 18-JUN-2002  
idopsis thaliana T-DNA flanking sequence GK-218E10-014201,  
omic survey sequence.

57345

57345.1 GI:21520464

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidof

REFERENCE

AUTHORS

Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., S

and Weisshaar, B.

A pipeline for automated high-throughput generation of F

(flanking sequence tags) from Arabidopsis thaliana T-DNA

transformed lines

Unpublished

2

REFERENCE

AUTHORS

Strizhov, N., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and We

A new Arabidopsis thaliana T-DNA mutagenised population

for flanking sequence tag based reverse genetics

Unpublished

3 (bases 1 to 50)

Direct Submission

Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institu

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829

This sequence is recovered from the left border of the T

indicates an insertion within the locus defined by clone

The sequences are generated at the MPI for Plant Breedir

in the context of the GABI-Kat project. GABI-Kat is part

German Plant Genomics program designated 'GABI'. Informa

line availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1. .50

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-218E10-014201"

/note="PCR was performed on DNA from Arabidopsis

plants (T1) which were transformed with the T-I

vector pAC161. The lines contain one or more T-

insertions. The DNA fragment(s) resulting from

were directly sequenced to determine the genomic

flanking the insertion. Sequences displaying si

similarity to the A. thaliana nuclear genome se

processed for submission. T-DNA derived sequenc

removed"

Query Match 54.5%; Score 12; DB 29; Length 50;

Best Local Similarity 75.0%; Pred. No. 2e+05; Indels 0;

Matches 15; Conservative 0; Mismatches 5;

QY 2 GACATCAGATCTCTCTCGGG 21

|||||

Db 23 GACAGCCCATCTCTCTCGG 4

Search completed: February 29, 2004, 11:20:00

Job time : 1706.43 secs

09:38:25 2004

us-10-090-326-7.max.rge

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

eic search, using sw model

February 29, 2004, 08:42:24 ; Search time 624.416 Seconds  
(without alignments)  
1388.275 Million cell updates/sec

IS-10-090-326-7

:0 atcctgtctccacgggtt 20

:IDENTITY NUC

lapop 10.0 , Gapext 1.0

1470272 seqs, 2167516995 residues

hits satisfying chosen parameters: 1685580

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

GenEmbl.\*

: gb\_ba.\*  
: gb\_htg.\*  
: gb\_in.\*  
: gb\_om.\*  
: gb\_ov.\*  
: gb\_pat.\*  
: gb\_ph.\*  
: gb\_pl.\*  
: gb\_pr.\*  
: gb\_ro.\*  
: gb\_sts.\*  
: gb\_sy.\*  
: gb\_un.\*  
: gb\_vi.\*  
: em\_ba.\*  
: em\_fun.\*  
: em\_hum.\*  
: em\_in.\*  
: em\_mu.\*  
: em\_om.\*  
: em\_or.\*  
: em\_ov.\*  
: em\_pat.\*  
: em\_ph.\*  
: em\_pl.\*  
: em\_ro.\*  
: em\_sts.\*  
: em\_un.\*  
: em\_vi.\*  
: em\_htg\_hum.\*  
: em\_htg\_in.\*  
: em\_htg\_other.\*  
: em\_htg\_mus.\*  
: em\_htg\_pln.\*  
: em\_htg\_rod.\*  
: em\_htg\_man.\*  
: em\_htg\_vrt.\*  
: em\_sy.\*  
: em\_htgo\_hum.\*  
: em\_htgo\_mus.\*  
: em\_htgo\_other.\*

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being p:  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	15	75.0	17	6	AX723803	AX723803
2	14.8	74.0	20	6	BD268717	BD268717
3	14.8	74.0	20	6	BD268720	BD268720
4	14.8	74.0	20	6	AR229114	AR229114
5	14.8	74.0	20	6	AR229117	AR229117
6	14.8	74.0	20	6	AR281377	AR281377
7	14.8	74.0	20	6	AR281380	AR281380
8	14.8	74.0	20	6	AR304586	AR304586
9	14.8	74.0	20	6	AR304589	AR304589
10	14.8	74.0	20	6	AR337582	AR337582
11	14.8	74.0	20	6	AR337585	AR337585
12	14.8	74.0	20	6	AX696154	AX696154
13	14.4	72.0	38	6	AR216216	AR216216
14	14	70.0	33	6	I11490	I11490 Sec
15	13.6	68.0	24	6	BD234781	BD234781
16	13.6	68.0	24	6	AX011544	AX011544
17	13.6	68.0	32	6	AX089510	AX089510
18	13.4	67.0	20	6	AX601037	AX601037
19	13.4	67.0	29	6	AR176562	AR176562
20	13.4	67.0	29	6	AR176564	AR176564
21	13.4	67.0	29	6	AR342701	AR342701
22	13.4	67.0	29	6	AR342703	AR342703
23	13.4	67.0	41	6	AX517020	AX517020
24	13.4	67.0	41	6	AX519531	AX519531
25	13.2	66.0	20	6	AX167919	AX167919
26	13.2	66.0	30	6	AR095317	AR095317
27	13.2	66.0	30	6	AR172127	AR172127
28	13.2	66.0	30	6	AR173470	AR173470
29	13.2	66.0	32	6	I69389	I69389 Sec
30	13.2	66.0	47	6	AR289265	AR289265
31	13.2	66.0	54	9	HUMC1A201	M22817 Hum
32	13.2	66.0	55	6	AR422169	AR422169
33	13.2	66.0	55	6	BD117722	BD117722
34	13	65.0	31	6	AX248870	AX248870
35	13	65.0	55	8	AJ594698	AJ594698
36	12.8	64.0	17	6	AX674525	AX674525
37	12.8	64.0	21	6	BD226165	BD226165
38	12.8	64.0	22	6	AX663735	AX663735
39	12.8	64.0	22	6	BD133427	BD133427
40	12.8	64.0	24	6	AX289046	AX289046
41	12.8	64.0	28	6	AR090871	AR090871
42	12.8	64.0	28	6	AR197906	AR197906
43	12.8	64.0	28	6	AR260060	AR260060
44	12.8	64.0	37	8	AJ590113	AJ590113
45	12.8	64.0	41	6	AX516800	AX516800
46	12.8	64.0	41	6	AX518956	AX518956
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65	12.8	64.0	60	14	AF466425	AF466425

64.0	60	14	AF466426	AF466426 Hepatitis	139	12.4	62.0	14	6	A89288	A89288 Se
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64.0	60	14	AF466457	AF466457 Hepatitis	c 170	12.4	62.0	60	14	AF466482	AF466482
64.0	60	14	AF466458	AF466458 Hepatitis	c 171	12.4	62.0	60	14	AF466483	AF466483
64.0	60	14	AF466459	AF466459 Hepatitis	c 172	12.4	62.0	60	14	AF466484	AF466484
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64.0	60	14	AF466490	AF466490 Hepatitis	c 176	12.4	62.0	60	14	AF466488	AF466488
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64.0	60	14	AF466501	AF466501 Hepatitis	c 185	12.2	61.0	25	6	AX533636	AX533636
64.0	60	14	AF466502	AF466502 Hepatitis	c 186	12.2	61.0	25	6	AX533637	AX533637
64.0	60	14	AF466503	AF466503 Hepatitis	c 187	12.2	61.0	25	6	AX533638	AX533638
64.0	60	14	AF466504	AF466504 Hepatitis	c 188	12.2	61.0	25	6	AX533639	AX533639
64.0	60	14	AF466505	AF466505 Hepatitis	c 189	12.2	61.0	25	6	AX533640	AX533640
64.0	60	14	AF466506	AF466506 Hepatitis	c 190	12.2	61.0	25	6	AX533641	AX533641
64.0	60	14	AF466508	AF466508 Hepatitis	c 191	12.2	61.0	25	6	AX533642	AX533642
64.0	60	14	AF466509	AF466509 Hepatitis	c 192	12.2	61.0	25	6	AX533643	AX533643
63.0	20	6	AX743539	AX743539 Sequence	c 193	12.2	61.0	29	6	AX010778	AX010778
63.0	20	6	AX774462	AX774462 Sequence	c 194	12.2	61.0	29	6	BD211699	BD211699
63.0	25	6	ES3850	ES3850 LONX gene a	c 195	12.2	61.0	31	6	AR043929	AR043929
63.0	27	6	AR040348	AR040348 Sequence	c 196	12.2	61.0	31	6	AR073462	AR073462
63.0	31	6	AX326596	AX326596 Sequence	c 197	12.2	61.0	31	6	193333	193333 Se
63.0	34	6	AX235755	AX235755 Sequence	c 198	12.2	61.0	31	6	AX022056	AX022056
63.0	41	6	A74298	A74298 Sequence 10	c 199	12.2	61.0	31	6	BD080633	BD080633
63.0	41	6	AR038839	AR038839 Sequence	c 200	12.2	61.0	31	6	BD087579	BD087579
63.0	41	6	BD232071	BD232071 Remedy re	c 201	12.2	61.0	32	6	128720	128720 Se
63.0	41	6	AX014733	AX014733 Sequence	c 202	12.2	61.0	32	6	189374	189374 Se
63.0	43	6	AX287618	AX287618 Sequence	c 203	12.2	61.0	33	6	E09062	E09062 DN
63.0	43	6	AX739903	AX739903 Sequence	c 204	12.2	61.0	33	6	E09066	E09066 DN
63.0	45	6	AR007987	AR007987 Sequence	c 205	12.2	61.0	33	6	AX163908	AX163908
63.0	45	6	AR433004	AR433004 Sequence	c 206	12.2	61.0	36	6	AX472710	AX472710
63.0	51	6	AX204414	AX204414 Sequence	c 207	12.2	61.0	37	6	132360	132360 Se
63.0	52	6	AR086666	AR086666 Sequence	c 208	12.2	61.0	37	6	AX809438	AX809438
63.0	55	6	A10481	A10481 oligonucleo	c 209	12.2	61.0	39	6	AX722230	AX722230
63.0	55	6	A13639	A13639 oligonucleo	c 210	12.2	61.0	39	6	AX722231	AX722231
62.0	14	6	A88021	A88021 Sequence 16	c 211	12.2	61.0	45	6	AR050513	AR050513

61.0	45	6	AR124641	Sequence	AR124641	Sequence	285	11.8	59.0	42	6	AX612023	AX612023
61.0	45	6	AX697100	Sequence	AX697100	Sequence	286	11.8	59.0	44	6	AR058903	AR058903
61.0	48	6	AX160227	Sequence	AX160227	Sequence	287	11.8	59.0	44	6	I36264	I36264
61.0	51	6	AR231224	Sequence	AR231224	Sequence	288	11.8	59.0	45	6	AR096938	AR096938
61.0	51	6	AR308005	Sequence	AR308005	Sequence	289	11.8	59.0	45	6	BD136133	BD136133
61.0	51	6	AX525468	Sequence	AX525468	Sequence	290	11.8	59.0	47	6	AR290943	AR290943
61.0	54	6	BD245074	Regions o	BD245074	Regions o	291	11.8	59.0	49	6	AX150267	AX150267
61.0	56	6	AR086650	Sequence	AR086650	Sequence	292	11.8	59.0	49	6	AX150276	AX150276
61.0	59	6	AX756512	Sequence	AX756512	Sequence	293	11.8	59.0	60	6	I87861	I87861
61.0	60	9	HUMSAU3A03	D49587 Homo sapien	D49587 Homo sapien	294	11.6	58.0	19	6	AX130820	AX130820	
61.0	60	9	HUMSAU3A12	D49596 Homo sapien	D49596 Homo sapien	295	11.6	58.0	20	6	AR268226	AR268226	
61.0	60	9	HUMSAU3A37	D49621 Homo sapien	D49621 Homo sapien	296	11.6	58.0	20	6	AX613642	AX613642	
61.0	60	9	HUMSAU3A39	D49623 Homo sapien	D49623 Homo sapien	297	11.6	58.0	21	6	AR183755	AR183755	
60.0	17	6	BD104906	Kit and m	BD104906 Kit and m	298	11.6	58.0	22	6	A79079	A79079	
60.0	24	6	AR111452	Sequence	AR111452	Sequence	299	11.6	58.0	22	6	AR208215	AR208215
60.0	24	6	AR111452	Sequence	AR111452	Sequence	300	11.6	58.0	23	6	AX454974	AX454974
60.0	24	6	AR159861	Sequence	AR159861	Sequence	301	11.6	58.0	24	6	E39982	E39982
60.0	24	6	I19889	Sequence 14	I19889	Sequence 14	302	11.6	58.0	24	6	AX292639	AX292639
60.0	24	6	I44680	Sequence 15	I44680	Sequence 15	303	11.6	58.0	24	6	BD174982	BD174982
60.0	24	6	I60457	Sequence 15	I60457	Sequence 15	304	11.6	58.0	25	6	AX378888	AX378888
60.0	24	6	I79555	Sequence 14	I79555	Sequence 14	305	11.6	58.0	25	6	BD170447	BD170447
60.0	24	6	AR213260	Sequence	AR213260	Sequence	306	11.6	58.0	26	6	BD160852	BD160852
60.0	24	6	AR216146	Sequence	AR216146	Sequence	307	11.6	58.0	27	6	A84004	A84004
60.0	24	6	AX343407	Sequence	AX343407	Sequence	308	11.6	58.0	27	6	AR091025	AR091025
60.0	27	6	AR109762	Sequence	AR109762	Sequence	309	11.6	58.0	27	6	AR099333	AR099333
60.0	28	6	A44445	Sequence 8	A44445	Sequence 8	310	11.6	58.0	27	6	AR198060	AR198060
60.0	28	6	AR009690	Sequence	AR009690	Sequence	311	11.6	58.0	27	6	AR260214	AR260214
60.0	28	6	I68088	Sequence 8	I68088	Sequence 8	312	11.6	58.0	27	6	AR321623	AR321623
60.0	28	6	AR241823	Sequence	AR241823	Sequence	313	11.6	58.0	27	6	AR391967	AR391967
60.0	28	6	AX696197	Sequence	AX696197	Sequence	314	11.6	58.0	27	6	AX235758	AX235758
60.0	30	6	A42577	Sequence 94	A42577	Sequence 94	315	11.6	58.0	27	6	BD061174	BD061174
60.0	30	6	A88766	Sequence 91	A88766	Sequence 91	316	11.6	58.0	28	6	AR18729	AR18729
60.0	30	6	AX037170	Sequence	AX037170	Sequence	317	11.6	58.0	28	6	AR129941	AR129941
60.0	30	6	AX037186	Sequence	AX037186	Sequence	318	11.6	58.0	28	6	E13294	E13294
60.0	30	6	BD066279	An antise	BD066279 An antise	319	11.6	58.0	28	6	BD132600	BD132600	
60.0	38	6	A86831	Sequence 15	A86831	Sequence 15	320	11.6	58.0	30	6	A84929	A84929
60.0	38	6	A86835	Sequence 19	A86835	Sequence 19	321	11.6	58.0	30	6	AR253029	AR253029
60.0	38	6	AR316941	Sequence	AR316941	Sequence	322	11.6	58.0	31	6	AX248587	AX248587
60.0	38	6	AR316945	Sequence	AR316945	Sequence	323	11.6	58.0	31	6	AX249526	AX249526
60.0	38	6	BD070407	Factor X	BD070407 Factor X	324	11.6	58.0	32	6	A18738	A18738	
60.0	38	6	BD070411	Factor X	BD070411 Factor X	325	11.6	58.0	33	6	AR075177	AR075177	
60.0	41	6	BD224821	Novel pla	BD224821 Novel pla	326	11.6	58.0	33	6	AR112344	AR112344	
60.0	56	8	AY199115	Arabidops	AY199115 Arabidops	327	11.6	58.0	33	6	I87870	I87870	
60.0	57	6	AR381796	Sequence	AR381796	Sequence	328	11.6	58.0	33	6	AR212987	AR212987
60.0	57	6	AR381820	Sequence	AR381820	Sequence	329	11.6	58.0	34	6	I92381	I92381
60.0	57	6	BD107773	Opsonic a	BD107773 Opsonic a	330	11.6	58.0	34	11	C75799	C75799	
59.0	17	6	AX725064	Sequence	AX725064	Sequence	331	11.6	58.0	37	6	AR427970	AR427970
59.0	18	6	AX785461	Sequence	AX785461	Sequence	332	11.6	58.0	37	6	BD057945	BD057945
59.0	20	6	AR107754	Sequence	AR107754	Sequence	333	11.6	58.0	39	6	AL8732	AL8732
59.0	20	6	AR199735	Sequence	AR199735	Sequence	334	11.6	58.0	42	6	AX283147	AX283147
59.0	20	6	AR373464	Sequence	AR373464	Sequence	335	11.6	58.0	42	6	AX283148	AX283148
59.0	20	6	AX060355	Sequence	AX060355	Sequence	336	11.6	58.0	42	6	AX787116	AX787116
59.0	20	6	AX241169	Sequence	AX241169	Sequence	337	11.6	58.0	42	6	AX787120	AX787120
59.0	22	6	AX486753	Sequence	AX486753	Sequence	338	11.6	58.0	43	6	A18731	A18731
59.0	22	6	A57530	Sequence 22	A57530	Sequence 22	339	11.6	58.0	47	6	AR291975	AR291975
59.0	24	6	A57532	Sequence 24	A57532	Sequence 24	340	11.6	58.0	48	6	A79783	A79783
59.0	24	6	AX003689	Sequence	AX003689	Sequence	341	11.6	58.0	48	6	AR018113	AR018113
59.0	25	6	AR340514	Sequence	AR340514	Sequence	342	11.6	58.0	48	6	AR300132	AR300132
59.0	25	6	AX079229	Sequence	AX079229	Sequence	343	11.6	58.0	48	6	BD082071	BD082071
59.0	25	6	AX079233	Sequence	AX079233	Sequence	344	11.6	58.0	50	6	AX199540	AX199540
59.0	25	6	AX079239	Sequence	AX079239	Sequence	345	11.6	58.0	51	6	AX159973	AX159973
59.0	25	6	AX079250	Sequence	AX079250	Sequence	346	11.6	58.0	51	6	AX199539	AX199539
59.0	25	6	AX288125	Sequence	AX288125	Sequence	347	11.6	58.0	51	6	AXJ590706	AXJ590706
59.0	27	6	BD140691	Nucleic a	BD140691 Nucleic a	348	11.6	58.0	54	8	HUMC1A2A	HUMC1A2A	
59.0	27	6	BD182143	Novel cha	BD182143 Novel cha	349	11.6	58.0	54	5	GGTHRS5A2	GGTHRS5A2	
59.0	30	6	BD235494	Deaturas	BD235494 Deaturas	350	11.6	58.0	57	5	AR138369	AR138369	
59.0	30	6	AR204083	Sequence	AR204083	Sequence	351	11.6	58.0	57	6	AR146879	AR146879
59.0	30	6	BD077089	Lipocalin	BD077089 Lipocalin	352	11.6	58.0	57	6	AR390982	AR390982	
59.0	31	11	BX545710	Arabidops	BX545710 Arabidops	353	11.6	58.0	57	6	AR390983	AR390983	
59.0	31	6	BD002655	Gene comp	BD002655 Gene comp	354	11.6	58.0	57	6	AX089676	AX089676	
59.0	41	6	AX517882	Sequence	AX517882	Sequence	355	11.6	58.0	57	6	AX089677	AX089677
59.0	42	6	AX612020	Sequence	AX612020	Sequence	356	11.6	58.0	57	6	AX090131	AX090131
59.0	42	6				357	11.6	58.0	57	6	AX090132	AX090132	

58.0	57	6	AX543227	Sequence	431	11.4	57.0	60	6	AR172689	AR172689
58.0	57	6	AX543228	Sequence	432	11.4	57.0	60	6	AR178633	AR178633
58.0	57	6	BD224575	Adeno-ass	433	11.4	57.0	60	6	BD231077	BD231077
58.0	60	6	AR177888	Sequence	434	11.4	57.0	60	6	AR181204	AR181204
58.0	60	6	BD015073	Recombina	435	11.4	57.0	60	6	AR199885	AR199885
57.0	14	6	A89271	Sequence 14	436	11.4	57.0	60	6	AR231833	AR231833
57.0	14	6	BD066784	An antise	437	11.4	57.0	60	6	AR343308	AR343308
57.0	16	6	AX235525	Sequence	438	11.4	57.0	60	6	AR349626	AR349626
57.0	17	6	AX531569	Sequence	439	11.4	57.0	60	6	AR391097	AR391097
57.0	17	6	AX531570	Sequence	440	11.4	57.0	60	6	AR431540	AR431540
57.0	17	6	AX531571	Sequence	441	11.4	57.0	60	6	BD062822	BD062822
57.0	17	6	AX531572	Sequence	442	11.2	56.0	17	6	BD259296	BD259296
57.0	17	6	AX758411	Sequence	443	11.2	56.0	17	6	AX422037	AX422037
57.0	18	6	AR410492	Sequence	444	11.2	56.0	17	6	AX422038	AX422038
57.0	18	6	AR410497	Sequence	445	11.2	56.0	17	6	AX422743	AX422743
57.0	18	6	AX317302	Sequence	446	11.2	56.0	17	6	AX422744	AX422744
57.0	18	6	AX317307	Sequence	447	11.2	56.0	17	6	AX531574	AX531574
57.0	18	6	AX317450	Sequence	448	11.2	56.0	17	6	AX735662	AX735662
57.0	18	6	AX356968	Sequence	449	11.2	56.0	17	6	BD202678	BD202678
57.0	18	6	AX554986	Sequence	450	11.2	56.0	18	6	AR293569	AR293569
57.0	19	6	AX590226	Sequence	451	11.2	56.0	19	6	AR067185	AR067185
57.0	20	6	AR136257	Sequence	452	11.2	56.0	19	6	AX477615	AX477615
57.0	20	6	BD247712	Antisense	453	11.2	56.0	19	6	AX505035	AX505035
57.0	20	6	AR268227	Sequence	454	11.2	56.0	20	6	BD141129	BD141129
57.0	20	6	AX592301	Sequence	455	11.2	56.0	20	6	AR075709	AR075709
57.0	20	6	AX644649	Sequence	456	11.2	56.0	20	6	AR076702	AR076702
57.0	21	6	AR279122	Sequence	457	11.2	56.0	20	6	AR153559	AR153559
57.0	21	6	AX057940	Sequence	458	11.2	56.0	20	6	BD262874	BD262874
57.0	24	6	AR140036	Sequence	459	11.2	56.0	20	6	BD266176	BD266176
57.0	24	6	AR165203	Sequence	460	11.2	56.0	20	6	I85587	I85587
57.0	24	6	AX443854	Sequence	461	11.2	56.0	20	6	AR182759	AR182759
57.0	25	6	AX197188	Sequence	462	11.2	56.0	20	6	AR300839	AR300839
57.0	25	6	AX197228	Sequence	463	11.2	56.0	20	6	AX224269	AX224269
57.0	25	6	AX447832	Sequence	464	11.2	56.0	20	6	AX370478	AX370478
57.0	25	6	AX533631	Sequence	465	11.2	56.0	20	6	AX719288	AX719288
57.0	25	6	AX533632	Sequence	466	11.2	56.0	20	6	AX805339	AX805339
57.0	25	6	AX533633	Sequence	467	11.2	56.0	21	6	AR124239	AR124239
57.0	25	6	AX533634	Sequence	468	11.2	56.0	21	6	I27417	I27417
57.0	26	6	AR140037	Sequence	469	11.2	56.0	21	6	I27450	I27450
57.0	27	6	AX105635	Sequence	470	11.2	56.0	22	6	E35028	E35028
57.0	28	6	AX111733	Sequence	471	11.2	56.0	22	6	I04331	I04331
57.0	28	6	AR140038	Sequence	472	11.2	56.0	22	6	BD165811	BD165811
57.0	28	6	BD097501	Novel mel	473	11.2	56.0	23	6	AX212235	AX212235
57.0	30	6	A26395	Origonucleo	474	11.2	56.0	23	6	BD143781	BD143781
57.0	30	6	AR021098	Sequence	475	11.2	56.0	23	6	BD168643	BD168643
57.0	30	6	AR140039	Sequence	476	11.2	56.0	24	6	AR004320	AR004320
57.0	30	6	BD229110	Sequence	477	11.2	56.0	24	6	AR080651	AR080651
57.0	30	6	AR308641	Sequence	478	11.2	56.0	24	6	AX444225	AX444225
57.0	30	6	AR431785	Sequence	479	11.2	56.0	24	6	AX548171	AX548171
57.0	31	6	AR300486	Sequence	480	11.2	56.0	25	6	AR302467	AR302467
57.0	32	6	AR428763	Sequence	481	11.2	56.0	25	6	AR302474	AR302474
57.0	33	6	AR027111	Sequence	482	11.2	56.0	25	6	AX448191	AX448191
57.0	36	6	E36446	DNA polymer	483	11.2	56.0	25	6	AX533644	AX533644
57.0	36	6	E36456	DNA polymer	484	11.2	56.0	25	6	BD175838	BD175838
57.0	36	6	E36458	DNA polymer	485	11.2	56.0	25	6	BD175845	BD175845
57.0	36	6	I13347	Sequence 1	486	11.2	56.0	26	6	AX675927	AX675927
57.0	36	6	I13357	Sequence 14	487	11.2	56.0	27	6	AX023887	AX023887
57.0	36	6	I13359	Sequence 16	488	11.2	56.0	27	6	BD182141	BD182141
57.0	36	6	AR359217	Sequence	489	11.2	56.0	27	6	BD186062	BD186062
57.0	36	6	BD085156	Sequence	490	11.2	56.0	28	6	BD186065	BD186065
57.0	36	8	ATH552316	Arabidops	491	11.2	56.0	28	6	AR090622	AR090622
57.0	38	6	AX565083	Sequence	492	11.2	56.0	28	6	AR197657	AR197657
57.0	39	6	AR007971	Sequence	493	11.2	56.0	28	6	AR259811	AR259811
57.0	39	6	I16905	Sequence 10	494	11.2	56.0	28	6	AR302941	AR302941
57.0	39	6	I69498	Sequence 10	495	11.2	56.0	28	6	AX024605	AX024605
57.0	42	6	AR018115	Sequence	496	11.2	56.0	28	6	AX598169	AX598169
57.0	42	6	AR079785	Sequence 12	497	11.2	56.0	28	6	BD091310	BD091310
57.0	42	6	AR018115	Sequence	498	11.2	56.0	28	6	BD223220	BD223220
57.0	45	6	AX612451	Sequence	499	11.2	56.0	29	6	AR039142	AR039142
57.0	46	6	AX665082	Sequence	500	11.2	56.0	29	6	AR065272	AR065272
57.0	47	6	AR291957	Sequence	501	11.2	56.0	29	6	BD061656	BD061656
57.0	49	6	E08249	linker. 9/1	502	11.2	56.0	30	6	I06862	I06862
57.0	49	6	I78449	Sequence 3	503	11.2	56.0	30	6	I07313	I07313

56.0	30	6	AR427956	AR427956 Sequence	c 577	11.2	56.0	57	6	BD141873
56.0	30	6	AR433332	AR433332 Sequence	578	11.2	56.0	58	6	A62961
56.0	30	6	AR433332	AR433332 Sequence	579	11.2	56.0	59	6	AR267016
56.0	30	10	RRNF116B	X66573 R.rattus Hn	c 580	11.2	56.0	59	6	AX113783
56.0	31	6	AR069595	AR069595 Sequence	c 581	11.2	56.0	60	6	E30083
56.0	31	6	AR091464	AR091464 Sequence	c 582	11.2	56.0	60	14	AF466492
56.0	31	6	AR104415	AR104415 Sequence	c 583	11.2	56.0	60	14	AF466507
56.0	31	6	AR260540	AR260540 Sequence	584	11	55.0	17	6	AX732402
56.0	31	6	AR248269	AR248269 Sequence	585	11	55.0	17	6	BD203109
56.0	31	6	AX329339	AX329339 Sequence	586	11	55.0	17	6	BD203110
56.0	31	6	AX743565	AX743565 Sequence	587	11	55.0	17	6	BD203111
56.0	31	8	ATH524599	ATH524599 Arabidops	588	11	55.0	18	6	AR073436
56.0	32	6	AR110560	AR110560 Sequence	589	11	55.0	18	6	BD250760
56.0	32	6	AR151780	AR151780 Sequence	c 590	11	55.0	18	6	AX443449
56.0	32	6	AR219996	AR219996 Sequence	591	11	55.0	20	6	AR136444
56.0	32	6	AR220713	AR220713 Sequence	c 592	11	55.0	20	6	E36664
56.0	32	6	BD063041	BD063041 Protease-	593	11	55.0	20	6	AR221423
56.0	34	6	AR302546	AR302546 Sequence	594	11	55.0	20	6	AR314814
56.0	34	6	AX101011	AX101011 Sequence	595	11	55.0	20	6	AX429760
56.0	34	6	AX472708	AX472708 Sequence	c 596	11	55.0	20	6	AX521736
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## ALIGNMENTS

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linear PAT 08-MAY-2003

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
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 artificial sequences.  
 1 (bases 1 to 20)  
 SHEPPARD,P.O., LASSER,G.W. and Bishop,P.D.  
 Inhibitors for use in hemostasis and immune function  
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 PF 17-FEB-2000 JP 2000599415  
 PR 15-FEB-1999 US 09/253604,22-NOV-1999 US 09/44  
 PAUL O SHEPPARD,GERALD W LASSER,PAUL D BISHOP PC  
 A61K38/00,A61P7/04,A61P9/08,A61P9/10,A61P17/02,A61P43/00  
 A61K39/395  
 PC A61K39/395,A61K45/00,C07K14/47,C12N15/09,A61K37/02,  
 CC Oligonucleotide ZC13651  
 FH Key Location/Qualifiers  
 FT source 1..20  
 /organism="Artificial Sequence".  
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 1. 20  
 Location/Qualifiers  
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 Query Match 74.0%; Score 14.8; DB 6; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 6.9e+03; Indels 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0;  
 Qy 3 CCTTGTCTCCTCCACGGTT 20  
 |||||  
 Db 1 CTTTGTCTCCTCCACGGTT 18  
 |||||  
 RESULT 3  
 BD268720/c  
 LOCUS  
 DEFINITION Inhibitors for use in hemostasis and immune function.  
 BD268720 20 bp DNA linear PAT

us-10-090-326-7.max.rge

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ACCESSION AR229117.1 GI:27268262
VERSION AR229117.1
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Sheppard,P.O., Lasser,G.W. and Bishop,P.D.
TITLE Methods of promoting blood flow within the vasculature o
JOURNAL Patent: US 648221-A 15 10-SEP-2002;
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 88.9%; Pred. No. 6.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CTTGTCTCTCCACGGTT 20
| | | | | | | | | | | | | | | |
Db 20 CTTGTCTCTCCACGGTT 3

RESULT 6
LOCUS AR281377
DEFINITION Sequence 12 from patent US 6518403.
ACCESSION AR281377
VERSION AR281377.1 GI:29717043
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Sheppard,P.O.
TITLE Antibodies that bind an adipocyte-specific protein homol
JOURNAL Patent: US 6518403-A 12 11-FEB-2003;
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"

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QY 3 CTTGTCTCTCCACGGTT 20
| | | | | | | | | | | | | | | |
Db 1 CTTGTCTCTCCACGGTT 18

RESULT 7
LOCUS AR281380/c
DEFINITION Sequence 15 from patent US 6518403.
ACCESSION AR281380
VERSION AR281380.1 GI:29717046
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Sheppard,P.O.
TITLE Antibodies that bind an adipocyte-specific protein homol
JOURNAL Patent: US 6518403-A 15 11-FEB-2003;
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74.0%; Score 14.8; DB 6; Length 20;  
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TTGTCTCTCCACGGTTT 20  
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TTGTCTCTCCACGGTTT 3

4586 20 bp DNA PAT 12-JUN-2003  
ence 12 from patent US 6544946.  
4586  
4586.1 GI:31693749

OWN.  
OWN.  
asified.  
bases 1 to 20)  
pard,P.O., Lasser,G.W. and Bishop,P.D.  
bitors for use in hemostasis and immune function  
nt: US 6544946-A 12 08-APR-2003;  
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TTGTCTCTCCACGGTTT 20  
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TTGTCTCTCCACGGTTT 18

4589 20 bp DNA PAT 12-JUN-2003  
ence 15 from patent US 6544946.  
4589  
4589.1 GI:31693752

OWN.  
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asified.  
bases 1 to 20)  
pard,P.O., Lasser,G.W. and Bishop,P.D.  
bitors for use in hemostasis and immune function  
nt: US 6544946-A 15 08-APR-2003;  
Location/Qualifiers  
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Conservative 0; Mismatches 2; Indels 0;

TTGTCTCTCCACGGTTT 20  
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TTGTCTCTCCACGGTTT 3

47582 20 bp DNA PAT 17-AUG-2003  
ence 12 from patent US 6566499.  
47582

VERSION AR337582.1 GI:33723983  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Sheppard,P.O.  
TITLE Adipocyte-specific protein homologs  
JOURNAL Patent: US 6566499-A 12 20-MAY-2003;  
FEATURES Location/Qualifiers  
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source /organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 74.0%; Score 14.8; DB 6; Length 20;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CCTTGTCTCTCCACGGTTT 20  
|||||  
Db 1 CTTTGTCTCTCCACGGTTT 18

RESULT 11  
AR337585/c  
LOCUS AR337585 20 bp DNA linear PAT  
DEFINITION Sequence 15 from patent US 6566499.  
ACCESSION AR337585  
VERSION AR337585.1 GI:33723986  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Sheppard,P.O.  
TITLE Adipocyte-specific protein homologs  
JOURNAL Patent: US 6566499-A 15 20-MAY-2003;  
FEATURES Location/Qualifiers  
1..20  
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/mol\_type="genomic DNA"

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Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CCTTGTCTCTCCACGGTTT 20  
|||||  
Db 20 CTTTGTCTCTCCACGGTTT 3

RESULT 12  
AX696154  
LOCUS AX696154 20 bp DNA linear PAT  
DEFINITION Sequence 53 from Patent WO03008640.  
ACCESSION AX696154  
VERSION AX696154.1 GI:29419314  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Whittaker,P.A., Meyers,D.A., Postma,D.S. and Bleesker,E.  
TITLE Asthma-associated gene  
JOURNAL Patent: WO 03008640-A 53 30-JAN-2003;  
Novartis AG (CH); Novartis Pharma GmbH (AT); Wake Fore  
University Health Sciences (US); Rijksuniversiteit te G  
(NL)

FEATURES Location/Qualifiers  
source 1..20

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us-10-090-326-7.max.rge

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/db\_xref="taxon:9606"

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Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCTCCACGG 18  
|||||  
CTGCTCTCCACGG 20

216 38 bp DNA linear PAT 25-SEP-2002  
nce 2 from patent US 6410710.

216.1 GI:23314670

wn.  
wn.  
ssified.  
ases 1 to 38)  
man,S. and Van Eyndhoven,W.  
ic acid encoding a TRAF-3 deletion isoform  
it: US 6410710-A 2 25-JUN-2002;  
Location/Qualifiers  
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72.0%; Score 14.4; DB 6; Length 38;  
ilarity 93.8%; Pred. No. 1.2e+04;  
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TTGTCTCTCCACGG 17  
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TTGTCTCTCCACGG 17

10 33 bp DNA linear PAT 26-JUL-1995  
nce 44 from Patent US 5407795.

10.1 GI:909008

wn.  
wn.  
ssified.  
ases 1 to 33)  
rg,J.A., Shen,L.-P. and Urdea,M.S.  
probes for use in solution phase sandwich  
it: US 5407795-A 44 18-APR-1995;  
Location/Qualifiers  
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/mol\_type="unassigned DNA"

70.0%; Score 14; DB 6; Length 33;  
ilarity 100.0%; Pred. No. 1.9e+04;  
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TTGTCTCTCCACG 16  
|||||  
TTGTCTCTCCACG 31

B0234781/c  
LOCUS  
DEFINITION

24 bp DNA linear PAT  
Polypeptide having immunogenic properties and modified b  
protein function.

ACCESSION  
BD234781.1 GI:33044551

VERSION  
JP 2002512801-A/4.

KEYWORDS

SOURCE  
synthetic construct

ORGANISM  
artificial sequences.

REFERENCE  
1 (bases 1 to 24)

AUTHORS  
Gissmann,L. and Jochmus,I.

TITLE  
Polypeptide having immunogenic properties and modified b  
protein function

JOURNAL  
Patent: JP 2002512801-A 4 08-MAY-2002;

COMMENT  
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICH

OS Artificial Sequence

PN JP 2002512801-A/4

PD 08-MAY-2002

PF 30-APR-1999 JP 2000546020

PR 30-APR-1998 DE 198 19 476.5

PI LUTZ GISSMANN,INGRID JOCHMUS

PC C12N15/09,A61K38/00,A61K48/00,C07K14/025,C12N1/15,C

PC C12N1/21,C12P21/02,C12N15/00,A61K37/02,C12N5/00 CC

Description of Artificial Sequence: Primer

PH Key Location/Qualifiers

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FT /organism='Artificial Sequence'.

Location/Qualifiers

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/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

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Query Match 68.0%; Score 13.6; DB 6; Length 24;

Best Local Similarity 80.0%; Pred. No. 3e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 1 ATCCTTGCTCTCCACGGTT 20

|||||

Db 21 ATCCTCTCTCTCTCGGTT 2

|||||

RESULT 16

AX011544/c

LOCUS 24 bp DNA linear PAT

DEFINITION Sequence 6 from Patent WO955876.

ACCESSION AX011544

VERSION AX011544.1 GI:9998083

KEYWORDS

SOURCE  
synthetic construct

ORGANISM  
artificial sequences.

REFERENCE  
1

AUTHORS  
Gissmann,L. and Jochmus,I.

TITLE  
Polypeptide with immunogenic properties and with a prote

JOURNAL  
modified biological functions

Patent: WO 995876-A 6 04-NOV-1999;

DEUTSCHES KREBSFORSCH (DE); GISSMANN LUTZ (DE); JOCHMUS :

Location/Qualifiers

1. .24

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="Primer"

ORIGIN

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Best Local Similarity 80.0%; Pred. No. 3e+04;

Matches 16; Conservative 0; Mismatches 4; Indels 0;

CTTGTCTCTCCACGGGTT 20  
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CTCTCTCTCTCTGGTT 2

9510 32 bp DNA linear PAT 21-MAR-2001

ence 2 from Patent WO0116299.

9510

9510.1 GI:13443747

etic construct

etic construct

icial sequences.

J.P.M., Riggs, B.L., Khosla, S. and Russel, S.T.

of dna encoding osteoprotegerin to prevent or inhibit metabolic

disorders

at: WO 0116299-A 2 08-MAR-2001;

FOUNDATION (US)

Location/Qualifiers

1..32

/organism="synthetic construct"

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/db\_xref="taxon:32630"

/note="A primer"

68.0%; Score 13.6; DB 6; Length 32;

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Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CTTGTCTCTCCACGGGTT 20

|||||

CTTATCATCCATGGGAT 28

1037 20 bp DNA linear PAT 17-FEB-2003

ence 132 from Patent WO02092851.

1037

1037.1 GI:28401110

etic construct

etic construct

icial sequences.

S.M.M. and Swinburne, J.E.

tic typing

nt: WO 02092851-A 132 21-NOV-2002;

AL HEALTH TRUST (GB); The British Horseracing Board (GB)

Location/Qualifiers

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/organism="synthetic construct"

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/db\_xref="taxon:32630"

/note="Primer"

67.0%; Score 13.4; DB 6; Length 20;

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Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CCTTGTCTCTCCAC 15

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CCTTGGCTCTCCAC 6

6562 29 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 5 from patent US 6312892.

ACCESSION AR176562

VERSION AR176562.1 GI:17918917

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)

AUTHORS Barany, F., Luo, J., Khanna, M. and Bergstrom, D.E.

TITLE High fidelity detection of nucleic acid differences by 1.

JOURNAL detection reaction

Patent: US 6312892-A 5 06-NOV-2001;

FEATURES Location/Qualifiers

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/organism="unknown"

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Query Match 67.0%; Score 13.4; DB 6; Length 29;

Best Local Similarity 93.3%; Pred. No. 3.9e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0;

Qy 3 CCTTGTCTCTCCACGG 17

|||||

Db 14 CCTTGTCTCTCCACGG 28

RESULT 20

AR176564

LOCUS

Sequence 7 from patent US 6312892.

ACCESSION AR176564

VERSION AR176564.1 GI:17918919

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)

AUTHORS Barany, F., Luo, J., Khanna, M. and Bergstrom, D.E.

TITLE High fidelity detection of nucleic acid differences by 1.

JOURNAL detection reaction

Patent: US 6312892-A 7 06-NOV-2001;

FEATURES Location/Qualifiers

1..29

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Query Match 67.0%; Score 13.4; DB 6; Length 29;

Best Local Similarity 93.3%; Pred. No. 3.9e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0;

Qy 3 CCTTGTCTCTCCACGG 17

|||||

Db 14 CCTTGTCTCTCCACGG 28

RESULT 21

AR342701

LOCUS

Sequence 5 from patent US 6576453.

ACCESSION AR342701

VERSION AR342701.1 GI:33737888

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)

AUTHORS Barany, F., Luo, J., Khanna, M. and Bergstrom, D.E.

TITLE Thermostable DNA ligase mutants

JOURNAL Patent: US 6576453-A 5 10-JUN-2003;

FEATURES Location/Qualifiers

1..29

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67.0%; Score 13.4; DB 6; Length 29;  
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Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TTGTCTCCACGG 17  
|||||  
TTGTCTCCACGG 28

2703 29 bp DNA linear PAT 17-AUG-2003  
ence 7 from patent US 6576453.  
2703  
2703.1 GI:33737890

own.  
own.  
assified.  
ases 1 to 29)  
y, F., Luo, J., Khanna, M. and Bergstrom, D. E.  
ostable DNA ligase mutants  
at: US 6576453-A 7 10-JUN-2003;  
Location/Qualifiers  
1. 29  
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67.0%; Score 13.4; DB 6; Length 29;  
ilarity 93.3%; Pred. No. 3.9e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TTGTCTCCACGG 17  
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TTGTCTCCACGG 28

7020 41 bp DNA linear PAT 05-OCT-2002  
ence 3218 from Patent WO02052044.  
7020  
7020.1 GI:23565323

sapiens (human)  
sapiens  
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
mura, Y., Sekine, A., Iida, A. and Saito, S.  
ction of genetic polymorphisms  
nt: WO 02052044-A 3218 04-JUL-2002;  
n (JP)  
Location/Qualifiers  
1. 41  
/organism="Homo sapiens"  
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67.0%; Score 13.4; DB 6; Length 41;  
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Conservative 1; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCCACGGGT 19  
|||||  
TTGTCTCCACGGGT 17

RESULT 24  
AX519531/c  
LOCUS  
DEFINITION  
Sequence 5729 from Patent WO02052044.  
ACCESSION  
AX519531  
VERSION  
AX519531.1 GI:23569850  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom

REFERENCE  
1  
AUTHORS  
Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE  
Detection of genetic polymorphisms  
JOURNAL  
Patent: WO 02052044-A 5729 04-JUL-2002;  
Riken (JP)  
FEATURES  
Location/Qualifiers  
source  
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QY 3 CCTGTCTCCACGGGT 19  
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DB 33 CCTGTCTCCACGGGT 17

RESULT 25  
AX167919/c  
LOCUS  
DEFINITION  
Sequence 103 from Patent WO0142307.  
ACCESSION  
AX167919  
VERSION  
AX167919.1 GI:14597239  
KEYWORDS  
SOURCE  
synthetic construct  
ORGANISM  
artificial sequences.

REFERENCE  
1  
AUTHORS  
Saito, K., Ohe, N. and Satch, H.  
TITLE  
Mutant er g(a) and test systems for transactivation  
JOURNAL  
Patent: WO 0142307-A 103 14-JUN-2001;  
Sumitomo Chemical Company, Limited (JP)  
FEATURES  
Location/Qualifiers  
source  
1. 20  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="Designed oligonucleotide primer for PCR"

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QY 2 TCCTTGTCTCCACGGGT 19  
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DB 20 TCCTTGTCTCCACGGAT 3

RESULT 26  
AR095317/c  
LOCUS  
DEFINITION  
Sequence 8 from patent US 6004557.  
ACCESSION  
AR095317  
VERSION  
AR095317.1 GI:10023086  
KEYWORDS  
SOURCE  
Unknown.

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own.
classified.
bases 1 to 30)
rds,S.John., Cox,J.Cooper., Webb,E.Ann. and Frazer,I.
ants of human papillomavirus antigens
nt: US 6004557-A 8 21-DEC-1999;
Location/Qualifiers
1..30
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66.0%; Score 13.2; DB 6; Length 30;
ilarity 83.3%; Pred. No. 4.9e+04;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

'CCCTGTCTCTCCACGGG 18
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'CCCTCTCTCTCCCGGG 3

'2127 30 bp DNA PAT 17-DEC-2001
ence 8 from patent US 6303128.
'2127
'2127.1 GI:17911618
own.
own.
classified.
(bases 1 to 30)
,E.Ann. and Edwards,S.John.
od for protein expression
nt: US 6303128-A 8 16-OCT-2001;
Location/Qualifiers
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66.0%; Score 13.2; DB 6; Length 30;
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Conservative 0; Mismatches 3; Indels 0; Gaps 0;

'CCCTGTCTCTCCACGGG 18
|||||
'CCCTCTCTCTCCCGGG 3

'3470 30 bp DNA PAT 17-DEC-2001
ence 8 from patent US 6306397.
'3470
'3470.1 GI:17913790
own.
own.
classified.
(bases 1 to 30)
rds,S.John., Cox,J.Cooper., Webb,E.Ann. and Frazer,I.
ants of human papilloma virus antigens
nt: US 6306397-A 8 23-OCT-2001;
Location/Qualifiers
1..30
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/mol_type="unassigned DNA"

66.0%; Score 13.2; DB 6; Length 30;
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Conservative 0; Mismatches 3; Indels 0; Gaps 0;

'CCCTGTCTCTCCACGGG 18
|||||
'CCCTCTCTCTCCCGGG 3

own.
own.
classified.
(bases 1 to 47)
Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 1000 25-MAR-2003;
Location/Qualifiers
1..47
/organism="unknown"
/mol_type="genomic DNA"

66.0%; Score 13.2; DB 6; Length 47;
Best Local Similarity 83.3%; Pred. No. 5.1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTTGCTCTCCACGGT 19
|||||
DB 2 TCCTTGCTCTCCACGGT 19

RESULT 31
HUMC1A20I
LOCUS Human mutant alpha-2 type I collagen (COL1A2) gene, Part
DEFINITION M22817 M20904
ACCESSION M22817.1 GI:179606
VERSION alpha-2 type I collagen; collagen; osteogenesis imperfec
KEYWORDS Homo sapiens (human)
SOURCE
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QY 1 ATCCTTGCTCTCCACGGG 18  
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DB 20 ATCCTTGCTCTCCACGGG 3

RESULT 29  
I69389  
LOCUS Sequence 2 from patent US 5677277.  
DEFINITION I69389  
ACCESSION I69389  
VERSION I69389.1 GI:2831511  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Yatsu,F.M., Alam,N.A. and Alam,S.S.  
TITLE Brain endothelial cell protein induced by nerve growth f  
JOURNAL Patent: US 5677277-A 2 14-OCT-1997;  
FEATURES Location/Qualifiers  
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source  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 66.0%; Score 13.2; DB 6; Length 32;  
Best Local Similarity 83.3%; Pred. No. 5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 ATCCTTGCTCTCCACGGG 18  
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DB 15 ATCCTTGCTCTCCACGGG 32

RESULT 30  
AR289265  
LOCUS Sequence 1000 from patent US 6537751.  
DEFINITION AR289265  
ACCESSION AR289265  
VERSION AR289265.1 GI:31676549  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 47)  
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
TITLE Biallelic markers for use in constructing a high density  
disequilibrium map of the human genome  
JOURNAL Patent: US 6537751-A 1000 25-MAR-2003;  
FEATURES Location/Qualifiers  
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source  
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ORIGIN  
Query Match 66.0%; Score 13.2; DB 6; Length 47;  
Best Local Similarity 83.3%; Pred. No. 5.1e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTTGCTCTCCACGGT 19  
|||||  
DB 2 TCCTTGCTCTCCACGGT 19

RESULT 31  
HUMC1A20I  
LOCUS Human mutant alpha-2 type I collagen (COL1A2) gene, Part  
DEFINITION M22817 M20904  
ACCESSION M22817.1 GI:179606  
VERSION alpha-2 type I collagen; collagen; osteogenesis imperfec  
KEYWORDS Homo sapiens (human)  
SOURCE

09:38:25 2004

us-10-090-326-7.max.rge

sapiens  
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ases 1 to 54)  
rup, R.J., Cohn, D.H., Cohen, T., and Byers, P.H.  
line for glycine substitution in the triple-helical domain of  
products of one alpha 2(I) collagen allele (COL1A2) produces  
osteogenesis imperfecta type IV phenotype  
ol. Chem. 263 (16), 7734-7740 (1988)

63  
nal source text: Human (individuals I-1 and II-4) skin  
blast DNA.  
utant alpha-2 type I collagen causes osteogenesis imperfecta.

Location/Qualifiers  
1. .54  
/organism="Homo sapiens"  
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/map="7q21.3-q22.1"  
1. .54  
/gene="COL1A2"  
<1. >54  
/gene="COL1A2"  
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/codon\_start=1  
/protein\_id="AA51846.1"  
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/translation="GPPGPPGPPRVSGG"  
osome 7q21.3-q22.1.

66.0%; Score 13.2; DB 9; Length 54;  
larity 83.3%; Pred. No. 5.1e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTCTCTCCACGGGT 19  
|||||  
TGGACCTCCACGGTGT 41

1169 55 bp DNA linear PAT 18-DEC-2003  
nce 13666 from patent US 6639063.  
1169  
1169.1 GI:40177279

wn.  
ssified.  
ases 1 to 55)  
ds, J.-B.D.M., Jobert, S. and Giordano, J.-Y.  
and encoded human proteins  
it: US 6639063-A 13666 28-OCT-2003;  
Location/Qualifiers  
1. .55  
/organism="unknown"  
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66.0%; Score 13.2; DB 6; Length 55;  
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Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTCTCTCCACGGGT 19  
|||||  
TCTCTCTCCACGGCT 1

7722 55 bp DNA linear PAT 18-SEP-2002

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

EST and encoded human protein.  
BD117722  
BD117722.1 GI:23212626  
JP 2002010789-A/9799.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo  
1 (bases 1 to 55)  
Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.  
EST and encoded human protein  
Patent: JP 2002010789-A 9799 15-JAN-2002;  
GENSET CORP  
OS Homo sapiens (human)  
PN JP 2002010789-A/9799  
PD 15-JAN-2002  
PF 07-AUG-2000 JP 2000280989  
PR 05-AUG-1999 US 60/147499  
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN  
GIORDANO  
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N15/00  
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FH Key Location/Qualifiers  
FT source 1. .55  
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FEATURES  
source

1. .55  
Location/Qualifiers  
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ORIGIN

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Best Local Similarity 83.3%; Pred. No. 5.1e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTGTCTCTCCACGGGT 19  
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18 TCCTCTCTCTCCACGGCT 1

Db

RESULT 34  
AX248870/c

LOCUS  
AX248870  
DEFINITION  
Sequence 949 from Patent WO0166800.  
ACCESSION  
AX248870  
VERSION  
AX248870.1 GI:15963493  
KEYWORDS  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1  
Cargill, M., Ireland, J.S. and Lander, E.S.  
Human single nucleotide polymorphisms  
Patent: WO 0166800-A 949 13-SEP-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)

Location/Qualifiers  
1. .31  
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ORIGIN

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Best Local Similarity 86.7%; Pred. No. 6.3e+04;  
Matches 13; Conservative 1; Mismatches 1; Indels 0;

QY 3 CCTGTCTCTCCACGG 17  
|||||  
|||||



TTGTCGCCACGG 10

4698 idopsis thaliana T-DNA flanking sequence, left border, clone 08.

4698 55 bp DNA linear PLN 23-OCT-2003  
 4698 GI:37944322  
 Border; T-DNA flanking sequence.  
 idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 aud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,  
 vin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
 niec, L., Caboche, M. and Lecharny, A.  
 A integration into the Arabidopsis genome depends on sequences  
 re-insertion sites  
 Rep. 3 (12), 1152-1157 (2002)  
 3535  
 6565  
 bases 1 to 55)  
 ergue, S.  
 ct Submision  
 dited (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
 on Crenieux, 91057 Evry cedex, FRANCE  
 was performed on DNA from transformants of Arabidopsis thaliana  
 its from INRA (Versailles). The DNA fragment (s) resulting from  
 PCR were directly sequenced from the left or the right border  
 determine the genomic sequence flanking the insertion. T-DNA  
 ved sequences were removed. Information to order the  
 responding mutant line and a link to a database providing a  
 hical display of the insertion site are available at  
 ://dbgap.versailles.inra.fr/publiclines/. This sequence has  
 generated in the framework of the French plant genomics  
 ram 'Genoplante' (http://www.genoplante.com and  
 ://genoplante-info.infobiogen.fr).  
 Location/Qualifiers  
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65.0%; Score 13; DB 8; Length 55;  
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GTCTCCACGG 17  
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 GTCTCCACGG 17

74525 idopsis thaliana T-DNA flanking sequence, left border, clone 08.

74525 17 bp DNA linear PAT 27-MAR-2003  
 74525 GI:29332873

> sapiens (human)  
 > sapiens  
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS  
 TITLE

JOURNAL  
 Patent: WO 03004526-A 2970 16-JAN-2003;  
 Molecular Engines Laboratories (FR)  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
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FEATURES  
 source

ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 17;  
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 Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 4 CTTCTCCTCCACGGT 19  
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 Db 17 CTTCTCCTCCACGAT 2

RESULT 37  
 BD226165

LOCUS  
 DEFINITION  
 BD226165 Glaucoma therapeutics and diagnostics based on a novel T  
 transcriptions factor.

ACCESSION  
 BD226165.1 GI:33035935

VERSION  
 JP 2002511265-A/16.

KEYWORDS  
 synthetic construct  
 SOURCE  
 synthetic construct  
 ORGANISM  
 artificial sequences.

REFERENCE  
 1 (bases 1 to 21)

AUTHORS  
 Sheffield, V.C., Alward, W.L.M., Stone, E.M., Nishimura, D.  
 Patil, S.

TITLE  
 Glaucoma therapeutics and diagnostics based on a novel T  
 transcriptions factor

JOURNAL  
 Patent: JP 2002511265-A 16 16-APR-2002;  
 THE UNIVERSITY OF IOWA RESEARCH FOUNDATION

COMMENT

OS Artificial Sequence  
 PN JP 2002511265-A/16  
 PD 16-APR-2002  
 PF 14-APR-1999 JP 2000543608  
 PR 15-APR-1998 US 60/081870, 22-MAY-1998 US 09/08  
 VAL C SHEFFIELD, WALLACE L M ALWARD, EDWIN M STONE, DARRYL  
 NISHIMURA,

PI SHIVA PATIL  
 PC C:2N15/00, A61K45/00, A61P27/06, C07K14/47, C12N1/15, C1  
 C12N1/21,  
 PC C12N5/10, C12P21/02, C12Q1/68, G01N33/15, G01N33/50, C12  
 C12N5/00

CC Description of Artificial Sequence: primer

FH Key Location/Qualifiers

FT source 1..21  
 FT /organism='Artificial Sequence'.  
 Location/Qualifiers

FEATURES  
 source

1..21  
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QY 2 TCCTGTCTCCTCCACGG 17  
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 Db 3 TCCTGTCTCCTCCACGG 18

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735 22 bp DNA linear PAT 22-MAR-2003  
nce 110 from Patent WO02097127.  
735  
735.1 GI:29163915

etic construct  
etic construct  
ical sequences.  
rs.N., Gehrman.M., Kallabis,H., Hall,R., Schulze,T. and  
el,C.  
and proteins for prevention, prediction, diagnosis, prognosis  
reatment of chronic lung disease  
it: WO 02097127-A 110 05-DEC-2002;  
Aktiengesellschaft (DE)  
Location/Qualifiers  
1..22  
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/note="M96233 reverse primer"

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Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGCTCTCCACCG 17  
TTGACCTCCACCG 4

.427 22 bp DNA linear PAT 18-SEP-2002  
d for assaying glutathione S-transferase, and probe and kit  
for.

.427  
.427.1 GI:23228372  
02058483-A/25.  
ntified  
ntified  
ssified.  
ases 1 to 22)  
mura,M., Yaguchi,H., Naito,S. and Hiraoka,I.  
d for assaying glutathione S-transferase, and probe and kit  
for  
it: JP 2002058483-A 25 26-FEB-2002;  
A PHARMACEUTICAL FACTORY INC  
human GSTM1B gene  
JP 2002058483-A/25  
26-FEB-2002  
14-AUG-2000 JP 2000245951  
MASUHIRO NISHIMURA,HIROSHI YAGUCHI,SHINSAKU NAITO,ISAO HIRAKA  
C12N15/09,C12Q1/68,G01N21/64,G01N21/78,G01N33/53,G01N33/566,  
C12N15/00  
Method for assaying glutathione S-transferase, and probe and  
kit therefor  
Key  
source  
Location/Qualifiers  
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1..22  
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Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 2 TCCTTGCTCTCCACCG 17  
|||||  
Db 18 TCCTTGACCTCCACCG 3  
|||||

RESULT 40  
AX289046 24 bp DNA linear PAT;  
LOCUS Sequence 808 from Patent WO0179548.  
DEFINITION AX289046  
ACCESSION AX289046  
VERSION AX289046.1 GI:17050729

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.  
TITLE Method of designing addressable array for detection of m  
JOURNAL sequence differences using ligase detection reaction  
PATENT: WO 0179548-A 808 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)

FEATURES  
1..24  
Location/Qualifiers  
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Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 2 TCCTTGCTCTCCACCG 17  
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Db 1 TCCTTGCTCTCCACCG 16  
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RESULT 41  
AR090871 28 bp DNA linear PAT  
LOCUS Sequence 991 from patent US 5994076.  
DEFINITION AR090871  
ACCESSION AR090871  
VERSION AR090871.1 GI:10017626

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Chenchik,A., Jolkhadze,G. and Bibilashvilli,R.  
TITLE Methods of assaying differential expression  
JOURNAL Patent: US 5994076-A 991 30-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..28  
/organism="unknown"  
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ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 28;  
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QY 2 TCCTTGCTCTCCACCG 17  
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Db 9 TCCTTGACCTCCACCG 24  
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RESULT 42  
AR197906 28 bp DNA linear PAT;  
LOCUS Sequence 991 from patent US 6352829.  
DEFINITION

```

7906
7906.1 GI:20247755
OWN.
OWN.
assified.
bases 1 to 28)
chik,A., Jokhadze,G. and Bibilashvilli,R.
ods of assaying differential expression
nt: US 6352829-A 991 05-MAR-2002;
Location/Qualifiers
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Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CTGTGCTCCACCG 17
|||||
CTTGACCTCCACCG 24

0060
0060.1 GI:27310571
OWN.
OWN.
assified.
bases 1 to 28)
chik,A., Jokhadze,G. and Bibilashvilli,R.
ods of assaying differential expression
nt: US 6489455-A 991 03-DEC-2002;
Location/Qualifiers
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Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CTGTGCTCCACCG 17
|||||
CTTGACCTCCACCG 24

0113
0113.1 GI:37939737
border; T-DNA flanking sequence.
idopsis thaliana (thale cress)
idopsis thaliana
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; eudicotyledons; core eudicots;
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
aud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
vin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
nec,L., Caboche,M. and Lecharny,A.
NA integration into the Arabidopsis genome depends on sequences
re-insertion sites

```

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```

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 37)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS,
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsi
plants from INRA (Versailles). The DNA fragment(s) resu
the PCR were directly sequenced from the left or the ri
to determine the genomic sequence flanking the insertion
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database provi
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This seq
been generated in the framework of the French plant gen
program 'genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
source
1..37
Location/Qualifiers
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/mol_type="genomic DNA"
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misc_feature
1..37
/note="T-DNA flanking sequence
left border"
ORIGIN
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Matches 14; Conservative 0; Mismatches 2; Indels 0;
QY 4 CTGTGCTCCACCGGT 19
Db 17 CGTGTCTCTGCACCGGT 32

RESULT 45
AX516800/C
LOCUS AX516800 41 bp DNA linear PAT
DEFINITION Sequence 2998 from Patent WO02052044.
ACCESSION AX516800
VERSION AX516800.1 GI:23564873
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hor
1
REFERENCE Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
AUTHORS Detection of genetic polymorphisms
TITLE Patent: WO 02052044-A 2998 04-JUL-2002;
JOURNAL Riken (JP)
FEATURES
source
1..41
Location/Qualifiers
/organism="Homo sapiens"
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/db_xref="taxon:9606"
ORIGIN
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Best Local Similarity 77.8%; Pred. No. 8.2e+04;
Matches 14; Conservative 1; Mismatches 3; Indels 0;
QY 2 TCCTGTGCTCTCCACCGGT 19
Db 21 YCCTGTGCTCTCCACAGCT 4

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: February 29, 2004, 09:43:11  
16 secs

09:38:25 2004

us-10-090-326-7.max.rng

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

.eic search, using sw model

February 29, 2004, 07:46:14 ; Search time 170.649 Seconds  
(without alignments)  
497.886 Million cell updates/sec

JS-10-090-326-7

l atcttgctccacgggtt 20

IDENTITY NUC

hapop 10.0 , Gapext 1.0

1373863 seqs, 2124099041 residues

bits satisfying chosen parameters: 3308108

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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l: Geneseqn1990s:.\*  
l: Geneseqn2000s:.\*  
l: Geneseqn2001as:.\*  
l: Geneseqn2001bs:.\*  
l: Geneseqn2002s:.\*  
l: Geneseqn2003as:.\*  
l: Geneseqn2003bs:.\*  
l: Geneseqn2003cs:.\*  
l: Geneseqn2004s:.\*

is the number of results predicted by chance to have a  
er than or equal to the score of the result being printed,  
ved by analysis of the total score distribution.

SUMMARIES

%	Query	Match	Length	DB	ID	Description
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95.0	47	9	Adel13859			Adel13859 CEA (6D)-1
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75.0	25	8	ACI58088			ACI58088 Human mic
74.0	20	7	ABX99012			ABX99012 Human AAG
74.0	20	7	ACD02563			ACD02563 Novel hum
74.0	20	7	ACD02560			ACD02560 Novel hum
74.0	20	7	ABX04524			ABX04524 Human adi
74.0	20	7	ABX04521			ABX04521 Human adi
74.0	20	9	ADC01943			ADC01943 Human zsi
74.0	20	9	ADC01940			ADC01940 Human zsi
74.0	20	9	AAD59886			AAD59886 ZC13651 o
74.0	20	9	AAD59889			AAD59889 ZC13650 o
74.0	25	8	ACK19038			ACK19038 Human mic
72.0	38	3	AAA95956			AAA95956 Human TRA
72.0	38	3	AAA95963			AAA95963 1.8 kb TR
71.0	25	8	ACI76567			ACI76567 Human mic
71.0	36	4	AAF84148			AAF84148 Human nov
70.0	33	2	AAQ45878			AAQ45878 CMV captu
69.0	25	8	ACI54322			ACI54322 Human mic
69.0	60	6	ABN35794			ABN35794 Human spl
68.0	24	3	AAZ24132			AAZ24132 HPV16 E7
68.0	24	6	AAK99483			AAK99483 Lipophili

62.0	14	2	AAV48580	Aav48580 junB gene	C 170	12.2	61.0	45	4	AAF31453	Aaf31453
62.0	17	7	ACC6823	Acc6823 Murine ol	C 171	12.2	61.0	45	8	ACD68356	Ac68356
62.0	18	4	AAF60706	Aaf60706 Human som	C 172	12.2	61.0	45	8	ACH04458	Ac604458
62.0	21	7	ACC41024	Acc41024 Perennial	C 173	12.2	61.0	45	8	ACD68002	Ac68002
62.0	21	9	ADC19995	Adc19995 Human COM	C 174	12.2	61.0	45	9	ADC18037	Adc18037
62.0	25	2	AAE65132	Aae65132 Primer 31	C 175	12.2	61.0	45	9	ADD70683	Ad70683
62.0	25	8	ACT155189	Act155189 Human mic	C 176	12.2	61.0	45	9	ADD39760	Ad39760
62.0	25	8	ACI82928	Act82928 Human mic	C 177	12.2	61.0	45	9	ADD70206	Ad70206
62.0	25	8	ACK29672	Act29672 Human mic	C 178	12.2	61.0	45	9	ADD38327	Ad38327
62.0	25	8	ACK16061	Act16061 Human mic	C 179	12.2	61.0	45	9	ADD39283	Ad39283
62.0	25	8	ACT186036	Act186036 Human mic	C 180	12.2	61.0	45	9	ADD38806	Ad38806
62.0	25	8	ACH53289	Ach53289 DNA target	C 181	12.2	61.0	45	9	ADD40237	Ad40237
62.0	25	8	ACH54112	Ach54112 DNA target	C 182	12.2	61.0	45	9	ADD50458	Ad50458
62.0	33	6	ABZ70235	Abz70235 Ribosomal	C 183	12.2	61.0	45	9	ADG20070	Adg20070
62.0	36	7	AA449055	Aad449055 RO38, re	C 184	12.2	61.0	45	9	ADG49981	Adg49981
62.0	36	7	ABX10180	Abx10180 Delta-des	C 185	12.2	61.0	45	9	ADG21539	Adg21539
62.0	47	6	ABK40861	Abk40861 Human obe	C 186	12.2	61.0	48	4	AAI76614	Aai76614
62.0	60	6	ABN50057	Abn50057 Human spl	C 187	12.2	61.0	50	4	AAI34322	Aai34322
61.0	17	6	ABV90369	Abv90369 Human POS	C 188	12.2	61.0	50	4	AAI34323	Aai34323
61.0	20	2	AAZ02725	Aaz02725 PCR prime	C 189	12.2	61.0	50	4	AAI34066	Aai34066
61.0	20	6	AB194148	Abi94148 Capture o	C 190	12.2	61.0	51	2	AAI56311	Aai56311
61.0	20	7	ABZ87914	Abz87914 Human oli	C 191	12.2	61.0	51	3	AAI77359	Aai77359
61.0	20	8	ACF79179	Acf79179 Mouse ger	C 192	12.2	61.0	51	3	AAI77274	Aai77274
61.0	21	2	AAZ25980	Aaz25980 Human pol	C 193	12.2	61.0	51	4	AAI28243	Aai28243
61.0	21	2	AAV99832	Aav99832 Human fla	C 194	12.2	61.0	51	4	AAI33152	Aai33152
61.0	24	6	ABK15074	Abk15074 Human HBG	C 195	12.2	61.0	51	6	ABT12805	Abt12805
61.0	24	6	AB184866	Abi84866 Capture o	C 196	12.2	61.0	54	1	AAI90962	Aai90962
61.0	24	6	ABV92434	Abv92434 Human POS	C 197	12.2	61.0	54	3	AAI261077	Aai261077
61.0	25	6	ABV92438	Abv92438 Human POS	C 198	12.2	61.0	57	6	AB151925	Ab151925
61.0	25	6	ABV92431	Abv92431 Human POS	C 199	12.2	61.0	59	3	AAI622394	Aai622394
61.0	25	6	ABV92435	Abv92435 Human POS	C 200	12.2	61.0	60	3	AAI296519	Aai296519
61.0	25	6	ABV92436	Abv92436 Human POS	C 201	12.2	61.0	60	6	ABN35991	Abn35991
61.0	25	6	ABV92437	Abv92437 Human POS	C 202	12.2	61.0	60	6	ABN37303	Abn37303
61.0	25	6	ABV92432	Abv92432 Human POS	C 203	12	60.0	17	6	ABD331521	Abd331521
61.0	25	6	ABV92433	Abv92433 Human POS	C 204	12	60.0	20	6	ADD44449	Add44449
61.0	25	6	ABV92439	Abv92439 Human POS	C 205	12	60.0	24	2	AAQ55447	Aaq55447
61.0	25	8	ACI93767	Act93767 Human mic	C 206	12	60.0	24	2	AAI88177	Aai88177
61.0	25	8	ACK07633	Act07633 Human mic	C 207	12	60.0	24	6	ABA05108	Ab05108
61.0	25	8	ACI54323	Act154323 Human mic	C 208	12	60.0	25	8	ACT178422	Act178422
61.0	25	8	ACK22927	Act22927 Human mic	C 209	12	60.0	25	8	ACT189158	Act189158
61.0	27	6	ABX03800	Abx03800 DNA encod	C 210	12	60.0	25	8	ACT113801	Act113801
61.0	31	2	AAQ71881	Aaq71881 LO-CD2a V	C 211	12	60.0	25	8	ACH59873	Act59873
61.0	31	2	AAV62599	Aav62599 LO-CD2a c	C 212	12	60.0	27	3	AAZ52085	Aaz52085
61.0	31	2	AAV22857	Aav22857 LO-CD2a h	C 213	12	60.0	27	8	AAI57203	Aai57203
61.0	31	2	AAI38592	Aai38592 Human gen	C 214	12	60.0	28	7	ABT9786	Abt9786
61.0	31	2	AAZ10124	Aaz10124 PCR prime	C 215	12	60.0	29	7	ABT32693	Abt32693
61.0	31	2	AAI06194	Aai06194 Human bia	C 216	12	60.0	30	2	AAQ83360	Aaq83360
61.0	32	2	AAI32839	Aai32839 Yeast GCN	C 217	12	60.0	30	3	AAZ35138	Aaz35138
61.0	32	2	AAQ90574	Aaq90574 Encodes r	C 218	12	60.0	31	2	AAI38733	Aai38733
61.0	32	2	AAQ90571	Aaq90571 Encodes r	C 219	12	60.0	33	5	AAH77404	Aah77404
61.0	33	2	AAZ47122	Aaz47122 Primer #2	C 220	12	60.0	33	5	AAH76993	Aah76993
61.0	33	3	AAZ47121	Aaz47121 Primer #1	C 221	12	60.0	33	6	ABA98625	Ab98625
61.0	33	3	AAQ08995	Aaq08995 Bacillus	C 222	12	60.0	33	9	ADC56925	Adc56925
61.0	36	6	ABK98981	Abk98981 Feline PC	C 223	12	60.0	36	4	ABK10987	Abk10987
61.0	36	6	ABN88049	Abn88049 Taxadiene	C 224	12	60.0	38	2	AAV56793	Aav56793
61.0	37	2	AAQ65478	Aaq65478 PCR prime	C 225	12	60.0	38	2	AAV56797	Aav56797
61.0	37	2	AAV65699	Aav65699 Helicobac	C 226	12	60.0	41	3	AAA37500	Aaa37500
61.0	37	9	ADC64348	Adc64348 Oligonuc	C 227	12	60.0	41	6	ABA98627	Ab98627
61.0	39	7	ACC69760	Acc69760 FLAG olig	C 228	12	60.0	41	6	AAI47559	Aai47559
61.0	39	7	ACC69761	Acc69761 FLAG olig	C 229	12	60.0	41	6	AAI47560	Aai47560
61.0	39	8	ADA38057	Ada38057 Flag olig	C 230	12	60.0	48	7	ABZ77301	Abz77301
61.0	39	8	ADA38058	Ada38058 Flag olig	C 231	12	60.0	53	9	ADC27807	Adc27807
61.0	40	7	ACA55276	Act55276 Rat Ige C	C 232	12	60.0	57	2	AAI05533	Aai05533
61.0	41	6	ABZ46214	Abz46214 Human ald	C 233	12	60.0	60	6	ABN50211	Abn50211
61.0	41	6	ABZ48946	Abz48946 Human ald	C 234	12	60.0	60	6	ABN33966	Abn33966
61.0	41	6	ABZ48371	Abz48371 Human org	C 235	12	60.0	60	6	ABN35001	Abn35001
61.0	45	2	AAQ14604	Aaq14604 5TG-Apal	C 236	11.8	59.0	17	7	ACC65504	Acc65504
61.0	45	2	AAV08809	Aav08809 PCR prime	C 237	11.8	59.0	19	7	ACT72215	Act72215
61.0	45	3	AAV58499	Aav58499 Human PRO	C 238	11.8	59.0	20	2	AAI06993	Aai06993
61.0	45	3	AAA37213	Aaa37213 Human PRO	C 239	11.8	59.0	20	4	AAI67060	Aai67060
61.0	45	4	AAF54319	Aaf54319 Probe #26	C 240	11.8	59.0	20	6	ABA95060	Ab95060
61.0	45	4			C 241	11.8	59.0	20	6	ABL52356	AbL52356
61.0	45	4			C 242	11.8	59.0	20	6		

59.0	20	6	ABT07420	Mammalian	Abt07420	C 316	11.6	58.0	25	6	ABX39852	Abk39852
59.0	20	6	AAD38471	Bovine MH	Rad38471	C 317	11.6	58.0	25	6	ABN89410	Abn89410
59.0	20	7	ACC70236	PCR prime	Acc70236	C 318	11.6	58.0	25	6	ABK89041	Abk89041
59.0	21	8	AAD56927	Human 604	Aad56927	C 319	11.6	58.0	25	7	ABX12293	Abx12293
59.0	22	4	AAQ94129	Human mpl	Raq94129	C 320	11.6	58.0	25	8	ACK18832	Ack18832
59.0	22	6	AAZ33726	Primer A	Raz33726	C 321	11.6	58.0	25	8	ACK26905	Ack26905
59.0	22	6	ABZ29902	Candida a	Abz29902	C 322	11.6	58.0	25	8	ACI01073	Act01073
59.0	22	3	AAA07348	M. tuberc	Aaa07348	C 323	11.6	58.0	25	8	ACI09664	Act09664
59.0	23	3	AAAO7348	PCR prime	Raa07348	C 324	11.6	58.0	25	8	ACK11841	Ack11841
59.0	24	4	AAAS5906	PCR prime	Ras5906	C 325	11.6	58.0	25	8	ACI38055	Act38055
59.0	24	4	AAAS08718	Forward P	Ras08718	C 326	11.6	58.0	25	8	ACI64770	Act64770
59.0	25	3	AAA87583	Rat hepat	Raa87583	C 327	11.6	58.0	25	8	ACI67995	Act67995
59.0	25	4	AAD02664	Human WTI	Rad02664	C 328	11.6	58.0	25	8	ACK19316	Ack19316
59.0	25	6	AAD21935	Target nu	Rad21935	C 329	11.6	58.0	25	8	ACI23979	Act23979
59.0	25	7	ABZ84508	Toxicolog	Abz84508	C 330	11.6	58.0	25	8	ACI01519	Act01519
59.0	25	8	ACI27143	Human mic	Act27143	C 331	11.6	58.0	25	8	ACK09850	Ack09850
59.0	25	8	ACI16451	Human mic	Act16451	C 332	11.6	58.0	25	8	ACI72440	Act72440
59.0	25	8	ACI38421	Human mic	Act38421	C 333	11.6	58.0	25	8	ACI64256	Act64256
59.0	25	8	ACK28100	Human mic	Act28100	C 334	11.6	58.0	25	8	ACK24323	Act24323
59.0	25	8	ACK22222	Human mic	Act22222	C 335	11.6	58.0	26	6	ABQ75990	Abq75990
59.0	25	8	ACI35185	Human mic	Act35185	C 336	11.6	58.0	27	2	AAV41481	Av41481
59.0	25	8	ACI16450	Human mic	Act16450	C 337	11.6	58.0	27	2	AAZ09730	Aaz09730
59.0	25	8	ACI67728	Human mic	Act67728	C 338	11.6	58.0	27	5	AAH78365	Aah78365
59.0	25	8	ACI51610	Human mic	Act51610	C 339	11.6	58.0	27	6	ABK67057	Abk67057
59.0	25	8	ACI78487	Human mic	Act78487	C 340	11.6	58.0	28	2	AAZ02385	Aaz02385
59.0	25	8	ACI83089	Human mic	Act83089	C 341	11.6	58.0	28	2	AAZ03202	Aaz03202
59.0	25	8	ACI28252	Human mic	Act28252	C 342	11.6	58.0	28	6	AAV69768	Av69768
59.0	26	4	AAD06276	Domestic	Rad06276	C 343	11.6	58.0	28	6	AAV69768	Av69768
59.0	26	4	AAD06278	Domestic	Rad06278	C 344	11.6	58.0	30	2	AAV60371	Av60371
59.0	27	2	AAZ80203	Beta-glob	Raz80203	C 345	11.6	58.0	31	4	AAI29860	Aai29860
59.0	27	7	ABZ21545	Humulus l	Abz21545	C 346	11.6	58.0	31	4	AAI30178	Aai30178
59.0	28	2	AAZ86510	Forward p	Raz86510	C 347	11.6	58.0	31	4	AAI31117	Aai31117
59.0	28	5	AAF80037	PCR prime	Raf80037	C 348	11.6	58.0	33	2	AAV05297	Av05297
59.0	28	9	AAD36214	Weed cont	Rad36214	C 349	11.6	58.0	33	2	AAZ09602	Aaz09602
59.0	30	2	AAAT41641	Endo-xylo	Rat41641	C 350	11.6	58.0	33	3	AAZ09602	Aaz09602
59.0	30	2	AAZ19510	Human lip	Raz19510	C 351	11.6	58.0	33	3	AAZ09602	Aaz09602
59.0	30	2	AAZ35207	Corn glob	Raz35207	C 352	11.6	58.0	33	3	AAZ09602	Aaz09602
59.0	31	2	AAV67924	Nucleotid	Rav67924	C 353	11.6	58.0	33	6	AAZ25996	Aaz25996
59.0	31	3	AAA78951	Human gen	Raa78951	C 354	11.6	58.0	35	2	AAQ24138	Aaq24138
59.0	31	3	ABV74474	UGT and c	Abv74474	C 355	11.6	58.0	36	2	AAQ58217	Aaq58217
59.0	40	2	AAZ82122	Probe for	Raz82122	C 356	11.6	58.0	37	2	AAV63966	Av63966
59.0	40	2	AAZ87111	IFN-gamma	Raz87111	C 357	11.6	58.0	37	2	AAZ81010	Aaz81010
59.0	40	2	AAZ87110	IFN-gamma	Raz87110	C 358	11.6	58.0	37	7	ACA54711	Ac54711
59.0	44	2	AAZ62424	Bovine be	Raz62424	C 359	11.6	58.0	39	7	ABT19445	Abt19445
59.0	44	2	AAV64121	Bovine be	Rav64121	C 360	11.6	58.0	41	6	ABZ60440	Abz60440
59.0	45	2	AAZ97216	Immunoglo	Raz97216	C 361	11.6	58.0	41	6	ABZ48553	Abz48553
59.0	47	3	AAZ68331	Human map	Raz68331	C 362	11.6	58.0	41	6	ABZ43276	Abz43276
59.0	49	4	AAD06895	Human oli	Rad06895	C 363	11.6	58.0	41	6	ABA95666	Ab95666
59.0	49	4	AAD06904	Human oli	Rad06904	C 364	11.6	58.0	41	7	ABZ79598	Abz79598
59.0	50	4	AAZ29516	Human SNP	Raz29516	C 365	11.6	58.0	41	7	AAZ54344	Aaz54344
59.0	50	6	ABZ03355	Human leu	Abz03355	C 366	11.6	58.0	42	4	AAI66856	Aai66856
59.0	50	6	ADD41480	Synthetic	Rad41480	C 367	11.6	58.0	42	4	AAI66857	Aai66857
59.0	51	4	AAZ27563	Human SNP	Raz27563	C 368	11.6	58.0	42	6	AAZ28168	Aaz28168
59.0	51	4	AAZ27653	Human SNP	Raz27653	C 369	11.6	58.0	42	6	AAZ28169	Aaz28169
59.0	51	4	AAZ31121	Human SNP	Raz31121	C 370	11.6	58.0	42	7	ACC72627	Acc72627
59.0	51	4	AAZ31236	Human SNP	Raz31236	C 371	11.6	58.0	42	7	ACC72628	Acc72628
59.0	60	2	AAV13216	Primer AS	Rav13216	C 372	11.6	58.0	42	7	ACC43213	Acc43213
59.0	60	6	ABN50088	Human spl	Abn50088	C 373	11.6	58.0	42	7	ACC43209	Acc43209
59.0	60	6	ABN59445	Human spl	Abn59445	C 374	11.6	58.0	48	2	AAV07413	Av07413
59.0	60	6	ABN46833	Human spl	Abn46833	C 375	11.6	58.0	48	2	AAV07413	Av07413
59.0	60	6	ABN42416	Human spl	Abn42416	C 376	11.6	58.0	50	4	AAH89689	Aah89689
58.0	19	3	AAA84452	Cyclin D3	Raa84452	C 377	11.6	58.0	50	6	ABZ05446	Abz05446
58.0	19	3	AAH59614	Cyclin D3	Rah59614	C 378	11.6	58.0	50	6	AAZ06001	Aaz06001
58.0	20	6	AAD34730	Human MEK	Rad34730	C 379	11.6	58.0	51	3	AAA07020	Aaa07020
58.0	21	2	AAZ61027	PCR prime	Raz61027	C 380	11.6	58.0	51	3	AAZ77148	Aaz77148
58.0	21	8	ADA27332	Human mic	Rad27332	C 381	11.6	58.0	51	3	AAZ77148	Aaz77148
58.0	22	2	AAV35216	ICE gene	Rav35216	C 382	11.6	58.0	51	4	AAI33955	Aai33955
58.0	23	6	ABX09450	Arteriosc	Abx09450	C 383	11.6	58.0	51	4	AAI76360	Aai76360
58.0	23	6	ABL99402	Left PCR	AbL99402	C 384	11.6	58.0	54	8	ACC49559	Acc49559
58.0	24	4	AAH45836	C album c	Rah45836	C 385	11.6	58.0	57	3	AAZ00113	Aaz00113
58.0	24	6	ABZ55114	C. Album	Abz55114	C 386	11.6	58.0	57	4	AAZ94539	Aaz94539
58.0	24	6	ABI91199	Capture o	Abi91199	C 387	11.6	58.0	57	4	AAZ93107	Aaz93107
58.0	24	6	ABI91198	Capture o	Abi91198	C 388	11.6	58.0	57	4	AAZ93106	Aaz93106

58.0	57	4	AAD08604	Aad08604	Primer IN	462	11.4	57.0	25	8	ACI10408	ACI10408
58.0	57	6	ABT03446	Abt03446	Human HIV	463	11.4	57.0	25	8	ACI43231	ACI43231
58.0	57	6	ART03447	Art03447	Human HIV	c 464	11.4	57.0	25	8	ACH57316	ACH57316
58.0	60	2	AQT051027	Aeq51027	5' fragme	465	11.4	57.0	26	4	AAF30582	AAF30582
58.0	60	6	ABN44635	Abn44635	Human spl	c 466	11.4	57.0	27	4	AAF57678	AAF57678
58.0	60	6	ABN440334	Abn440334	Human spl	c 467	11.4	57.0	27	4	AAF30672	AAF30672
58.0	60	6	ABN41630	Abn41630	Human spl	468	11.4	57.0	28	4	AAF30583	AAF30583
58.0	60	6	ABN41074	Abn41074	Human spl	c 469	11.4	57.0	28	5	AAI71936	AAI71936
58.0	60	6	ABN38683	Abn38683	Human spl	470	11.4	57.0	30	2	AAQ14283	AAQ14283
58.0	60	6	ABN46459	Abn46459	Human spl	471	11.4	57.0	30	2	AAQ37670	AAQ37670
58.0	60	6	ABN43803	Abn43803	Human spl	c 472	11.4	57.0	30	3	AAZ50560	AAZ50560
58.0	60	6	ABN32832	Abn32832	Human spl	c 473	11.4	57.0	30	3	AAA30665	AAA30665
58.0	60	6	ABN34626	Abn34626	Human spl	474	11.4	57.0	30	4	AAF30584	AAF30584
58.0	60	6	ABN33037	Abn33037	Human spl	c 475	11.4	57.0	30	9	ADC22635	ADC22635
58.0	60	6	ABN39120	Abn39120	Human spl	476	11.4	57.0	31	4	ACC81025	ACC81025
58.0	60	6	ABN44650	Abn44650	Human spl	477	11.4	57.0	31	4	AAF84963	AAF84963
57.0	16	2	AXX61158	Aax61158	Human chr	478	11.4	57.0	32	4	AAF30585	AAF30585
57.0	16	7	ACC42403	Acc42403	Mouise acy	c 479	11.4	57.0	33	2	AAT31736	AAT31736
57.0	17	6	ABV90365	Abv90365	Human POS	480	11.4	57.0	33	6	ABL58191	ABL58191
57.0	17	6	ABV90368	Abv90368	Human POS	481	11.4	57.0	36	2	AAQ79555	AAQ79555
57.0	17	6	ABV90366	Abv90366	Human POS	482	11.4	57.0	36	2	AAQ79543	AAQ79543
57.0	17	6	ABV90367	Abv90367	Human POS	483	11.4	57.0	36	2	AAQ79553	AAQ79553
57.0	17	7	ABZ61854	Abz61854	Human H-R	c 484	11.4	57.0	36	2	AAQ4258	AAQ4258
57.0	17	7	ACD64741	Acd64741	HCV minus	485	11.4	57.0	36	6	AAQ42545	AAQ42545
57.0	17	7	ACD57928	Acd57928	HCV DNazzy	486	11.4	57.0	36	6	AAQ42535	AAQ42535
57.0	17	9	ADB41409	Adb41409	Tumour su	487	11.4	57.0	36	6	AAQ42547	AAQ42547
57.0	18	2	AAV44606	Aav44606	Human unc	488	11.4	57.0	36	8	ACH00389	ACH00389
57.0	18	2	AAV54355	Aax54355	NK-KB ant	489	11.4	57.0	36	8	ACH00377	ACH00377
57.0	18	3	AAV33799	Aaa33799	Low adeno	490	11.4	57.0	36	8	ACH00387	ACH00387
57.0	18	3	AAF19921	Aaf19921	Human NF-	491	11.4	57.0	38	9	ADC64130	ADC64130
57.0	18	6	ABK30181	Abk30181	Human UGT	492	11.4	57.0	41	8	ACC41994	ACC41994
57.0	18	6	ABK98395	Abk98395	Mouise sma	c 493	11.4	57.0	42	2	AAT77149	AAT77149
57.0	18	7	ABZ95615	Abz95615	Human NF-	c 494	11.4	57.0	46	9	ADC64129	ADC64129
57.0	19	6	ABX03574	Abx03574	Human ner	c 495	11.4	57.0	47	3	AAZ68568	AAZ68568
57.0	20	2	AAV36332	Aav36332	Human BRC	496	11.4	57.0	50	6	ABZ02282	ABZ02282
57.0	20	3	AACT73707	Aac73707	Human IL-	c 497	11.4	57.0	50	6	ABZ01231	ABZ01231
57.0	20	6	ABN85727	Abn85727	Human FSA	498	11.4	57.0	51	4	AAI32625	AAI32625
57.0	20	6	AAZ34731	Aaz34731	Human MEK	499	11.4	57.0	51	4	AAI32787	AAI32787
57.0	20	7	ACC49981	Acc49981	sox9f pri	c 500	11.4	57.0	51	4	AAI27191	AAI27191
57.0	20	7	AD531148	Aad531148	SOX-9 DNA	501	11.4	57.0	60	2	AAV40187	AAV40187
57.0	20	9	ADD22547	Add22547	Flatfish	c 502	11.4	57.0	60	6	ABN32962	ABN32962
57.0	21	2	AAQ71316	Aaq71316	Primer fo	c 503	11.4	57.0	60	6	ABN58762	ABN58762
57.0	21	2	AAQ91386	Aaq91386	Primer fo	c 504	11.4	57.0	60	6	ABN37104	ABN37104
57.0	21	4	AAC84519	Aac84519	Human gly	c 505	11.4	57.0	60	6	ABN39406	ABN39406
57.0	21	4	AAAF95940	Aaf95940	Human gen	506	11.2	56.0	17	2	AAA22478	AAA22478
57.0	21	4	AA542709	Aas42709	T. gondii	507	11.2	56.0	17	3	AAAF07098	AAAF07098
57.0	21	4	ABL51705	Abi51705	Human GFR	c 508	11.2	56.0	17	6	ABN08564	ABN08564
57.0	22	9	ABE16166	Abi6166	G-coupled	c 509	11.2	56.0	17	6	ABN08565	ABN08565
57.0	23	7	ABZ76186	Abz76186	Arabidops	510	11.2	56.0	17	6	ABK18433	ABK18433
57.0	24	2	AAAT17881	Aat17881	IL-11 rec	511	11.2	56.0	17	6	ABK17727	ABK17727
57.0	24	4	AAF30581	Aaf30581	Human COM	512	11.2	56.0	17	6	ABK18432	ABK18432
57.0	24	6	ABQ04620	Abq04620	Oligonucl	513	11.2	56.0	17	6	ABV90370	ABV90370
57.0	24	6	ABQ04579	Abq04579	Oligonucl	514	11.2	56.0	17	3	AAZ91442	AAZ91442
57.0	24	6	ABQ10907	Abq10907	Oligonucl	c 515	11.2	56.0	18	3	AAZ70948	AAZ70948
57.0	24	6	ABQ00302	Abq00302	Oligonucl	c 516	11.2	56.0	18	3	AAZ70948	AAZ70948
57.0	24	6	ABQ10948	Abq10948	Oligonucl	c 517	11.2	56.0	18	9	AAE43411	AAE43411
57.0	25	5	AAI62264	Aai62264	Soybean 3	518	11.2	56.0	19	2	AAQ82533	AAQ82533
57.0	25	5	AAI62304	Aai62304	Soybean 3	c 519	11.2	56.0	19	6	ABK41090	ABK41090
57.0	25	6	ABQ12443	Abq12443	Oligonucl	c 520	11.2	56.0	19	6	ABK44408	ABK44408
57.0	25	6	ABQ12484	Abq12484	Oligonucl	c 521	11.2	56.0	19	6	ABT03925	ABT03925
57.0	25	6	ABQ12484	Abq12484	Oligonucl	c 522	11.2	56.0	19	7	ABZ84512	ABZ84512
57.0	25	6	ABV52430	Abv52430	Human POS	c 523	11.2	56.0	19	8	ACD13528	ACD13528
57.0	25	6	ABV92428	Abv92428	Human POS	c 524	11.2	56.0	19	8	ADA97829	ADA97829
57.0	25	6	ABV92427	Abv92427	Human POS	c 525	11.2	56.0	20	2	AAT00612	AAT00612
57.0	25	6	ABV92429	Abv92429	Human POS	526	11.2	56.0	20	2	AAZ22628	AAZ22628
57.0	25	8	ACI65495	Act65495	Human mic	527	11.2	56.0	20	2	AAZ78590	AAZ78590
57.0	25	8	ACI30050	Act30050	Human mic	c 528	11.2	56.0	20	2	AAZ06158	AAZ06158
57.0	25	8	ACI17094	Act17094	Human mic	c 529	11.2	56.0	20	2	AAZ01942	AAZ01942
57.0	25	8	ACK29930	Ack29930	Human mic	530	11.2	56.0	20	2	AAZ83697	AAZ83697
57.0	25	8	ACI34056	Act34056	Human mic	531	11.2	56.0	20	2	AAZ19193	AAZ19193
57.0	25	8	ACI18817	Act18817	Human mic	532	11.2	56.0	20	2	AAZ27332	AAZ27332
57.0	25	8	ACI86651	Act86651	Human mic	533	11.2	56.0	20	3	AACT1588	AACT1588
57.0	25	8	ACK12962	Act12962	Human mic	534	11.2	56.0	20	3	AACT1591	AACT1591



56.0	20	3	AAC73141	Forward p	c 608	11.2	56.0	25	8	ACH53698	Ach53698
56.0	20	4	AAD14641	DEN-1 PDK	c 609	11.2	56.0	25	8	ACH64773	Ach64773
56.0	20	4	AAC84227	Human PKC	c 610	11.2	56.0	25	8	ACH55441	Ach55441
56.0	20	6	ABL90920	Human pro	c 611	11.2	56.0	25	8	ACH55317	Ach55317
56.0	20	7	ABZ85243	Human Oli	c 612	11.2	56.0	25	9	ADE86830	Ade86830
56.0	20	7	ABZ98576	Human ICA	c 613	11.2	56.0	26	2	AAT10247	Aat10247
56.0	20	7	ACC43096	Probe use	c 614	11.2	56.0	26	6	ABS51750	Ab51750
56.0	20	8	ACC99689	Apol PCR	c 615	11.2	56.0	27	3	AAA39575	Aaa39575
56.0	20	8	ACH11199	Human pro	c 616	11.2	56.0	27	3	ADA01452	Ada01452
56.0	20	9	ACF79244	Human neu	c 617	11.2	56.0	27	7	ADA01448	Ada01448
56.0	20	9	ADE13476	HLA class	c 618	11.2	56.0	27	7	ABZ21543	Abz21543
56.0	21	2	ANT05918	COX II se	c 619	11.2	56.0	28	2	AAQ24484	Aaq24484
56.0	21	3	AAA11510	Human dys	c 620	11.2	56.0	28	2	AAQ24484	Aaq24484
56.0	21	3	AAA36965	Human dys	c 621	11.2	56.0	28	2	AAQ24484	Aaq24484
56.0	21	4	AAF6280	Human gen	c 622	11.2	56.0	28	3	AAZ88940	Aaz88940
56.0	21	4	AAF6280	Human gen	c 623	11.2	56.0	28	3	AAZ88940	Aaz88940
56.0	21	6	ABK56113	Human sin	c 624	11.2	56.0	28	6	ABK66654	Abk66654
56.0	21	8	ADA49835	Human mit	c 625	11.2	56.0	28	7	ABZ83529	Abz83529
56.0	22	3	AAAG6698	Rice cyto	c 626	11.2	56.0	29	2	AAV49799	Aav49799
56.0	23	5	AAD13607	H(A12-M)d	c 627	11.2	56.0	29	2	AAV08884	Aav08884
56.0	23	6	AAAL42661	Rice seed	c 628	11.2	56.0	30	2	AAQ45423	Aaq45423
56.0	24	2	AAQ42195	HCV c33c	c 629	11.2	56.0	30	2	AAQ45423	Aaq45423
56.0	24	2	AAQ72292	Serotonin	c 630	11.2	56.0	30	4	AAQ26644	Aad26644
56.0	24	6	ABQ00673	Oligonucl	c 631	11.2	56.0	31	2	AAZ27962	Aaz27962
56.0	24	6	ABQ11635	Oligonucl	c 632	11.2	56.0	31	2	AAZ27962	Aaz27962
56.0	24	6	ABQ05307	Oligonucl	c 633	11.2	56.0	31	2	AAZ27962	Aaz27962
56.0	24	6	ABQ11594	Oligonucl	c 634	11.2	56.0	31	3	AAA95630	Aaa95630
56.0	24	6	ABQ05348	Oligonucl	c 635	11.2	56.0	31	3	AAA95630	Aaa95630
56.0	24	6	ABT03574	Human Cux	c 636	11.2	56.0	31	6	AAAL41247	Aal41247
56.0	24	7	ABV77502	A. margin	c 637	11.2	56.0	31	6	AAAL41247	Aal41247
56.0	25	4	AAF44581	Mouse DSS	c 638	11.2	56.0	31	7	ABX93832	Abx93832
56.0	25	6	AAAG62207	Porcine r	c 639	11.2	56.0	31	7	ABX93832	Abx93832
56.0	25	6	AAAG62207	Porcine r	c 640	11.2	56.0	31	7	ABX93832	Abx93832
56.0	25	6	ABN13457	Human GDM	c 641	11.2	56.0	32	6	ABV73854	Abv73854
56.0	25	6	ABN13463	Human GDM	c 642	11.2	56.0	33	4	AAV15834	Aav15834
56.0	25	6	ABN13464	Human GDM	c 643	11.2	56.0	33	4	AAV15834	Aav15834
56.0	25	6	ABN13462	Human GDM	c 644	11.2	56.0	33	4	AAV15834	Aav15834
56.0	25	6	ABN13458	Human GDM	c 645	11.2	56.0	33	4	AAV15834	Aav15834
56.0	25	6	ABN13460	Human GDM	c 646	11.2	56.0	34	6	ABN80848	Abn80848
56.0	25	6	ABN13461	Human GDM	c 647	11.2	56.0	34	6	ABN80848	Abn80848
56.0	25	6	ABN13459	Human GDM	c 648	11.2	56.0	34	9	ADC54184	Adc54184
56.0	25	6	ABN13456	Human GDM	c 649	11.2	56.0	35	3	AAQ35855	Aaq35855
56.0	25	6	ABN13465	Human GDM	c 650	11.2	56.0	36	3	AAQ35855	Aaq35855
56.0	25	6	ABX72713	Cryptococ	c 651	11.2	56.0	37	3	AAZ39031	Aaz39031
56.0	25	6	ABQ13130	Oligonucl	c 652	11.2	56.0	37	4	AAI66269	Aai66269
56.0	25	6	ABQ13171	Oligonucl	c 653	11.2	56.0	38	2	AAV58260	Aav58260
56.0	25	6	ABV92440	Human POS	c 654	11.2	56.0	38	5	AAI5541	Aai5541
56.0	25	8	ACI30309	Human mic	c 655	11.2	56.0	38	5	AAI5541	Aai5541
56.0	25	8	ACI00641	Human mic	c 656	11.2	56.0	39	2	AAQ38124	Aaq38124
56.0	25	8	ACK06224	Human mic	c 657	11.2	56.0	40	4	AAQ38124	Aaq38124
56.0	25	8	ACI44890	Human mic	c 658	11.2	56.0	40	8	ACC85304	Acc85304
56.0	25	8	ACI09083	Human mic	c 659	11.2	56.0	41	3	AAA77202	Aaa77202
56.0	25	8	ACI84783	Human mic	c 660	11.2	56.0	41	4	AAQ84467	Aaq84467
56.0	25	8	ACI84782	Human mic	c 661	11.2	56.0	41	5	AAQ84467	Aaq84467
56.0	25	8	ACI96776	Human mic	c 662	11.2	56.0	41	6	ABL40246	AbL40246
56.0	25	8	ACI36129	Human mic	c 663	11.2	56.0	41	6	ABT08106	Abt08106
56.0	25	8	ACI95679	Human mic	c 664	11.2	56.0	41	6	ABT08106	Abt08106
56.0	25	8	ACK05421	Human mic	c 665	11.2	56.0	41	6	ABT08106	Abt08106
56.0	25	8	ACI02211	Human mic	c 666	11.2	56.0	41	6	ABT08106	Abt08106
56.0	25	8	ACK06920	Human mic	c 667	11.2	56.0	41	6	ABT08106	Abt08106
56.0	25	8	ACI83951	Human mic	c 668	11.2	56.0	41	6	ABT08106	Abt08106
56.0	25	8	ACI75696	Human mic	c 669	11.2	56.0	41	6	ABT08106	Abt08106
56.0	25	8	ACI32391	Human mic	c 670	11.2	56.0	41	6	ABT08106	Abt08106
56.0	25	8	ACI02256	Human mic	c 671	11.2	56.0	41	6	ABT08106	Abt08106
56.0	25	8	ACI60399	Human mic	c 672	11.2	56.0	41	7	ABZ25674	Abz25674
56.0	25	8	ACK19877	Human mic	c 673	11.2	56.0	42	2	AAI65339	Aai65339
56.0	25	8	ACI72680	Human mic	c 674	11.2	56.0	44	4	AAQ06072	Aaq06072
56.0	25	8	ACK03261	Human mic	c 675	11.2	56.0	44	4	AAQ06072	Aaq06072
56.0	25	8	ACI32570	Human mic	c 676	11.2	56.0	45	4	AAQ06072	Aaq06072
56.0	25	8	ACK03391	Human mic	c 677	11.2	56.0	45	4	AAQ06072	Aaq06072
56.0	25	8	ACH52395	DNA target	c 678	11.2	56.0	47	3	AAZ66343	Aaz66343
56.0	25	8	ACH62756	DNA target	c 679	11.2	56.0	47	3	AAZ66343	Aaz66343
56.0	25	8			c 680	11.2	56.0	48	2	AAZ66343	Aaz66343

56.0	48	4	AAAL40776	AAAL40776 5' PCR pr	c 754	11	55.0	20	2	AAZ03662	Aaz03662
56.0	49	6	ABL51371	ABL51371 Mouse pho	755	11	55.0	20	2	AAZ96025	Aax96025
56.0	50	4	AAAL34028	AAAL34028 Human SNP	c 756	11	55.0	20	3	AAAL1387	Aaa11387
56.0	50	4	AAAL34411	AAAL34411 Human SNP	757	11	55.0	20	4	AAAG67719	Aac67719
56.0	50	4	AAAL31517	AAAL31517 Human SNP	758	11	55.0	20	6	ABN83208	Abn83208
56.0	50	4	AAAL31754	AAAL31754 Human SNP	759	11	55.0	20	6	AAAD39528	Aad39528
56.0	50	4	AAAL31755	AAAL31755 Human SNP	c 760	11	55.0	20	6	ABS52091	Abs52091
56.0	50	4	AAAH70677	AAAH70677 Human cer	c 761	11	55.0	20	6	ABS52083	Abs52083
56.0	50	4	AAAF76766	AAAF76766 T flavus	762	11	55.0	20	6	ABO75982	Abg75982
56.0	50	6	ABZ07347	ABZ07347 Human leu	763	11	55.0	20	6	AAAL43887	Aal43887
56.0	50	6	ABZ01635	ABZ01635 Human leu	764	11	55.0	20	7	AAAD50868	Aad50868
56.0	50	6	ABZ08003	ABZ08003 Human leu	765	11	55.0	20	7	ACC49247	Acc49247
56.0	50	6	ABZ05012	ABZ05012 Human leu	c 766	11	55.0	20	8	ABT19438	Abt19438
56.0	50	8	ADA21055	ADA21055 Codon-opt	c 767	11	55.0	20	8	ACC99693	Acc99693
56.0	50	8	ADA21083	ADA21083 Codon-opt	768	11	55.0	21	2	AAT86480	Aat86480
56.0	51	3	AAA77291	AAA77291 Human clo	769	11	55.0	22	3	AAZ50457	Aaz50457
56.0	51	4	AAAL29407	AAAL29407 Human SNP	770	11	55.0	22	6	ABL58459	Abi58459
56.0	51	4	AAAL31137	AAAL31137 Human SNP	771	11	55.0	22	7	ACA61738	Acc61738
56.0	51	4	AAAL28244	AAAL28244 Human SNP	772	11	55.0	22	9	ADB66806	Adb66806
56.0	51	4	AAI76324	AAI76324 Human sil	773	11	55.0	23	2	AAT40438	Aat40438
56.0	51	4	AAI76325	AAI76325 Human sil	774	11	55.0	23	2	AXX81852	Aax81852
56.0	51	4	AAH90461	AAH90461 Human clo	775	11	55.0	23	3	AAZ88927	Aaz88927
56.0	51	6	ABA82897	ABA82897 Human pro	c 776	11	55.0	23	3	AAH87966	Aah87966
56.0	51	6	AAI67893	AAI67893 Forward o	777	11	55.0	23	7	ABT21539	Abt21539
56.0	51	6	AAI67894	AAI67894 Reverse o	778	11	55.0	24	2	AAV14051	Aav14051
56.0	53	4	AAH74871	AAH74871 Oligonuc	c 779	11	55.0	24	4	AAH27936	Aah27936
56.0	53	4	AAH74872	AAH74872 Oligonuc	c 780	11	55.0	24	5	AAAS12647	Aas12647
56.0	53	6	ABA99040	ABA99040 Kpn-BB'-X	c 781	11	55.0	24	6	ABT08330	Abt08330
56.0	53	7	ADA48045	ADA48045 AttB reco	c 782	11	55.0	24	6	ABQ03485	Abq03485
56.0	53	8	ACF06160	ACF06160 Nucleic a	c 783	11	55.0	24	6	ABA95103	AbA95103
56.0	54	2	AAE64481	AAE64481 Rabbit st	784	11	55.0	24	6	ABT85588	Abt85588
56.0	54	2	AAZ06778	AAZ06778 PCR prime	c 785	11	55.0	24	6	ABT88589	Abt88589
56.0	54	3	AAZ61088	AAZ61088 Forward p	786	11	55.0	25	2	AXX01263	Aax01263
56.0	54	3	AAAC31088	AAAC31088 Human sec	c 787	11	55.0	25	3	AAZ50505	Aaz50505
56.0	54	3	AAAT73934	AAAT73934 GFP Glu(G	c 788	11	55.0	25	6	ABS55623	Abs55623
56.0	56	3	AAZ58962	AAZ58962 Primer fo	789	11	55.0	25	7	ABZ37305	Abz37305
56.0	56	3	AAZ58994	AAZ58994 Primer fo	790	11	55.0	25	7	ABZ37259	Abz37259
56.0	57	2	AAQ22693	AAQ22693 Gal alpha	791	11	55.0	25	8	ACT83971	Act83971
56.0	57	3	AAAS2452	AAAS2452 Human I-k	c 792	11	55.0	25	8	ACT77426	Act77426
56.0	57	4	AAH50027	AAH50027 Bacterial	793	11	55.0	25	8	ACI40266	Act40266
56.0	57	6	ABL51346	ABL51346 Human pho	c 794	11	55.0	25	8	ACT02709	Act02709
56.0	58	6	ABR86543	ABR86543 PCR prime	795	11	55.0	25	8	ACI38244	Act38244
56.0	59	3	AAAS90146	AAAS90146 PCR prime	796	11	55.0	25	8	ACI63359	Act63359
56.0	59	5	AAF82659	AAF82659 Primer us	797	11	55.0	25	8	ACI89300	Act89300
56.0	60	2	AAAT31935	AAAT31935 RIP14-2 c	798	11	55.0	25	8	ACI08603	Act08603
56.0	60	2	AAV54568	AAV54568 GFP-Beari	799	11	55.0	25	8	ACI51740	Act51740
56.0	60	2	AAH89224	AAH89224 Sense pri	c 800	11	55.0	25	8	ACT72890	Act72890
56.0	60	3	AAZ39408	AAZ39408 Human tra	801	11	55.0	25	8	ACK26915	Act26915
56.0	60	6	ABN40965	ABN40965 Human spl	802	11	55.0	25	8	ACI39822	Act39822
56.0	60	6	ABN43418	ABN43418 Human spl	803	11	55.0	25	8	ACI39802	Act39802
56.0	60	6	ABN38688	ABN38688 Human spl	804	11	55.0	25	8	ACK16388	Act16388
56.0	60	6	ABN44193	ABN44193 Human spl	805	11	55.0	25	8	ACK09986	Act09986
56.0	60	6	ABN35520	ABN35520 Human spl	806	11	55.0	25	8	ACK06083	Act06083
56.0	60	6	ABN319793	ABN319793 Human spl	807	11	55.0	25	8	ACT01511	Act01511
56.0	60	6	ABN47129	ABN47129 Human spl	808	11	55.0	25	8	ACT27896	Act27896
56.0	60	6	ABN35928	ABN35928 Human spl	c 809	11	55.0	25	8	ACK04844	Act04844
56.0	60	6	ABN319401	ABN319401 Human spl	c 810	11	55.0	25	8	ACK04844	Act04844
56.0	60	6	ABN36165	ABN36165 Human spl	811	11	55.0	25	8	ACT84573	Act84573
56.0	60	6	ABN33072	ABN33072 Human spl	812	11	55.0	25	8	ACT62323	Act62323
56.0	60	6	ABN39300	ABN39300 Human spl	813	11	55.0	25	8	ACT66136	Act66136
56.0	60	6	ABN50630	ABN50630 Human spl	814	11	55.0	25	8	ACT194039	Act194039
56.0	60	6	ABN38748	ABN38748 Human spl	815	11	55.0	25	8	ACK04077	Act04077
56.0	60	6	AAAL46473	AAAL46473 Human spl	c 816	11	55.0	25	8	ACI93701	Act93701
55.0	17	2	AAQ06859	AAQ06859 Sequence	817	11	55.0	25	8	ACT151741	Act151741
55.0	17	2	AAA22909	AAA22909 Integrin	c 818	11	55.0	25	8	ACH52389	Ach52389
55.0	17	2	AAA22911	AAA22911 Integrin	c 819	11	55.0	25	8	ACH53320	Ach53320
55.0	17	7	ABT38399	ABT38399 Tumour su	c 820	11	55.0	25	8	ACH53464	Ach53464
55.0	18	2	AAZ41165	AAZ41165 Human G-a	c 821	11	55.0	25	8	ACH53338	Ach53338
55.0	18	2	AAZ19536	AAZ19536 Human G-a	c 822	11	55.0	25	9	ADC53865	Adc53865
55.0	18	6	ABK68847	ABK68847 PCR prime	823	11	55.0	25	9	ADD94046	Add94046
55.0	18	7	ACC43590	ACC43590 Probe use	824	11	55.0	26	2	AAV80399	Aav80399
55.0	20	2	AAAT08229	AAAT08229 p193, PCR	825	11	55.0	26	2	AAV68616	Aav68616
55.0					c 826	11	55.0	26	3	AAAC66157	Aac66157

55.0	26	6	AB565327	Ab565327 A. thalia	900	11	55.0	45	7	ACA58031	Aca58031
55.0	27	2	AAV94296	AAV94296 Mouse IL-	901	11	55.0	45	7	ACA71758	Aca71758
55.0	27	2	AAV94355	AAV94355 Mouse IL-	902	11	55.0	45	7	ABX92398	Abx92398
55.0	27	2	AAV83628	AAV83628 PCR prime	903	11	55.0	45	7	ACA66139	Aca66139
55.0	27	4	AAF30904	AAF30904 Yeast HMG	904	11	55.0	45	8	ADA24699	Ada24699
55.0	27	7	ABX33943	ABX33943 Human int	905	11	55.0	45	8	ACD29740	Acd29740
55.0	28	4	AAH20878	AAH20878 Tobacco p	906	11	55.0	45	8	ADA12360	Ada12360
55.0	29	2	AAQ24564	AAQ24564 NANBH pep	907	11	55.0	45	8	ACD29155	Acd29155
55.0	29	2	AAQ64062	AAQ64062 Anti-canc	908	11	55.0	45	9	ADB73666	Adb73666
55.0	30	2	AAT00205	AAT00205 Thrombin	909	11	55.0	45	9	ADB76382	Adb76382
55.0	30	2	AAT18017	AAT18017 Chemokine	910	11	55.0	45	9	ADC43808	Adc43808
55.0	30	2	AAT98806	AAT98806 Primer 63	911	11	55.0	45	9	ADC61568	Adc61568
55.0	30	2	AAT65532	AAT65532 Oligonucl	912	11	55.0	45	9	ADC63532	Adc63532
55.0	30	2	AAT63002	AAT63002 c-mpl rec	913	11	55.0	45	9	ADC66632	Adc66632
55.0	30	2	AAV55444	AAV55444 Primer 12	914	11	55.0	45	9	ADC68756	Adc68756
55.0	30	4	AAF70757	AAF70757 Thrombin	915	11	55.0	45	9	ADC62816	Adc62816
55.0	30	6	AD34667	AD34667 PCR prime	916	11	55.0	45	9	ADC67881	Adc67881
55.0	30	6	AA94552	AA94552 Rice XB3	917	11	55.0	45	9	ADC41201	Adc41201
55.0	31	2	AAQ80843	AAQ80843 MHC 1 reg	918	11	55.0	45	9	ADC67256	Adc67256
55.0	31	2	AAT59839	AAT59839 Regulator	919	11	55.0	45	9	ADC62192	Adc62192
55.0	31	4	AAI31136	AAI31136 Human sin	920	11	55.0	45	9	ADC53863	Adc53863
55.0	31	4	AAI29843	AAI29843 Human sin	921	11	55.0	45	9	ADC41825	Adc41825
55.0	31	6	AAI42078	AAI42078 Human Glu	922	11	55.0	45	9	ADE45194	Ade45194
55.0	31	6	AB564553	AB564553 Human K+a	923	11	55.0	45	9	ADE35248	Ade35248
55.0	31	6	AB564526	AB564526 Human K+a	924	11	55.0	45	9	ADD72335	Add72335
55.0	31	6	AB564541	AB564541 Human K+a	925	11	55.0	45	9	ADD72335	Add72335
55.0	31	7	ACD43786	ACD43786 Human gen	926	11	55.0	45	9	ADD72335	Add72335
55.0	32	2	AAV66474	AAV66474 PCR prime	927	11	55.0	45	9	ADD72335	Add72335
55.0	32	2	AAQ45872	AAQ45872 CMV ampli	928	11	55.0	45	10	ADE48494	Ade48494
55.0	33	6	ABK50198	ABK50198 Acid phos	929	11	55.0	45	10	ADE89595	Ade89595
55.0	33	7	ABX13121	ABX13121 Rat volta	930	11	55.0	45	10	AAZ65844	Aaz65844
55.0	35	1	AA60031	AA60031 Sequence	931	11	55.0	47	3	AAH88310	Aah88310
55.0	35	1	AAV31803	AAV31803 Human cyt	932	11	55.0	48	7	ACD55114	Acd55114
55.0	35	3	AA75439	AA75439 PCR prime	933	11	55.0	48	7	ACD55264	Acd55264
55.0	35	3	AA70686	AA70686 CMV IE ge	934	11	55.0	50	2	AA76096	Aat76096
55.0	35	5	AAH45499	AAH45499 PCR prime	935	11	55.0	50	2	AA76096	Aat76096
55.0	35	6	AD42077	AD42077 CMV IE pr	936	11	55.0	50	3	AA33350	Aaa33350
55.0	35	8	AA62309	AA62309 PCR prime	937	11	55.0	50	3	AAF19472	Aaf19472
55.0	35	9	AA60101	AA60101 CMV genom	938	11	55.0	50	6	ABZ04864	Abz04864
55.0	36	2	AA708949	AA708949 Reverse p	939	11	55.0	50	6	ABZ04864	Abz04864
55.0	36	2	AAV66305	AAV66305 3' PCR pr	940	11	55.0	50	6	ABZ04775	Abz04775
55.0	36	2	AAV32680	AAV32680 Delta thi	941	11	55.0	50	6	ABZ07384	Abz07384
55.0	36	2	AAV52688	AAV52688 HGV rever	942	11	55.0	50	6	ABZ00264	Abz00264
55.0	36	2	AAV16496	AAV16496 PCR prime	943	11	55.0	50	6	ABZ03945	Abz03945
55.0	36	2	AAV02543	AAV02543 USS856134	944	11	55.0	50	6	ABZ95166	Abz95166
55.0	36	2	AAV82239	AAV82239 Hepatitis	945	11	55.0	50	7	ABQ80025	Abq80025
55.0	36	8	ACC78362	ACC78362 Bag-1 DNA	946	11	55.0	51	3	AA77280	Aaa77280
55.0	37	3	AA71618	AA71618 Shuttle v	947	11	55.0	51	4	AAI31657	Aai31657
55.0	38	9	AD19639	AD19639 Oreochrom	948	11	55.0	51	4	AAI30798	Aai30798
55.0	39	2	AAQ70222	AAQ70222 HTLV1 pep	949	11	55.0	51	4	AAI76332	Aai76332
55.0	40	2	AA792660	AA792660 BNLFI gen	950	11	55.0	51	4	AAI76786	Aai76786
55.0	40	6	AAAD27751	AAAD27751 HPIV3 wil	951	11	55.0	51	4	AAI75196	Aai75196
55.0	41	8	ABT19439	ABT19439 Aspergill	952	11	55.0	51	4	AAI76994	Aai76994
55.0	42	6	AAI41023	AAI41023 Sense PCR	953	11	55.0	51	4	AAI76995	Aai76995
55.0	42	8	ACC84885	ACC84885 S. antibi	954	11	55.0	51	4	AAI75197	Aai75197
55.0	43	6	ABZ49419	ABZ49419 Human UDP	955	11	55.0	51	4	AAH79615	Aah79615
55.0	44	6	ABAO1121	ABAO1121 HBV prime	956	11	55.0	51	4	AAH80006	Aah80006
55.0	44	7	ABZ37310	ABZ37310 URE adapt	957	11	55.0	51	5	ABL00588	Ab100588
55.0	44	7	ABZ37312	ABZ37312 URE adapt	958	11	55.0	51	5	ABL00199	Ab100199
55.0	44	7	ABZ37309	ABZ37309 URE adapt	959	11	55.0	52	5	AA84164	Aac84164
55.0	44	7	ABZ37319	ABZ37319 URE adapt	960	11	55.0	52	5	ACD95182	Acd95182
55.0	44	7	ABZ37311	ABZ37311 URE adapt	961	11	55.0	53	2	AAQ98133	Aaq98133
55.0	44	7	ABZ37321	ABZ37321 URE adapt	962	11	55.0	53	7	ACD94369	Acd94369
55.0	44	7	ABZ37322	ABZ37322 URE adapt	963	11	55.0	53	8	AA57536	Aad57536
55.0	44	7	ABZ37320	ABZ37320 URE adapt	964	11	55.0	53	8	AA57540	Aad57540
55.0	44	7	ACC79259	ACC79259 Hepatitis	965	11	55.0	54	2	AAI9719	Aai9719
55.0	45	2	AAZ34026	AAZ34026 Human PRO	966	11	55.0	54	6	AAK98828	Aak98828
55.0	45	3	AA88529	AA88529 PRO540 hy	967	11	55.0	55	2	AAZ22253	Aaz22253
55.0	45	3	AA78702	AA78702 Human PRO	968	11	55.0	57	6	ABK17232	Abk17232
55.0	45	4	AA91594	AA91594 Human PRO	969	11	55.0	57	7	ACD93496	Acd93496
55.0	45	7	ACD42559	ACD42559 Novel hum	970	11	55.0	58	2	AAQ8076	Aaq8076
55.0	45	7	ACA63594	ACA63594 Novel hum	971	11	55.0	58	3	AAZ39001	Aaz39001
55.0	45	7			972	11	55.0	58	4	AA02515	Aad02515

55.0 58 4 AAD02507  
 55.0 58 5 AAh74651  
 55.0 58 6 AAS19340  
 55.0 58 6 AAL41026  
 55.0 59 2 AAV84664  
 55.0 60 6 ABN46615  
 55.0 60 6 ABN40542  
 55.0 60 6 ABN41690  
 55.0 60 6 ABN58812  
 55.0 60 6 ABN48282  
 55.0 60 6 ABN36290  
 55.0 60 6 ABN32535  
 55.0 60 6 ABN41141  
 55.0 60 6 ABN41378  
 55.0 60 6 ABN34235  
 55.0 60 6 ABN58555  
 55.0 60 6 ABN37680  
 55.0 60 6 ABN40893  
 55.0 60 6 ABN58749  
 55.0 60 6 ABN32303  
 55.0 60 6 ABN58956  
 55.0 60 6 ABN49924  
 55.0 60 6 ABN35175  
 55.0 60 6 ABN35938  
 55.0 60 6 ABN38311  
 55.0 60 6 ABN41092  
 55.0 60 6 ABN43683

## ALIGNMENTS

Standard; DNA; 20 BP.

2 (first entry)

PCR primer SEQ ID NO:7.

; carcinoembryonic antigen; adenocarcinoma; oesophagus;  
 ; PCR primer; ss.

ss.

L-Al.

2.

; 2002WO-US006504.

1; 2001US-0273277P.

IV PITTSBURGH.

Luketich JD, Raja S, Kelly LA, Finkelstein SD;

732795/79.

PCR method for detecting malignancies, e.g. adenocarcinoma of  
 the lung comprises conducting a PCR amplification on a DNA sample in  
 a mixture.

page 33; 141pp; English.

The invention describes a multiplex polymerase chain reaction  
 comprising conducting PCR on a DNA sample in a reaction  
 mixture in first and second amplification stages, each with one  
 or more cycles comprising denaturing, annealing and elongating steps  
 along with a step may be conducted at the same temperature as the

CC annealing step. The second amplification stage of (M1) is cond  
 CC different reaction conditions from that of the first amplifica  
 CC to modulate the relative rate of production of the first ampli  
 CC first primer set and a second amplicon by a second primer set  
 CC first and second amplification stages. Also described: (1) an  
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) in  
 CC PCR diagnostic; (3) rapid detection of a malignancy or of meta  
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use i  
 CC automated PCR system. (M1) is useful for detecting malignancie  
 CC adenocarcinoma of the oesophagus. (M1) eliminates contaminatio  
 CC decreases the time it takes to carry out a PCR reaction. The p  
 CC sequence represents a PCR primer for human CEA (carcinoembryon  
 CC antigen), which is used in an example from the present inventi  
 XX  
 SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0;  
 QY 1 ATCCTTGTCCTCCACGGGTT 20  
 |||||  
 Db 1 ATCCTTGTCCTCCACGGGTT 20  
 |||||  
 RESULT 2  
 ADE13859  
 ID ADE13859 standard; DNA; 47 BP.  
 XX  
 AC ADE13859;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE CEA(6D)-1,2 related oligonucleotide SEQ ID NO:22.  
 XX  
 KW carcinoembryonic antigen; CEA; CEA(6D)-1; 2; cytostatic; vacci  
 KW tumour antigen; immunotherapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 EN WO2003085087-A2.  
 XX  
 PD 16-OCT-2003.  
 XX  
 PF 09-APR-2003; 2003WO-US010916.  
 XX  
 PR 09-APR-2002; 2002US-0372972P.  
 XX  
 PA (AVET) AVENTIS PASTEUR LTD.  
 PA (THER-) THERION BIOLOGICS INC.  
 XX  
 PI Parrington M, Zhang L, Rovinski B, Gritz LR, Greenhalgh T;  
 XX  
 DR WPI; 2003-877029/81.  
 XX  
 PT New isolated DNA molecule comprising the carcinoembryonic anti  
 PT 1,2 sequence, useful for diagnosing, preventing and treating ca  
 PT determining the effectiveness of a chemotherapeutic or other t  
 PT regimen.  
 XX  
 FS Disclosure; SEQ ID NO 22; 56pp; English.  
 XX  
 CC The present invention describes an isolated DNA molecule compri  
 CC carcinoembryonic antigen (CEA) (6D)-1,2 sequence of 2106 bp (se  
 CC ADE13861), or its fragment. Also described: (1) an expression v  
 CC comprising the nucleic acid sequence CEA(6D)-1,2, or its fragme  
 CC (1) in a pharmaceutical carrier; and (3) preventing or treating  
 CC comprising administering to a host the expression vector of (1)  
 CC 1,2 has cytostatic activity, and can be used in vaccines. The C  
 CC nucleic acid and target polypeptide are useful for diagnosing, the  
 CC and treating cancer, predicting prognosis, or determining the  
 CC effectiveness of a chemotherapeutic or other treatment regimen.

vector may be used for the insertion and expression of CEA (6D) c acid encoding tumour antigens for the immunotherapeutic use. The target polypeptides are useful in generating used in screening assays or for immunotherapy. The present presents an oligonucleotide which is given in the tion of the present invention.

BP; 9 A; 16 C; 12 G; 10 T; 0 U; 0 Other;

ilarity 95.0%; Score 19; DB 9; Length 47;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

'CCTTGCTCCACGGGT 19

'CCTTGCTCCACGGGT 47

andard; DNA; 17 BP.

(first entry)

onucleotide associated with tumour suppression, SEQ ID 1490.  
virucide; neuroprotective; nootropic; neuroleptic; murine;  
ression; tumour reversion; apoptosis; virus resistance;  
se; tumour; cell degeneration; cancer; Alzheimer's disease;  
ia; ss.

s.

6-A2.

; 2002WO-IB004210.

; 2001FR-00011979.

ECULAR ENGINES LAB.

Amson R, Tuijnder M;

33167/31.

d nucleic acid, useful for treating viral diseases associated and cell degeneration, also related polypeptides, antibodies cted cells.

Page 205; 738pp; French.

invention relates to murine oligonucleotides (ACC62754- which are associated with tumour suppression, tumour apoptosis and virus resistance. The oligonucleotides are 1) as probes and primers for detecting, identifying, and/or amplifying nucleic acid, e.g. as one component of a in vitro as (anti)sense reagents; and (2) for production of polypeptides. The oligonucleotides are useful for preparation uicals for prevention and/or treatment of viral diseases that erised by development of tumours or cell degeneration, Y cancer but also Alzheimer's disease and schizophrenia

BP; 2 A; 8 C; 2 G; 5 T; 0 U; 0 Other;

ilarity 75.0%; Score 15; DB 7; Length 17;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

'CCTTGCTCCAC 15

Db  
|||  
2 ATCCTTGCTCCAC 16

RESULT 4

ACI58088  
ID ACI58088 standard; DNA; 25 BP.

XX AC ACI58088;

XX DT 13-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 58079.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expres  
genetic variation; biallelic marker; polymorphism; human;  
cross-species comparison.

XX OS Homo sapiens.

XX FN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX DR WPI; 2003-567553/53.

XX PT New array of nucleic acid probes, useful for in situ hybridizat  
Southern, Northern or dot-blot hybridization to identify or det  
sequence or specific mutations of any gene.

XX PS Claim 1; SEQ ID NO 58079; 9pp; English.

XX CC The invention discloses a microarray comprising a plurality of  
acid probes including one of 2,018,500 fully defined sequences,  
perfect match, perfect mismatch, antisense match or antisense m  
Also disclosed is a method of gene expression analysis. The arr  
in monitoring gene expression levels by hybridisation to a DNA  
in analysis of genetic variation or in hybridisation of tag-lab  
compounds. The nucleic acid probes are specifically designed fo  
of at least one target sequence. The method of analysis compris  
hybridising at least one or more nucleic acids to at least two  
nucleic acid probes and detecting the hybridisation. The nuclei  
probes are attached to a solid support. The analysis comprises  
gene expression levels, identifying biallelic markers or polymo  
or family members of a gene and a cross-species comparison. Eac  
nucleic acids further comprises a tag sequence. The array of nu  
probes is useful in in situ hybridisation, in Southern, Northern  
blot hybridisation to identify or detect the sequence or specif  
mutations of any gene, in mapping the 5' termini of mRNA molecu  
primer extensions or in screening cDNA or genomic libraries or  
for additional subclones containing segments of DNA that have b  
isolated and previously sequenced. The sequence presented is on  
nucleic acid probes incorporated in the microarray. Note: The s  
data for this patent can also be obtained in electronic format  
from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 3 A; 8 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 8; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0;

QY 1 ATCCTTGCTCCAC 15

Db 3 ATCCTTGCTCCAC 17

XX SQ Sequence 20 BP, 2 A; 9 C; 3 G; 6 T; 0 U; 0 Other;  
Query Match 74.0%; Score 14.8; DB 7; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;  
QY 1 ATCCTGTCTCCACGGG 18  
||||| ||||| |||||  
DB 3 ATCCTGTCTCCACGGG 20  
RESULT 6  
ACD02563/c  
ID ACD02563 standard; DNA; 20 BP.  
XX  
AC ACD02563;  
DT  
XX 31-JUL-2003 (first entry)  
DE  
XX Novel human zsig37 sequencing primer ZC13650.  
XX  
KW Blood flow; vasodilation; wound repair; platelet inhibition; t  
KW vascular occlusion; ischaemic reperfusion injury; microvascula  
KW adipocyte complement related protein; intestinal strangulation  
KW angioplasty; coronary artery bypass graft; endarterectomy; an  
KW anastomosis; stroke; cardiopulmonary bypass ischaemia; inflam  
KW myocardial infarction; percutaneous transluminal angioplasty;  
KW post-trauma vasospasm; prosthetic biomaterial; fibroblast recu  
KW wound retraction; human; zsig37; primer; ss; sequencing; PCR.  
XX  
OS Homo sapiens.  
XX  
XX US2003022838-A1.  
XX  
PD 30-JAN-2003.  
XX  
XX 25-JUN-2002; 2002US-00180762.  
XX  
XX 19-FEB-1999; 99US-00253604.  
XX 22-NOV-1999; 99US-00444794.  
XX 17-FEB-2000; 2000US-00506855.  
XX 19-JUL-2000; 2000US-00619740.  
XX  
XX (SHEP/) SHEPPARD P O.  
XX (LASS/) LASSER G W.  
XX (BISH/) BISHOP P D.  
XX  
XX Sheppard PO, Lasser GW, Bishop PD;  
XX  
XX WPI; 2003-456304/43.  
XX  
XX Promoting blood flow or inducing vasodilation within vasculat  
XX mammal, or pacifying damaged collagenous tissues or pacifying  
XX prosthetic biomaterial, by administering adipocyte complement r  
XX protein.  
XX  
XX Example 1; Page 24; 46pp; English.  
XX  
XX The invention relates to a method of promoting blood flow or ir  
XX vasodilation within the vasculature of a mammal, pacifying dam  
XX collagenous tissues or surface of prosthetic biomaterial, media  
XX repair, inhibiting platelet adhesion, activation or accretion,  
XX vascular occlusion, protecting ischaemic myocardium from reper  
XX injury or mediating tumour metastasis, comprising administering  
XX complement related protein. The method is useful for promoting  
XX within the vasculature of a mammal, where the mammal suffers fr  
XX vascular injury, where the injury is due to vascular reconstruct  
XX comprises angioplasty, coronary artery bypass graft, endarterec  
XX microvascular repair or anastomosis of a vascular graft, or the  
XX due to trauma, stroke or aneurysm. The method is useful for pac  
XX damaged collagenous tissues within a mammal, where the damaged  
XX collagenous tissues are due to injury associated with ischaemic  
XX

standard; DNA; 20 BP.  
3 (first entry)  
SNP analysis PCR primer, #39.  
; primer; ss; asthma; bronchial hyperresponsiveness;  
truction; chronic bronchial inflammation;  
rial disease; asthma-associated gene; AAGA; allele-specific;  
leotide polymorphism; SNP; genetic profile; gene therapy;  
gene therapy; adult distress respiratory syndrome;  
structive pulmonary; chronic bronchitis; dyspnea.  
as.  
40-A2.  
3.  
2; 2002WO-EP007847.  
1; 2001US-0305649P.  
VARTIS AG.  
VARTIS-ERFINDUNGEN VERW GES MEH.  
IV WAKE FOREST HEALTH SCI.  
JKSUNIV GRONINGEN.  
PA, Meyers DA, Postma DS, Bleeker ER;  
239359/23.  
f whether a subject has or is at risk of developing a disease  
zed by bronchial hyperresponsiveness, comprises determining the  
or bioactivity level of an asthma-associated gene.  
Page 27; 70pp; English.  
ion discloses a method for determining a disease (e.g asthma)  
ay obstruction or chronic bronchial inflammation. Asthma is a  
rial disease, so discovery of the asthma susceptibility genes  
fy the fundamental mechanisms behind asthma. One such gene is  
-associated gene, AAGA. Also disclosed is an allele-specific  
pligonucleotide probe capable of detecting a polymorphism, an  
ynucleotide, and encoded polypeptide, which is a variant  
ated with bronchial hyperresponsiveness and methods for  
omically selecting a therapy to be administered to an  
having asthma, comprising determining an AAGA genetic profile  
ing the individual's genetic profile to an AAGA genetic  
profile, monitoring the effectiveness of treatment (e.g. gene  
antisense gene therapy) of a subject and identifying a  
which binds to or modulates the activity of AAGA. The  
nucleotide, encoded by it, antibody to the polypeptide,  
nucleotide, is useful for preparing a medicament for treating  
characterised by bronchial hyperresponsiveness, or inflammatory  
ive airways diseases, e.g. adult distress respiratory  
chronic obstructive pulmonary, chronic bronchitis or dyspnea.  
is useful for prognosing, diagnosing or confirming that a  
subject has a genetic defect which causes or contributes to  
ilar disease or disorder, for ascertaining an individual's  
on to develop bronchial responsiveness and for customising a  
c the individual according to the individual's genetic profile.  
es presented in ABX98968-ABX99053 and ABX99064-ABX99066 are  
s which were used to amplify sequences used in human AAGA  
struction and primers used to analyse AAGA single nucleotide  
ms (SNPs)

The injury comprises trauma injury, ischaemia, intestinal an, or injury associated with pre- and post-establishment of the mammal suffers from cardiopulmonary bypass ischaemia and a, myocardial infarction, or post-trauma vasospasm. The post-spasm comprises stroke, percutaneous transluminal angioplasty, my, accidental vascular trauma or surgical-induced vascular method is useful for pacifying the surface of a prostatic for use in association with a mammal, where the surface of ic biomaterial is coated with collagen or collagen fragments, brin or fibrinectin. The method is useful for mediating wound in a mammal, where the method enhances progression in wound progression in wound healing comprises reduction in a, reduction in fibroblast recruitment, wound retraction, or a infection. The method is useful for inhibiting platelet ctivation or accretion. The method is useful for minimising clusion by increasing patency time in a patient in need of the The method is useful for inducing vasodilation within the of a mammal. The method is useful for protecting ischemic from reperfusion injury. The method is useful for mediating stasis. The present sequence represents the human adipocyte related protein zsig27 DNA sequencing primer

BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

74.0%; Score 14.8; DB 7; Length 20;  
ilarity 88.9%; Pred. No. 2.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCTCCACGGGTT 20  
|||||||  
TTGTCTCTCCACGGGTT 3

andard; DNA; 20 BP.

(first entry)

zsig37 sequencing primer ZC13651.

vasodilation; wound repair; platelet inhibition; tumour; clusion; ischaemic reperfusion injury; microvascular repair; mplement related protein; intestinal strangulation; trauma; ; coronary artery bypass graft; endarterectomy; aneurysm; infarction; cardiopulmonary bypass ischaemia; inflammation; vasospasm; percutaneous transluminal angioplasty; infection; ction; human; zsig37; primer; ss; sequencing; PCR.

3.

3-AL.

2002US-00180762.  
99US-00253604.  
99US-0044794.  
2000US-00506855.  
2000US-00619740.

PPARD P O.  
SER G W.  
TOP P D.

Lasser GW, Bishop PD;

6304/43.

Promoting blood flow or inducing vasodilation within vasculatur mammal, or pacifying damaged collagenous tissues or pacifying e prostatic biomaterial, by administering adipocyte complement re protein.

Example 1; Page 23; 46pp; English.

The invention relates to a method of promoting blood flow or in vasodilation within the vasculature of a mammal, pacifying dama collagenous tissues or surface of prostatic biomaterial, mediat repair, inhibiting platelet adhesion, activation or accretion, vascular occlusion, protecting ischaemic myocardium from reperf injury or mediating tumour metastasis, comprising administering complement related protein. The method is useful for promoting within the vasculature of a mammal, where the mammal suffers fr vascular injury, where the injury is due to vascular reconstruc comprises angioplasty, coronary artery bypass graft, endarterec microvascular repair or anastomosis of a vascular graft, or the due to trauma, stroke or aneurysm. The method is useful for pac damaged collagenous tissues within a mammal, where the damaged collagenous tissues are due to injury associated with ischaemia reperfusion. The injury comprises trauma injury, ischaemia, int strangulation, or injury associated with pre- and post-establis blood flow. The mammal suffers from cardiopulmonary bypass isch recesitation, myocardial infarction, or post-trauma vasospasm. trauma vasospasm comprises stroke, percutaneous transluminal an endarterectomy, accidental vascular trauma or surgical-induced trauma. The method is useful for pacifying the surface of a pro biomaterial for use in association with a mammal, where the sur the prostatic biomaterial is coated with collagen or collagen f gelatin, fibrin or fibrinectin. The method is useful for mediat repair within a mammal, where the method enhances progression i healing and progression in wound healing comprises reduction in inflammation, reduction in fibroblast recruitment, wound retrac reduction in infection. The method is useful for inhibiting pia adhesion, activation or accretion. The method is useful for min vascular occlusion by increasing patency time in a patient in n treatment. The method is useful for inducing vasodilation withi vasculature of a mammal. The method is useful for protecting is myocardium from reperfusion injury. The method is useful for me tumour metastasis. The present sequence represents the human ad complement related protein zsig27 DNA sequencing primer

Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 7; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CCTTGTCTCTCCACGGGTT 20  
| | | | | | | | | | | | | | | | | |  
Db 1 CTTTGTCTCTCCACGGGTT 18

RESULT 8

ABX04524/c

ID ABX04524 standard; DNA; 20 BP.

AC ABX04524;

DT 13-JAN-2003 (first entry)

Human adipose complement related protein zsig37 primer ZC13650.

Human; ss; primer; adipocyte complement related protein; zsig37; chromosome 17q25.2; blood flow; vulnerary; antibacterial; vasot; anticoagulant; immunosuppressive; damaged collagenous tissue; complement activation; thrombosis; trauma; ischaemia; reperfusio; intestinal strangulation; cardiopulmonary bypass ischaemia; myocardial infarction; post-trauma vasospasm; stroke; percutaneous transluminal angioplasty; endarterectomy; accidental vascular trauma; surgical-induced vascular trauma; haemostasis; wound healing; antimicrobial.

primer; adipocyte complement related protein; zsig37;  
17q25.2; blood flow; vulnery; antibacterial; vasotrophic;  
ant; immunosuppressive; damaged collagenous tissue;  
activation; thrombosis; trauma; ischaemia; reperfusion;  
strangulation; cardiopulmonary bypass ischaemia;  
infarction; post-trauma vasospasm; stroke;  
as transliminal angioplasty; endarterectomy;  
vascular trauma; surgical-induced vascular trauma;

Human; zsg37; ss; chromosome 17q25.2; vascular occlusion; vascular adpocyte complement related protein; vascular injury; vascular reconstruction; trauma; stroke; aneurysm; plaque rupture; vasculature; diabetes; atherosclerosis; blood flow; vasorelaxant; tranquiliser; vulnerable; cerebroprotective; antiatherosclerotic sequencing; primer.



35.  
31.  
3.  
); 2000US-00619740.  
3; 99US-00253604.  
3; 99US-00444794.  
); 2000US-00506855.  
MOGENETICS INC.  
), Lasser GW, Bishop PD;  
'07011/67.  
vascular occlusion or inducing vasodilation within the  
; of a mammal, by administering an adipocyte complement related  
; ig37 that promotes blood flow.  
SEQ ID NO 15; 44pp; English.  
on relates to a method for minimising vascular occlusion or  
usodilation within a mammal, involving administering a  
comprising an adipocyte complement related protein, zsig37.  
is useful for minimising vascular occlusion and inducing  
n in a mammal suffering from acute vascular injury which may  
ascular reconstruction, trauma, stroke or aneurysm. The  
jury is due to plaque rupture, degradation of the vasculature,  
ns associated with diabetes and atherosclerosis.  
ion of the formulation promotes blood flow or elicits a  
t response. This sequence represents a primer used to sequence  
ng the human zsig37 polypeptide of the invention.  
BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;  
74.0%; Score 14.8; DB 9; Length 20;  
ilarity 88.9%; Pred. No. 2.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
TTGTCTCTCCACGGGTT 20  
TTGTCTCTCCACGGTTT 3  
andard; DNA; 20 BP.  
(first entry)  
7 cDNA sequencing primer #8.  
37; ss; chromosome 17q25.2; vascular occlusion; vasodilation;  
complement related protein; vascular injury;  
construction; trauma; stroke; aneurysm; plaque rupture;  
; diabetes; atherosclerosis; blood flow; vasorelaxant;  
r; vulnery; cerebroprotective; antiatherosclerotic;  
primer.  
s.  
1.  
; 2000US-00619740.  
; 99US-00253604.

PR 22-NOV-1999; 99US-00444794.  
PR 17-FEB-2000; 2000US-00506855.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Sheppard PO, Lasser GW, Bishop PD;  
XX WPI; 2003-707011/67.  
DR Minimizing vascular occlusion or inducing vasodilation within  
XX vasculture of a mammal, by administering an adipocyte comple  
PT protein, zsig37 that promotes blood flow.  
PT Example 1; SEQ ID NO 12; 44pp; English.  
XX The invention relates to a method for minimising vascular ocl  
XX inducing vasodilation within a mammal, involving administering  
CC formulation comprising an adipocyte complement related protein  
CC The method is useful for minimising vascular occlusion and ind  
CC vasodilation in a mammal suffering from acute vascular injury  
CC be due to vascular reconstruction, trauma, stroke or aneurysm.  
CC vascular injury is due to plaque rupture, degradation of the v  
CC complications associated with diabetes and atherosclerosis.  
CC Administration of the formulation promotes blood flow or elicit  
CC vasorelaxant response. This sequence represents a primer used  
CC cDNA encoding the human zsig37 polypeptide of the invention.  
XX Sequence 20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;  
SQ Query Match 74.0%; Score 14.8; DB 9; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;  
Qy 3 CCTGTCTCTCCACGGGTT 20  
Db 1 CTTGTCTCTCCACGGTTT 18  
RESULT 12  
AAD59886  
ID AAD59886 standard; DNA; 20 BP.  
AC AAD59886;  
XX  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE  
XX  
KW Adipocyte complement related protein; collagenous surface pacif  
KW wound healing; tumour metastasis; gene therapy; thrombogenic; f  
KW Acip; zsig37; ss.  
XX  
OS Homo sapiens.  
XX  
XX US2003144208-A1.  
XX  
PD 31-JUL-2003.  
XX  
XX 07-FEB-2003; 2003US-00360186.  
PF  
XX  
XX 19-FEB-1999; 99US-00253604.  
PR 22-NOV-1999; 99US-00444794.  
PR 17-FEB-2000; 2000US-00506855.  
PR 19-JUL-2000; 2000US-00619740.  
XX  
XX (SHEP/) SHEPPARD P O.  
PA (LASS/) LASSER G W.  
PA (BISH/) BISHOP P D.  
XX  
XX Sheppard PO, Lasser GW, Bishop PD;  
XX WPI; 2003-755532/71.  
XX

blood flow within the vasculature of a mammal, comprising an adipocyte complement related protein to reduce blood flow and complement activity within the vasculature.

Page 24; 48pp; English.

ion relates to a method of promoting blood flow within the vasculature of a mammal. The method involves administering an adipocyte complement related protein (Acrp) to the mammal to reduce thrombogenic activity within the vasculature. Methods and compositions are useful in promoting blood flow within the vasculature of a mammal, in pacifying collagenous surfaces, in modulating blood flow or mediating tumour metastasis. The invention is also a gene therapy. The present sequence is an oligo used to identify adipocyte complement related protein homologue (zsig37) DNA

20 BP; 2 A; 7 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 9; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.7e+03;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

TTGTCTCTCCACGGTT 20  
|||||||  
TTGTCTCTCCACGGTT 18

Standard; DNA; 20 BP.

3 (first entry)

Oligo used to identify human zsig37 DNA.

complement related protein; collagenous surface pacification; gene therapy; tumour metastasis; gene therapy; thrombogenic; human; 37; ss.

ss.

38-A1.

3.

3; 2003US-00360186.

3; 99US-00253604.

3; 99US-00444794.

3; 2000US-00506855.

3; 2000US-00619740.

3PPARD P O.

3SER G W.

3SHOP P D.

3, Lasser GW, Bishop PD;

755532/71.

blood flow within the vasculature of a mammal, comprising an adipocyte complement related protein to reduce blood flow and complement activity within the vasculature.

Page 24; 48pp; English.

ion relates to a method of promoting blood flow within the vasculature of a mammal. The method involves administering an adipocyte complement related protein (Acrp) to the mammal to reduce thrombogenic activity within the vasculature. Methods and compositions are useful in promoting blood flow within the

CC vasculature of a mammal, in pacifying collagenous surfaces, in  
CC wound healing or mediating tumour metastasis. The invention is  
CC useful in gene therapy. The present sequence is an oligo used  
CC human adipocyte complement related protein homologue (zsig37)  
XX

Sequence 20 BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 9; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.7e+03;  
Matches 16; Conservative 2; Mismatches 0; Indels 0;

OY 3 CCTTCTCTCTCCACGGTT 20  
|||||||  
DB 20 CCTTCTCTCTCCACGGTT 3

RESULT 14

ACK19038

ID ACK19038 standard; DNA; 25 BP.

XX ACK19038;

XX 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 119019.

XX EST; ss; probe; expressed sequence tag; microarray; gene expres-  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.

OS Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization  
PT Southern, Northern or dot-blot hybridization to identify or del-  
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 119019; 9pp; English.

CC The invention discloses a microarray comprising a plurality of  
CC acid probes including one of 2,018,500 fully defined sequences,  
CC perfect match, perfect mismatch, antisense match or antisense  
CC Also disclosed is a method of gene expression analysis. The array  
CC in monitoring gene expression levels by hybridisation to a DNA  
CC in analysis of genetic variation or in hybridisation of tag-lab-  
CC compounds. The nucleic acid probes are specifically designed for  
CC of at least one target sequence. The method of analysis compris-  
CC hybridising at least one or more nucleic acids to at least two  
CC nucleic acid probes and detecting the hybridisation. The nucleic  
CC probes are attached to a solid support. The analysis comprises  
CC gene expression levels, identifying biallelic markers or polymor-  
CC or family members of a gene and a cross-species comparison. Each  
CC nucleic acids further comprises a tag sequence. The array of nu-  
CC probes is useful in in situ hybridisation, in Southern, Northern  
CC blot hybridisation to identify or detect the sequence or speci-  
CC mutations of any gene, in mapping the 5' termini of mRNA molec-  
CC primer extensions or in screening cDNA or genomic libraries or  
CC for additional subclones containing segments of DNA that have b-  
CC isolated and previously sequenced. The sequence presented is or  
CC nucleic acid probes incorporated in the microarray. Note: The i-

us patent can also be obtained in electronic format directly at seqdata.uspto.gov/sequence.html

BP; 1 A; 7 C; 7 G; 10 T; 0 U; 0 Other;  
 74.0%; Score 14.8; DB 8; Length 25;  
 ilarity 88.9%; Pred. No. 2.7e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTGTGCTCTCCACGGT 19  
 ||||| |||||  
 CTGTGCTCTCCACGGT 24

andard; DNA; 38 BP.

(first entry)

3 cDNA PCR forward primer ZnRING.

-3; tumour necrosis factor receptor-associated factor 3;  
 AF-3; delta221 TRAF-3; immunosuppressive; antiarthritic;  
 cal; antiinflammatory; antianaemic; antipsoriatic;  
 c; antithyroid; antitumour; anti-HIV; antibacterial;  
 opthalmological; antiallergic; antiatherosclerotic;  
 neuroprotective; haemostatic; CD40 signalling inhibitor;  
 y; necrosis factor kappaB activator; autoimmune disease;  
 disease; allergy; PCR primer; ss.

S.

-A1.

; 200WO-US006503.

; 99US-00268544.

V COLUMBIA NEW YORK.

Van Eindhoven W;

87425/55.

necrosis factor (TNF) receptor-associated factor deletion  
 r identifying an agent that inhibits CD-40 mediated cellular  
 od for inhibiting e.g. rheumatoid arthritis and diabetes

Page 166; 170pp; English.

sequence is a PCR primer which was used in the isolation and  
 ation of tumour necrosis factor receptor (TNF)-associated  
 RAP-3) cDNA clones from the D1.1 Jurkat T cell line. TRAF-3  
 including delta130 and delta221 TRAF-3 deletion isoforms, are  
 inhibiting activation of a CD40 ligand on a wide range of  
 ing B cells, fibroblasts, endothelial cells, epithelial  
 lls, basophils, macrophages, Reed-Steinberg cells, dendritic  
 l cells or smooth muscle cells expressing CD40 on the cell  
 e proteins are also useful for treating conditions associated  
 adiated intracellular signalling, such as organ rejection as a  
 ransplantation or an immune response after receiving gene  
 may be useful for treating an CD40-dependent immune response  
 suffering from an autoimmune disease such as rheumatoid  
 myasthenia gravis, systemic lupus erythematosus, Grave's  
 topathic thrombocytopenia purpura, haemolytic anaemia,  
 litus, a drug-induced autoimmune disease (drug-induced  
 iasis or hyper immunoglobulin (Ig)E syndrome. The proteins

CC may also be used to treat an immune response associated with a  
 CC infectious disease such as Reiter's syndrome, spondyloarthritis  
 CC disease, human immunodeficiency virus (HIV) infection, syphilis  
 CC tuberculosis. They may be used to treat an allergic response,  
 CC atherosclerosis, reperfusion injury and chronic inflammatory a  
 CC diseases such as vasculitis, scleroderma or multiple sclerosis  
 XX

SQ Sequence 38 BP; 11 A; 9 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 72.0%; Score 14.4; DB 3; Length 38;  
 Best Local Similarity 93.8%; Pred. No. 4.2e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0;

QY 2 TCCTTGCTCTCCACGG 17  
 ||||| |||||  
 Db 32 TACTTGCTCTCCACGG 17

RESULT 16

AAA95963/c

ID AAA95963 standard; DNA; 38 BP.

XX AC AAA95963;

XX 19-JAN-2001 (first entry)

1.8 kb TRAF-3 cDNA forward primer 5'CRAP-EST2(186).F.

Human; TRAF-3; tumour necrosis factor receptor-associated facto  
 delta130 TRAF-3; delta221 TRAF-3; immunosuppressive; antiarthr  
 dermatological; antiinflammatory; antianaemic; antipsoriatic;  
 antidiabetic; antithyroid; antitumour; anti-HIV; antibacterial;  
 uropathic; opthalmological; antiallergic; antiatherosclerotic;  
 vasotropic; neuroprotective; haemostatic; CD40 signalling inhib  
 gene therapy; necrosis factor kappaB activator; autoimmune dise  
 infectious disease; allergy; 3'-RACE primer; ss.

XX OS Homo sapiens.

XX PN WO2000053629-A1.

XX PD 14-SEP-2000.

XX PF 10-MAR-2000; 2000WO-US006503.

XX PR 11-MAR-1999; 99US-00268544.

XX PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX PI Lederman S, Van Eindhoven W;

XX DR WPI; 2000-587425/55.

PT Novel tumor necrosis factor (TNF) receptor-associated factor de  
 PT isoforms for identifying an agent that inhibits CD-40 mediated  
 PT signaling and for inhibiting e.g. rheumatoid arthritis and diab  
 PT mellitus.

XX Example 2; Page 59; 170pp; English.

CC The present sequence is a primer which was used to generate a 1  
 CC tumour necrosis factor receptor (TNF)-associated factor 3 (TRAF  
 CC clone by 3'-RACE. TRAF-3 isoforms, including delta130 and delta  
 CC deletion isoforms, are useful for inhibiting activation of a CD  
 CC on a wide range of cells including B cells, fibroblasts, endothe  
 CC cells, epithelial cells, T cells, basophils, macrophages, Reed-  
 CC cells, dendritic cells, renal cells or smooth muscle cells expri  
 CC CD40 on the cell surface. The proteins are also useful for treat  
 CC conditions associated with CD40-mediated intracellular signalin  
 CC as organ rejection as a result of transplantation or an immune  
 CC after receiving gene therapy. It may be useful for treating an (c  
 CC dependent immune response in patients suffering from an autoimmu  
 CC disease such as rheumatoid arthritis, myasthenia gravis, system:

mus, Grave's disease, idiopathic thrombocytopenia purpura, anaemia, diabetes mellitus, a drug-induced autoimmune disease (lupus), psoriasis or hyper immunoglobulin (Ig)E syndrome. ns may also be used to treat an immune response associated with disease such as Reiter's syndrome, spondyloarthritis, Lyme disease, immunodeficiency virus (HIV) infection, syphilis or is. They may be used to treat an allergic response, rosis, reperfusion injury and chronic inflammatory autoimmune uch as vasculitis, scleroderma or multiple sclerosis

8 BP; 11 A; 8 C; 13 G; 6 T; 0 U; 0 Other;

72.0%; Score 14.4; DB 3; Length 38;  
milarity 93.8%; Pred. No. 4.2e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CCTTGTCCTCCACGG 17  
|||||  
ACTTGTCCTCCACGG 17

-andard; DNA; 25 BP.

1 (first entry)

array DNA oligonucleotide SEQ ID NO 76558.

robe; expressed sequence tag; microarray; gene expression;  
iation; biallelic marker; polymorphism; human;  
es comparison.

is.

.0-A1.

.

; 2002US-00098263.

; 2001US-0276759P.

YMETRIX INC.

;

.67953/53.

of nucleic acid probes, useful for in situ hybridization, in  
northern or dot-blot hybridization to identify or detect the  
specific mutations of any gene.

Q ID NO 76558; 9pp; English.

on discloses a microarray comprising a plurality of nucleic  
including one of 2,018,500 fully defined sequences, or its  
ch, perfect mismatch, antisense match or antisense mismatch.  
sed is a method of gene expression analysis. The array is used  
ng gene expression levels by hybridisation to a DNA library,  
of genetic variation or in hybridisation of tag-labelled  
The nucleic acid probes are specifically designed for analysis  
one target sequence. The method of analysis comprises  
at least one or more nucleic acids to at least two or more  
d probes and detecting the hybridisation. The nucleic acid  
ion levels, identifying biallelic markers or polymorphisms,  
members of a gene and a cross-species comparison. Each of the  
ds further comprises a tag sequence. The array of nucleic acid  
seful in in situ hybridisation, in Southern, Northern or dot-  
isation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molec  
CC primer extensions or in screening cDNA or genomic libraries or  
CC for additional subclones containing segments of DNA that have  
CC isolated and previously sequenced. The sequence presented is o  
CC nucleic acid probes incorporated in the microarray. Note: The  
CC data for this patent can also be obtained in electronic format  
CC from USPTO at segdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 8 A; 7 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 8; Length 25;  
Best Local Similarity 84.2%; Pred. No. 5.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTTGTCCTCCACGGTT 20  
|||||  
Db 25 TCCGTGTCCTCCACGGCTT 7

RESULT 18

AAF84148

ID AAF84148 standard; DNA; 36 BP.

XX AAF84148;

XX

DT 07-SEP-2001 (first entry)

XX Human novel betal-like subunit cDNA amplifying 3' primer SCNIB

XX Sodium channel; sensory neurone specific channel; betal-like s

KW SNS; therapeutic; pain; analgesic; PCR primer; ss.

XX Homo sapiens.

XX WO200144293-A2.

XX 21-JUN-2001.

XX 14-DEC-2000; 2000WO-GB004802.

XX 17-DEC-1999; 99GB-00029970.

XX (GLAX ) GLAXO GROUP LTD.

XX Plumpton M, Powell AJ, Sanseau P;

XX WPI; 2001-398:29/42.

XX Novel sub-unit for voltage-gated sodium channel proteins for pr

XX agents useful for treating pain.

XX Example; Page 8; 31pp; English.

XX The invention provides a novel betal-like sub-unit for voltage-

XX sodium ion channel polypeptide, specifically a sensory neurone

XX channel (SNS) subunit. The novel betal-like subunit is useful f

XX producing a therapeutic agent which is useful treating pain in

XX The subunit can be expressed by standard recombinant methodolog

XX Sequences AAF84147-48 represent PCR primers for amplifying the

XX novel sodium channel betal-like subunit cDNA fragment

XX Sequence 36 BP; 6 A; 13 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 36;

Best Local Similarity 84.2%; Pred. No. 5.2e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 1 ATCCTTCTCCTCCACGGTT 19

Db 6 ATCCTATTCCTCCACTGTT 24

RESULT 19

standard; DNA; 33 BP.

(revised)  
(first entry)

probe CMV.GB.20.

ure; amplifier; hybridisation; assay; detection; CMV;  
irus; solution phase; comb-type branched polynucleotide;  
extension; binding site; ligation; template; linker; ss.

1.

; 92WO-US011170.

; 91US-00813590.

RON CORP.

Shen L, Urdea MS;

27341/28.

for detection of cytomegalovirus - in a solution phase  
oridisation assay.

pe 63; 71pp; English.

amplified soln. phase nucleic acid sandwich hybridisation  
ys two multimers: (1) an amplifier probe having a first  
that binds to CMV and a second segment (B\*) that hybridises to  
lifer multimer having a first segment (B\*) that hybridises to  
(B) and fifteen iterations of a segment (C), wherein segment  
s to three labeled oligonucleotides. CMV amplifier probes are  
345840-74. CMV capture probes are given in AAQ45875-84. Each  
robe contained, in addition to the sequences complementary to a  
ences, the 5' extension given in AAQ45885, complementary to a  
he amplifier multimer. Each capture probe contained, in  
the sequences complementary to the CMV sequences, a  
sequence given in AAQ45886, complementary to the DNA bound to  
ase. (Updated on 25-MAR-2003 to correct PN field.)

BP; 5 A; 11 C; 8 G; 7 T; 0 U; 2 Other;

70.0%; Score 14; DB 2; Length 33;  
larity 100.0%; Pred. No. 6.4e+03;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TGTCCTCCAG 16

|||||

TGTCCTCCAG 31

standard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 54313.

be; expressed sequence tag; microarray; gene expression;  
ation; biallelic marker; polymorphism; human;  
s comparison.

XX Homo sapiens.  
OS US2003104410-A1.  
PN 05-JUN-2003.  
XX 15-MAR-2002; 2002US-00098263.  
XX 16-MAR-2001; 2001US-0276759P.  
XX (AFFY-) AFFYMETRIX INC.  
XX Mittmann MP;  
XX WPI; 2003-567953/53.  
XX New array of nucleic acid probes, useful for in situ hybridizat  
Southern, Northern or dot-blot hybridization to identify or det  
sequence or specific mutations of any gene.  
XX Claim 1; SEQ ID NO 54313; 9pp; English.

CC The invention discloses a microarray comprising a plurality of  
CC acid probes including one of 2,018,500 fully defined sequences,  
CC perfect match, perfect mismatch, antisense match or antisense m  
CC Also disclosed is a method of gene expression analysis. The arr  
CC in monitoring gene expression levels by hybridisation to a DNA  
CC in analysis of genetic variation or in hybridisation of tag-lab  
CC compounds. The nucleic acid probes are specifically designed fo  
CC of at least one target sequence. The method of analysis compris  
CC hybridising at least one or more nucleic acids to at least two  
CC nucleic acid probes and detecting the hybridisation. The nucle  
CC probes are attached to a solid support. The analysis comprises  
CC gene expression levels, identifying biallelic markers or polymo  
CC or family members of a gene and a cross-species comparison. Eac  
CC nucleic acids further comprises a tag sequence. The array of nu  
CC probes is useful in situ hybridisation, in Southern, Northern  
CC blot hybridisation to identify or detect the sequence or specifi  
CC mutations of any gene, in mapping the 5' termini of mRNA molecu  
CC primer extensions or in screening cDNA or genomic libraries or  
CC for additional subclones containing segments of DNA that have b  
CC isolated and previously sequenced. The sequence presented is on  
CC nucleic acid probes incorporated in the microarray. Note: The s  
CC data for this patent can also be obtained in electronic format  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX Sequence 25 BP; 1 A; 8 C; 4 G; 12 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 8; Length 25;  
Best Local Similarity 88.2%; Pred. No. 7.9e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 4 CTGTGCTCCACGGT 20

Db 1 CTGTGCTCCACGGT 17

RESULT 21

ABN35794

ID ABN35794 standard; DNA; 60 BP.

XX ABN35794;

XX

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:854

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

OS

XX

9-A2.

2.

1; 2001WO-IB001903.

0; 2000US-0221607P.

1; 2001US-0287724P.

MPUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

257383/30.

ucleotide libraries comprising oligonucleotides which  
y hybridize to mRNAs transcribed from a transcription unit of a  
eul for detecting tissue-, pathology-, and developmental-  
enes.

SEQ ID NO 8542; 47pp; English.

t invention describes oligonucleotide libraries for detecting  
RNAs that populate a (sub-)transcriptome, where the (sub-  
ome comprises messenger RNAs transcribed from multiple  
ion units that populate a genome. The library comprises several  
ptides, each capable of hybridising selectively to a set of  
RNAs transcribed from a given transcription unit of the genome,  
les one or more messenger RNA splice variants. The  
tide libraries are useful for detecting mRNAs from a  
sample, in expression profiling studies, in qualitatively or  
rely characterising the corresponding transcriptome, and in  
RNA transcripts and splice variants of human or animal  
mes. The libraries may also be used as specialised mini  
:o detect transcripts of a sub-transcriptome under a particular  
or pathological state, and so allowing the detection of tissue  
ology-specific genes such as those genes only expressed in  
issue under a specific pathological condition; to detect  
:al specific genes; and to detect RNA transcripts and splice  
: a transcriptome of a patient suffering from a particular  
ABN27253 to ABN59589 represent oligonucleotide sequences from  
s and mice, which are used in the exemplification of the  
ention N.B. The sequence data for this patent did not form  
printed specification, but was obtained in electronic format  
om WIPO at ftp.wipo.int/pub/published\_pct\_sequences

) BP; 11 A; 22 C; 7 G; 20 T; 0 U; 0 Other;

69.0%; Score 13.8; DB 6; Length 60;

ilarity 88.2%; Pred. No. 8.2e+03;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CCTGTGCTCCACGG 17

|||||

CCTGTGCTCCTGG 36

andard; DNA; 24 BP.

) (first entry)

rotein primer 2.

immunogenic; active immunization; primer; ss.

.lomavirus.

v2.

XX 04-NOV-1999.  
PD 30-APR-1999; 99WO-DE001331.  
PF 30-APR-1998; 98DE-01019476.  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA Gissmann L, Jochmus I;  
XX WPI; 2000-023362/02.  
DR Immunogenic protein with altered biological function, useful f  
XX immunization.  
PT Example 1; Page 28; 33pp; German.  
XX This invention describes the construction of a novel polypepti  
CC immunogenic and altered biological function of a protein, wher  
CC polypeptide has regions of the protein of about 10-40 amino ac  
CC different order. The polypeptide, or its DNA, is useful for ac  
CC immunization without cross-reactivity and problems associated  
CC biological function of the protein. AAZ24131-ZZ4143 represent  
CC used in the construction of the peptides of the invention  
XX Sequence 24 BP; 10 A; 3 C; 10 G; 1 T; 0 U; 0 Other;  
SQ Query Match 68.0%; Score 13.6; DB 3; Length 24;  
Best Local Similarity 80.0%; Pred. No. 9.7e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0;  
QY 1 ATCCTGTGCTCCACGGTT 20  
|||||  
Db 21 ATCCTGCTCCTCCTGGTT 2  
|||||  
RESULT 23  
AAK99483/c  
ID AAK99483 standard; DNA; 24 BP.  
XX AAK99483;  
AC AAK99483;  
XX 27-JUN-2002 (first entry)  
DT Lipophilin C cDNA sense PCR primer P14.  
XX Immunogenic epitope; hormonally regulated organ; malignant tum  
KW Lipophilin; human; PCR; primer; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH misc\_binding 1..24  
FT /\*tag= a  
FT /bound moiety= "Lipophilin C cDNA nucleotides 1  
FT /note= "Bound to nucleotides 107-130 of Lipophi  
XX US2002034739-A1.  
PN 21-MAR-2002.  
XX 07-JUL-1998; 98US-00110716.  
XX 07-JUL-1998; 98US-00110716.  
XX (LEHR/) LEHRER R I.  
PA (ZHAO/) ZHAO C.  
PA (GLAS/) GLASGOW B J.  
XX Lehrer RI, Zhao C, Glasgow BJ;  
XX WPI; 2002-338922/37.

on comprises the amino acid and coding sequence of a novel

CCCTGTCTCTCCACGGGTT 20  
|||||  
CCCTGTCTCTCCCATGTT 5

standard; DNA; 32 BP.

(first entry)

protegerin gene 3' Bam HI PCR primer.

oprotegerin; OPG; osteopathic; cytostatic; gene therapy;  
genesis inhibition; multiple myeloma; Paget's disease;  
osteoporosis; secondary osteopetrosis; osteopaenia;  
hyperparathyroidism; PCR primer; ss.

is.

-A1.

..

); 2000WO-US023755.

); 99US-0151415P.

FO FOUND MEDICAL EDUCATION RES.

Riggs BL, Khosla S, Russel ST;

65890/27.

or preventing osteoclastic overactivity in a mammal, involves  
pluripotent mammalian cells genetically altered with a  
d molecule encoding osteoprotegerin.

Page 32; 73pp; English.

sequence was used to amplify the osteoprotegerin (OPG) gene  
in example illustrating an invention relating to a method for  
or preventing osteoclastic overactivity in a mammal. The  
olives contacting pluripotent mammalian cells with a composition  
a nucleic acid molecule encoding osteoprotegerin, its variant  
ally active fragment to yield genetically altered mammalian  
introducing the cells into the mammal to alter  
genesis. The composition is useful for inhibiting or  
osteoclastic overactivity in a mammal having multiple myeloma,  
metastatic lesions, hypercalcaemia, involutional osteoporosis,  
osteopetrosis, Paget's disease, refractory hyperparathyroidism  
nia, especially osteolytic lesions, and for introducing  
nucleic acid into unfractionated bone marrow cells of a mammal

; BP; 6 A; 9 C; 8 G; 9 T; 0 U; 0 Other;

ilarity 68.0%; Score 13.6; DB 5; Length 32;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CCCTGTCTCTCCACGGGTT 20  
|||||  
CCCTTATCATCCATGGGAT 28

standard; DNA; 20 BP.

DT 16-APR-2003 (first entry)  
XX  
DE Multiplex group PCR primer #186.  
XX  
KW Racing potential; horse; grandpaternal DNA; over-represented; l  
KW grandmother; performance; progeny horse; PCR; primer; ss.  
XX  
OS Unidentified.  
XX  
PN WO200292851-A2.  
XX  
PD 21-NOV-2002.  
XX  
PF 15-MAY-2002; 2002WO-GB002273.  
XX  
PR 15-MAY-2001; 2001GB-00011886.  
XX  
PA (ANIM-) ANIMAL HEALTH TRUST.  
PA (BRHO-) BRITISH HORSERACING BOARD.  
XX  
PI Birns MM, Swinburne JE;  
XX  
DR WPI; 2003-129314/12.  
XX  
PT Determining the racing potential of a horse comprises measuring  
PT grandpaternal or grandmaternal DNA from the selected grandmothe  
PT over-represented in the genome of the horse.  
XX  
PS Example 2; Page 24; 49pp; English.  
XX  
CC The invention relates to a novel method for determining racing  
CC of a horse. The method comprises measuring: whether grandpatern  
CC over-represented in the genome of the horse; or in the case whe  
CC the grandmothers was selected for breeding on the basis of raci  
CC performance, whether grandmaternal DNA from the selected grandm  
CC over-represented in the genome of the horse which indicates the  
CC horse has good racing potential. The method of the invention in  
CC for determining the racing potential of a horse or for obtaini  
CC progeny horse with good racing potential. This polynucleotide  
CC represents a PCR primer used in the detection method of over-  
CC representation of DNA from male grandparents of the invention  
XX  
SQ Sequence 20 BP; 7 A; 2 C; 8 G; 3 T; 0 U; 0 Other;  
Query Match 67.0%; Score 13.4; DB 7; Length 20;  
Best Local Similarity 93.3%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;  
QY 1 ATCCTGTCTCTCCAC 15  
Db 20 ATCCTGTCTCTCCAC 6  
RESULT 28  
ACI58089  
ID ACI58089 standard; DNA; 25 BP.  
XX  
AC ACI58089;  
XX  
XX 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 58080.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expres  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.



09:38:25 2004

us-10-090-326-7.max.rng

: 2002US-00098263.

: 2001US-0276759P.

CMETRIX INC.

;  
67953/53.

f nucleic acid probes, useful for in situ hybridization, in  
orthern or dot-blot hybridization to identify or detect the  
specific mutations of any gene.

2 ID NO 58080; 9pp; English.

on discloses a microarray comprising a plurality of nucleic  
including one of 2,018,500 fully defined sequences, or its  
ch, perfect mismatch, antisense match or antisense mismatch.  
sed is a method of gene expression analysis. The array is used  
ig gene expression levels by hybridisation to a DNA library,  
of genetic variation or in hybridisation of tag-labelled  
The nucleic acid probes are specifically designed for analysis  
one target sequence. The method of analysis comprises  
at least one or more nucleic acids to at least two or more  
i probes and detecting the hybridisation. The nucleic acid  
attached to a solid support. The analysis comprises monitoring  
sion levels, identifying biallelic markers or polymorphisms,  
members of a gene and a cross-species comparison. Each of the  
ds further comprises a tag sequence. The array of nucleic acid  
seful in in situ hybridisation, in Southern, Northern or dot-  
isation to identify or detect the sequence or specific  
f any gene, in mapping the 5' termini of mRNA molecules by  
sions or in screening cDNA or genomic libraries or subclones  
nal subclones containing segments of DNA that have been  
i previously sequenced. The sequence presented is one of the  
i probes incorporated in the microarray. Note: The sequence  
is patent can also be obtained in electronic format directly  
at seqdata.uspto.gov/sequence.html

BP; 4 A; 8 C; 4 G; 9 T; 0 U; 0 Other;

ilarity 67.0%; Score 13.4; DB 8; Length 25;

Conservative 0; Pred. No. 1.2e+04;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CTTGTCTCTCCAC 15  
|||||  
CTTGTCTCCAC 17

andard; DNA; 31 BP.

(first entry)

2 nucleotide polymorphism (SNP) COL7A1 9.

quence; genotype; disease; forensic; paternity testing;  
eotide polymorphism; SNP; ss.

3.

Location/Qualifiers  
replace(16,T)  
/\*tag= a  
/standard\_name= "single nucleotide polymorphism"

-A2.

PD 13-SEP-2001.

XX 07-MAR-2001; 2001WO-US007268.

XX 07-MAR-2000; 2000US-0187510P.

XX 22-MAY-2000; 2000US-0206129P.

XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.

XX Cargill M, Ireland JS, Lander ES;

XX WPI; 2001-522952/57.

XX Nucleic acid molecules from the human genome which include poly  
sites, useful in methods for predicting the presence, absence o  
of a particular phenotype or disorder (e.g. diabetes) associate  
particular genotype.

XX Claim 1; Page 86; 145pp; English.

XX The invention relates to the identification of nucleic acid mol  
CC (AAI29513-AAI31314) from the human genome which include polymor  
CC which can predispose individuals to disease. Various genes from  
CC of individuals were resequenced and single nucleotide polymorph  
CC (SNPs) in these genes discovered. The method is useful for pred  
CC presence, absence or severity of a particular phenotype or diso  
CC diabetes) associated with a particular genotype. The nucleic ac  
CC containing the polymorphic sites may be useful in forensics and  
CC testing

XX SQ Sequence 31 BP; 6 A; 12 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 67.0%; Score 13.4; DB 4; Length 31;

Best Local Similarity 93.3%; Pred. No. 1.2e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 3 CTTGTCTCTCCACGG 17

|||||  
24 CTTGTCTCTCCACGG 10

RESULT 30

ABZ02460

ID ABZ02460 standard; DNA; 50 BP.

XX AC ABZ02460;

XX DT 09-JAN-2003 (first entry)

XX Human leukocyte gene expression profiling probe SEQ ID NO 2451.

XX TV; leukocyte; gene expression profiling; allograft rejection;  
XX atherosclerosis; congestive heart failure; systemic lupus eryth  
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infectio  
XX ss.

XX OS Homo sapiens.

XX EN WO200257414-A2.

XX PD 25-JUL-2002.

XX PF 22-OCT-2001; 2001WO-US047856.

XX PR 20-OCT-2000; 2000US-0241994P.

XX PR 08-JUN-2001; 2001US-0296764P.

XX PA (BIOC-) BIOCARDIA INC.

XX PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phill:  
XX Ly N, Woodward R, Quatermous T, Johnson F;

XX WPI; 2002-636525/68.

DR

for leukocyte expression profiling, diagnosing a disease, or (the rate of) progression of a disease, e.g. atherosclerosis or heart failure, comprises diagnostic oligonucleotides.

age 405; Opp; English.

ion relates to a system for detecting gene expression, which one or two isolated DNA molecules that detect expression of a gene corresponds to any of 8143 oligonucleotides AB208152) each having 50 base pairs (bp). The system is useful for expression profiling. It is particularly useful for a disease, monitoring (rate of) progression of a disease, therapeutic outcome, determining prognosis for a patient, disease complications in an individual or monitoring response in an individual. The diseases include cardiac allograft kidney allograft rejection, liver allograft rejection, renal allograft rejection, systemic lupus erythematosus, arthritis, osteoarthritis or cytomegalovirus infection

0 BP; 6 A; 14 C; 12 G; 18 T; 0 U; 0 Other;

milarity 67.0%; Score 13.4; DB 6; Length 50;

Conservative 93.3%; Pred. No. 1.2e+04; Mismatches 1; Indels 0; Gaps 0;

TGTCCTCCACGGGT 19  
|||||||  
TGTCCTCCACGGGT 25

standard; DNA; 20 BP.

1 (first entry)

rogen receptor alpha search PCR primer 75.

endent transcriptional factor; oestrogen receptor; ER; coid receptor protein; GR; mineralocorticoid receptor protein; some proliferator-activated receptor protein; PPAR; ne receptor protein; PR; pregnane X receptor protein; PXR; mone receptor protein; TR; vitamin D receptor protein; VDR; ation; ERalpha; breast cancer; PCR primer; probe; ss.

ns.

7-Al.

1.

0; 2000WO-JP008553.

9; 99JP-00348022.

9; 99JP-00370667.

0; 2000JP-00207011.

0; 2000JP-00220508.

0; 2000JP-00234053.

0; 2000JP-00235460.

0; 2000JP-00235461.

0; 2000JP-00235463.

MITOMO CHEM CO LTD.

Ohe N, Satoh H;

367866/38.

endent transcriptional factors, nucleic acids encoding them and rising them and a specified reporter gene, useful for screening

PT agents for the treatment of breast cancer.

XX

PS Example 9; Page 231; 276pp; English.

XX

CC The present invention relates to ligand dependent transcriptional factors, including oestrogen receptor (ER) alpha and beta protein, glucocorticoid receptor protein (GR), mineralocorticoid receptor protein (MR) peroxisome proliferator-activated receptor protein (PPAR), pxx receptor protein (PR), pregnane X receptor protein (PXR), thyr receptor protein (TR) and vitamin D receptor protein (VDR), th acids encoding them and cells comprising them and a specified gene for the ligand dependent transcriptional factor. These pr useful in the modulation of ligand dependent transcriptional f activity. The cells, mutant ERalpha and the polynucleotide enc may be used in assays for qualitatively analysing an activity transactivation of a reporter gene by a test ERalpha, for scre mutant ligand dependent transcriptional factors, for evaluat activity for transactivation of a reporter gene by a test ERal for screening a compound useful for treating a disorder of a m CC ERalpha, especially breast cancer

XX SQ Sequence 20 EP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 4; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTCTCTCCACGGGT 19

|||||  
Db 20 TCCTCTCTCCACGGGT 3

RESULT 32

AAQ21480/c

ID AAQ21480 standard; DNA; 22 BP.

XX

AC AAQ21480;

XX

DT 25-MAR-2003 (revised)

DT 01-JUN-1992 (first entry)

XX

DE CTP synthetase gene mutation-specific probe #3.

XX

XX MDR; chemotherapy; PCR; cytosine triphosphate synthetase;

KW

splice acceptor site; ss.

XX

OS Synthetic.

XX

PH Key Location/Qualifiers

FT misc\_difference 11

FT /\*tag= a

FT /note= "mutation"

XX

PN WO9201811-A.

XX

PD 06-FEB-1992.

XX

PF 25-JUL-1990; 90GB-00016287.

XX

PR 25-JUL-1990; 90GB-00016287.

XX

PR 11-APR-1991; 91US-00682975.

XX

PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.

XX

PI Meuth M;

XX

DR WPI; 1992-064967/08.

XX

PT Assay method for CTP synthetase mutation(s) - utilising polymers;

PT reaction to reveal the presence of the multiple drug resistance

XX

PT indicative of a mutation.

XX

PS Example 2; Page 28; 46pp; English.

was purified from white blood cells of patients with acute or solid tumour cells. The DNA or cDNA (reverse transcribed) was amplified using the PCR technique (see e.g. AAQ23749-primers designed to amplify regions potentially containing mutations). The critical mutation can then be detected in the product using a mutation-specific probe. This probe is end-labeled then hybridised to a slot or dot blot. (Updated on 25-MAR-97 rect PA field.)

BP; 9 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

ilarity 66.0%; Score 13.2; DB 2; Length 22;

Conservative 83.3%; Pred. No. 1.5e+04;

CTGTGCTCTCCACGGGT 19

TAIGTCTCTCCACGGT 3

andard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 119020.

obe; expressed sequence tag; microarray; gene expression;

iation; biallelic marker; polymorphism; human;

es comparison.

S.

0-Al.

; 2002US-00098263.

; 2001US-0276759P.

YMETRIX INC.

67953/53.

f nucleic acid probes, useful for in situ hybridization, in orthern or dot-blot hybridization to identify or detect the specific mutations of any gene.

Q ID NO 119020; 9pp; English.

on discloses a microarray comprising a plurality of nucleic including one of 2,018,500 fully defined sequences, or its ch, perfect mismatch, antisense match or antisense mismatch. sed is a method of gene expression analysis. The array is used ng gene expression levels by hybridisation to a DNA library, of genetic variation or in hybridisation of tag-labelled. The nucleic acid probes are specifically designed for analysis one target sequence. The method of analysis comprises at least one or more nucleic acids to at least two or more d probes and detecting the hybridisation. The nucleic acid attached to a solid support. The analysis comprises monitoring sion levels, identifying biallelic markers or polymorphisms, embers of a gene and a cross-species comparison. Each of the ds further comprises a tag sequence. The array of nucleic acid seful in in situ hybridization, in Southern, Northern or dot- isation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molec  
CC primer extensions or in screening cDNA or genomic libraries or  
CC for additional subclones containing segments of DNA that have  
CC isolated and previously sequenced. The sequence presented is o  
CC nucleic acid probes incorporated in the microarray. Note: The  
CC data for this patent can also be obtained in electronic format  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX

SQ Sequence 25 BP; 2 A; 7 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 8; Length 25;

Best Local Similarity 83.3%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

OY 2 TCCTGTCTCTCCACGGGT 19

Db 7 TCCTGTCTCTCCACGGGT 24

RESULT 34

AAT31832/c

ID AAT31832 standard; DNA; 30 BP.

XX AAT31832;

XX AAT31832;

DT 11-JAN-1997 (first entry)

DE Primer for amplifying HPV E7 protein fragment coding region.

XX Human papilloma virus; E6; E7; deletion mutant; HPV; immune res

KW humoral immune response; cellular immune response; vaccine; ss.

XX Synthetic.

XX WO9619496-A1.

XX 27-JUN-1996.

XX 20-DEC-1995; 95WO-AU000868.

XX 20-DEC-1994; 94AU-00000157.

XX (CSLC-) CSL LTD.

XX (UYQU) UNIV QUEENSLAND.

XX Edwards SJ, Cox J, Webb EA, Frazer I;

XX WPI; 1996-309518/31.

XX Vaccine variants of human papilloma virus antigens - contain va

XX E6 and/or E7 protein, pref. deletion mutants, and are used to t

XX prevent HPV infection.

XX Example 3; Page 13; 37pp; English.

XX A variant of the human papilloma virus (HPV) E6 or E7 protein w

XX elicits a humoral and/or cellular immune response against HPV c

XX in vaccines against HPV or to treat HPV infection. The variant

XX preferably a deletion mutant comprising at least half, and pref

XX -thirds of full length E6 or E7 protein starting from the N- or

XX terminal, or is a full length E6 moiety fused to a full length

XX peptide which optionally has a linkage moiety and a foreign prote

XX immunogenicity of, the fusion protein. Two primers (AAT31829, A

XX were used to amplify the 198 C-terminal bases of the HPV E7 pro

XX for its use in an E6/E7 fusion construct

XX SQ Sequence 30 BP; 9 A; 4 C; 14 G; 3 T; 0 U; 0 Other;

XX Query Match 66.0%; Score 13.2; DB 2; Length 30;

XX Best Local Similarity 83.3%; Pred. No. 1.5e+04;

XX Matches 15; Conservative 0; Mismatches 3; Indels 0;

TCCTTGCTCTCCACGGG 18  
|||||  
TCCTCTCTCTCCCGGG 3

tandard; DNA; 32 BP.

6 (first entry)

primer #2.

thelial cell protein; cerebral arteriole smooth muscle cell; protein; collateral cerebrovascular circulation; human; cular disease; intracerebral haemorrhage; aneurysm; migraine; id haemorrhage; intracerebral atherosclerosis; lipohyalinosis; 's disease; subcortical arteriopathic encephalopathy; therapy; isease; blood brain barrier; brain oedema formation; primer; cle cell; radioimmunoassay; polymerase chain reaction; PCR; rk-A; ss.

Al.

5.

5; 95WO-US005659.

4; 94US-00239889.

3 DEV FOUND.

Alam NA, Alam SS;

103939/51.

ilo: dalton protein secreted by brain endothelial cells - cerebral arteriole smooth muscle cell proliferation and is improving cerebral collateral cerebrovascular circulation.

Page 12; 33pp; English.

nd AAT02497 represent amplification primers for a 200 bp region brain trk-A gene. The amplified fragment encodes the lar domain of the neurotrophic protein. The peptide encoded by ed sequence was used to isolate a 67 kDa brain endothelial in. This protein stimulates proliferation of cerebral arteriole le cells. The protein can be used in the regulation of the ion of cerebral arteriole smooth muscle cells, and can be ad to improve collateral cerebrovascular circulation in humans. o be used to treat cerebrovascular diseases which result from ion of fragile brain vessels due to the under- or over- of the protein. These include intracerebral haemorrhage, id haemorrhage due to aneurysms, migraine, intracerebral osis, lipohyalinosis, Bingwanger's disease or subcortical ic encephalopathy, Moyamoya disease and impairment of the ic barrier with brain oedema formation. Oligonucleotides can be o inhibit the production of this protein. These ptides are preferably triplex forming or antisense. The ptides can be used to treat diseases which involve increased le cell proliferation from overproduction of the protein. The f these diseases can be measured by measuring the serum ion of the protein by radioimmunoassay

2 BP; 5 A; 12 C; 5 G; 10 T; 0 U; 0 Other;

ilarity 66.0%; Score 13.2; DB 2; Length 32;  
nilarity 83.3%; Pred. No. 1.5e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCCTTGCTCTCCACGGG 18  
|||||  
Db 15 ATCCTTGCTCTCCACGGG 32

RESULT 36

ABA95667/C

ID ABA95667 standard; DNA; 41 BP.

XX

AC ABA95667;

XX

DT 25-MAR-2002 (first entry)

XX

DE Human splicing protein 10.56 probe #2.

XX

KW Human; splicing protein 10.56; cytostatic; haemostatic; viruci immunomodulatory; antiinflammatory; gene therapy; tumour; haem HIV infection; immunological disease; inflammation; probe; ss.

XX

OS Homo sapiens.

XX

PN WO200192315-A1.

XX

PD 06-DEC-2001.

XX

PF 21-MAY-2001; 2001WO-CN0000828.

XX

PR 24-MAY-2000; 2000CN-00115832.

XX

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-090028/12.

XX

PT Human splicing protein 10.56 and encoding polynucleotide, used diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation.

XX

PS Example 6; Page 20; 34pp; English.

XX

CC The present invention relates to human splicing protein 10.56 AAM48273). The protein and its coding sequence are useful in t diagnosis and treatment of malignant tumours, haemopathy, HIV immunological diseases and various inflammations. The present a probe, which was used in an example from the present inventi

XX

SQ Sequence 41 BP; 8 A; 12 C; 11 G; 10 T; 0 U; 0 Other;

XX

Query Match 66.0%; Score 13.2; DB 6; Length 41;

Best Local Similarity 83.3%; Pred. No. 1.5e+04;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 ATCCTTGCTCTCCACGGG 18

Db 27 AGCCTTGCTCTCTAGG 10

XX

XX

XX

XX

XX

XX

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XX

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XX

XX

XX

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XX

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XX

XX

XX

XX

XX

d.  
23-NOV-1998; 98US-0109732P.  
(GEST ) GENSET.  
Cohen D, Blumenfeld M, Chumakov I;  
WPI; 2000-013267/01.  
Novel biallelic markers used to construct a high density diseq  
map of the human genome.  
Claim 1; Page 444; 2745pp; English.  
AAZ65654 to AAZ69578 represent human biallelic markers from the  
invention, which contain a polymorphic base at position 24 of t  
nucleotide sequences. AAZ69579 to AAZ77440 represent amplificat  
primers for the biallelic markers. The biallelic markers of the  
have a variety of uses: they can be used for high density mappi  
human genome, and in complex association studies and haplotypir  
which are useful in determining the genetic basis for disease s  
CC Compositions and methods of the invention can also be useful fo  
CC identification of the targets for the development of pharmaceut  
CC agents and diagnostic methods, as well as the characterisation  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other trea  
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3  
CC 3367, are not actually given a sequence in the Sequence Listing  
CC present invention  
XX  
SQ Sequence 47 BP; 12 A; 13 C; 6 G; 16 T; 0 U; 0 Other;  
Query Match 66.0%; Score 13.2; DB 3; Length 47;  
Best Local Similarity 83.3%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
QY 2 TCCTTGTCCTCCACGGGT 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 TCCTTCTCCTCGAAGGCT 19  
| | | | | | | | | | | | | | | | | | | | | |  
RESULT 39  
AAF89887/c  
ID AAF89887 standard; DNA; 48 BP.  
XX  
AC AAF89887;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE PCR primer for human nuclear regulatory factor-1 (NRF-1) cDNA.  
XX  
KW mitochondrial function; mitochondrial biogenesis; UCP gene; NRF  
KW uncoupling protein gene; PGC gene; nuclear regulatory factor ge  
KW peroxisome proliferator-activated receptor gamma coactivator ge  
KW PPAR-gamma coactivator gene; type 2 diabetes mellitus; PCR prim  
XX Homo sapiens.  
OS  
XX WO200135096-A2.  
FN  
XX 17-MAY-2001.  
PD  
XX 13-NOV-2000; 2000WO-US031119.  
PF  
XX 10-NOV-1999; 99US-0164533P.  
PR  
XX (MITO-) MITOKOR.  
PA  
XX Anderson CM, Clevenger W, Becker DK, Grako KA;  
PI  
XX WPI; 2001-335965/35.  
DR  
XX Treating a disease associated with altered mitochondrial functi  
PT

invention relates to a novel kind of polypeptide, human sigma  
.55, polynucleotides for encoding this polypeptide and a DNA  
on process to produce the polypeptide. The present invention  
ses the method of applying the polypeptide in treating various  
uch as psychogenic disease, heart-originating asthma, acute  
ased by morphine analgesic and progesterone dysfunction. The  
ention also discloses the antagonist resisting the polypeptide  
atment effect. The present invention also discloses the  
of the polynucleotides for encoding human sigma receptor  
polynucleotide sequence represents a probe of the human sigma  
.55 protein of the invention  
BP; 6 A; 13 C; 17 G; 5 T; 0 U; 0 Other;  
66.0%; Score 13.2; DB 7; Length 41;  
ilarity 83.3%; Pred. NO. 1.5e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
TTGTCTCTCCACGGGTT 20  
| | | | | | | | | | | | | | | | | | | | | |  
TCGTCTCTCCACAGGCT 9  
andard; DNA; 47 BP.  
(first entry)  
elated biallelic marker SEQ ID NO:1000.  
e; biallelic marker; high density disequilibrium map;  
; haplotype; phenotype; polymorphic base; genotyping;  
; hybridisation; identification; characterisation; diagnosis;  
eotide polymorphism; SNP; ds.  
s.  
Location/Qualifiers  
replace(24,T)  
/\*tag= a  
/standard\_name= "single nucleotide polymorphism"  
2.  
99WO-IB000822.

betes mellitus, involves administering an agent that increases al mass in cells of the individual.

Page 146; 184pp; English.

s AAF9986-88 were used to amplify epitope-tagged human nuclear factor-1 (NRF-1) cDNA. The amplified sequence was used in the invention. The specification describes a method for the disease associated with altered mitochondrial function. The invention describes administering an agent that increases mitochondrial function, in cells of the individual. The invention describes increasing mitochondrial biogenesis by induction of a peroxisome or -activated receptor gamma (PPAR- $\gamma$ ) coactivator gene (PGC-1 or PGC-1 $\alpha$ ) protein gene (UCP gene), and/or a nuclear regulatory gene (NRF gene). The agents are useful for treating a disease with altered mitochondrial function such as diabetes, e.g., diabetes mellitus.

8 BP; 18 A; 7 C; 16 G; 7 T; 0 U; 0 Other;

milarity  
66.0%; Score 13.2; DB 5;  
83.3%; Pred. No. 1.5e+04;  
Length 48;

Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
--------------	----	------------	----	--------	----	------	----

CCTTGTCTCCACGGT 19

[illegible]

CCTTGTA<sup>CT</sup>CCATGGAT 6

standard; DNA; 60 BP.

2 (first entry)

ced transcript detection oligonucleotide SEQ ID NO:16879.

se; rat; splice transcript; detection; RNA transcript;  
 iant; transcriptome; oligonucleotide library: ss.

ns.

9-A2.

2.

1; 2001WO-IB001903.

0: 2000US-0221607P.

1; 2001US-0287724P.

MPUGEN INC.

Wasserman A, Mintz E, Mintz L, Faiqler S;

257383/30.

nucleotide libraries comprising oligonucleotides which hybridize to mRNAs transcribed from a transcription unit of a gene. This method is useful for detecting tissue-, pathology-, and developmental-specific genes.

SEQ ID NO 16879; 47pp; English.

t invention describes oligonucleotide libraries for detecting RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple genes that populate a genome. The library comprises several oligonucleotides, each capable of hybridizing selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, where the set of messenger RNAs comprises one or more messenger RNAs transcribed from a given splice variant. The

CC oligonucleotide libraries are useful for detecting mRNAs from  
CC biological sample, in expression profiling studies, in qualitative  
CC quantitatively characterising the corresponding transcriptome,  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised  
CC libraries to detect transcripts of a sub-transcriptome under a  
CC biological or pathological state, and so allowing the detection  
CC - and pathology-specific genes such as those genes only expressed  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and  
CC variants of a transcriptome of a patient suffering from a part  
CC disorder. ABN27253 to ABN5989 represent oligonucleotide sequences  
CC in rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not  
CC part of the printed specification, but was obtained in electro  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 60 BP; 15 A; 12 C; 21 G; 12 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 6; Length 60;  
Best Local Similarity 83.3%; Pred. No. 1.5e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 2 TCCTTGTCCTCCACGGT 19

33 TCCTTGTTCCTATGGGT 16  
db

RESULT 41

ABN35011/C

ID ABN35011 standard; DNA; 60 BP.

AC ABN35011;

DT 15-JUL-2002 (first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:7

Human; mouse; rat; splice transcript; detection; RNA transcript  
splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

PN WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-IB001903.

PR 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

PA (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription genome, useful for detecting tissue-, pathology-, and development specific genes.

PS Example 1; SEQ ID NO 7759; 47bp; English.

The present invention describes oligonucleotide libraries for messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises oligonucleotides, each capable of hybridising selectively to a messenger RNA transcribed from a given transcription unit of a genome which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting RNAs from

sample, in expression profiling studies, in qualitatively or  
 ely characterising the corresponding transcriptome, and in  
 NA transcripts and splice variants of human or animal  
 mes. The libraries may also be used as specialised mini  
 o detect transcripts of a sub-transcriptome under a particular  
 or pathological state, and so allowing the detection of tissue  
 logy-specific genes such as those genes only expressed in  
 saue under a specific pathological condition; to detect  
 al specific genes; and to detect RNA transcripts and splice  
 a transcriptome of a patient suffering from a particular  
 BN27253 to ABN59589 represent oligonucleotide sequences from  
 s and mice, which are used in the exemplification of the  
 ention. N.B. The sequence data for this patent did not form  
 printed specification, but was obtained in electronic format  
 om WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 18 A; 12 C; 20 G; 10 T; 0 U; 0 Other;

ilarity 66.0%; Score 13.2; DB 6; Length 60;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTGTCTCCACGGGT 19  
 ||||| |||||  
 CTTGTCTTCACTGGT 3

andard; DNA; 60 BP.

(first entry)

ed transcript detection oligonucleotide SEQ ID NO:10055.

e; rat; splice transcript; detection; RNA transcript;  
 ant; transcriptome; oligonucleotide library; ss.

s.

-A2.

; 2001WO-IB001903.

; 2000US-0221607P.

; 2001US-0287724P.

PUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

37383/30.

cleotide libraries comprising oligonucleotides which  
 hybridize to mRNAs transcribed from a transcription unit of a  
 ful for detecting tissue-, pathology-, and developmental-  
 nes.

SEQ ID NO 10055; 47pp; English.

invention describes oligonucleotide libraries for detecting  
 NAs that populate a (sub-)transcriptome, where the (sub-  
 me comprises messenger RNAs transcribed from multiple  
 on units that populate a genome. The library comprises several  
 tides, each capable of hybridising selectively to a set of  
 NAs transcribed from a given transcription unit of the genome,  
 es one or more messenger RNA splice variants. The  
 tide libraries are useful for detecting mRNAs from a  
 sample, in expression profiling studies, in qualitatively or

CC quantitatively characterising the corresponding transcriptome,  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcripts. The libraries may also be used as specialised  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC biological or pathological state, and so allowing the detection  
 CC - and pathology-specific genes such as those genes only expressed  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and  
 CC variants of a transcriptome of a patient suffering from a part;  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequer  
 CC rats, humans and mice, which are used in the exemplification of  
 CC present invention. N.B. The sequence data for this patent did r  
 CC part of the printed specification, but was obtained in electron  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX

Sequence 60 BP; 20 A; 11 C; 18 G; 11 T; 0 U; 0 Other;

Query Match 66.0%; Score 13.2; DB 6; Length 60;  
 Best Local Similarity 83.3%; Pred. NO. 1.5e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 3 CTTGTCTCTCCACGGGTT 20  
 ||||| |||||  
 Db 23 CTTGTCTTCAAGGGTT 6

RESULT 43

AAV71103

ID AAV71103 standard; DNA; 35 BP.

AC AAV71103;

DT 05-FEB-1999 (first entry)

PCR primer used to amplify the dnaE gene of Thermus thermophilu  
 Alpha subunit; DNA Polymerase III-type enzyme; chromosomal repl  
 DNA amplification; DNA sequencing; dnaE gene; PCR primer; ss.

Synthetic.

Thermus thermophilus.

WO9845452-A2.

15-OCT-1998.

08-APR-1998; 98WO-US006921.

08-APR-1997; 97US-00823407.

(UYRQ ) UNIV ROCKEFELLER.

Yurieva O, Kuriyan J, Odonnell ME, Jeruzalmi D;

WPI; 1998-594486/50.

PT New isolated DNA Polymerase III-type enzymes - used to develop  
 PT for the amplification and sequencing of DNA, particularly by PC  
 PS Example 10; Page 79; 153pp; English.

CC PCR primers AAV71102-03 were used to amplify the dnaE gene of T  
 CC thermophilus. This gene encodes the alpha subunit of the T. the  
 CC DNA Polymerase III-type enzyme (DP3). DP3 functions as a chromo  
 CC replicase, and is a holoenzyme. The products can be used for DN  
 CC amplification and sequencing. They can provide faster and longe  
 CC production in PCR, and higher quality of DNA sequencing ladders  
 CC compared to other DNA polymerases

Sequence 35 BP; 4 A; 7 C; 12 G; 8 T; 0 U; 4 Other;

Query Match 65.0%; Score 13; DB 2; Length 35;  
 Best Local Similarity 76.5%; Pred. NO. 1.9e+04;

Conservative 2; Mismatches 2; Indels 0; Gaps 0;

TCTTGTCTCCACGG 17  
 ||||| | | | | |  
 TCTTGTCTCCAGSG 22

standard; DNA; 35 BP.

0 (first entry)

ermophilus dnaE PCR primer #4.

rase III; dnaE gene; alpha subunit; thermostable;  
 sis; speed; accuracy; processivity; frameshift; holoenzyme;  
 exonuclease; proofreading; PCR; primer; ss.

ermophilus.

Al.

9.

8; 98WO-US007070.

8; 98WO-US007070.

IV ROCKEFELLER.

Kuriyan J, O'donnell ME, Jeruzalmi D;

611306/52.

Y50014.

ed thermostable DNA polymerase III-type enzyme, used  
 ly for the amplification and sequencing of nucleic acids.

; Page 79; 156pp; English.

nce represents Thermus thermophilus dnaE PCR primer #4, used  
 r #3 (AAZ30923) to amplify a portion of the thermus  
 us dnaE gene. The dnaE gene encodes the alpha subunit of a  
 mostable DNA polymerase holoenzyme which corresponds to DNA  
 III (Pol III) of E. coli. Pol III-type enzymes have a high  
 ty (>50 kb) and rapid rate of synthesis (750 nucleotides/s).  
 consists of 18 subunits of 10 different types. The DNA polymerase  
 a catalytic unit and consists of the alpha (DNA polymerase),  
 "-5' exonuclease) and theta subunits. The beta subunit  
 clamp") is ring-shaped and encircles DNA and slides along it  
 aring the Pol III holoenzyme to the template. It is the beta  
 ich is responsible for the high processivity and speed. The  
 lex (composed of gamma, delta, delta', chi and psi subunits) is  
 loader" which couples ATP hydrolysis to assembly of beta  
 and DNA. A dimer of the tau subunit acts as a "macromolecular  
 , holding together molecules of core polymerase and one  
 f gamma complex, forming the Pol III\* subassembly. Two beta  
 ociate with the two cores within Pol III\* to form the  
 s capable of replicating both strands of duplex DNA  
 usly. The Thermus thermophilus Pol III-type enzyme can be used  
 ar cloning techniques such as PCR (polymerase chain reaction).  
 t limitations of enzymes previously used in PCR are that they  
 to synthesize extended lengths of nucleotides, and in the  
 f Tag (Thermus aquaticus) polymerase, the lack of 3'-5'  
 e activity and the subsequent inability to excise misinserted  
 s (proofreading)

5 BP; 4 A; 7 C; 12 G; 8 T; 0 U; 4 Other;

Query Match 65.0%; Score 13; DB 2; Length 35;  
 Best Local Similarity 76.5%; Pred. No. 1.9e+04;  
 Matches 13; Conservative 2; Mismatches 2; Indels 0;

QY 1 ATCCTTGTCTCCACGG 17  
 ||||| | | | | |  
 Db 6 ATCCTTGTCTCCAGSG 22

RESULT 45

ACC54203/c

ID ACC54203 standard; DNA; 17 BP.

XX AC ACC54203;

XX DT 27-JUN-2003 (first entry)

XX DE Human tumour suppressor sequence #2970.

XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppress

XX KW tumour regression; apoptosis; virus resistance; diagnosis;

XX KW cellular degeneration.

XX OS Homo sapiens.

XX PN FR2826373-A1.

XX PD 27-DEC-2002.

XX PF 20-JUN-2001; 2001FR-00008139.

XX PR 20-JUN-2001; 2001FR-00008139.

XX PA (MOLE-) MOLECULAR ENGINES LAB SA.

XX PI Tuijnder M, Telerman A, Amson R;

XX DR WPI; 2003-250498/25.

XX PT New nucleic acid sequences associated with tumor suppression,

XX PT apoptosis or virus resistance are useful to diagnose and treat

XX PT disease, development of tumor cells and cell degeneration.

XX PS Claim 1; Page 726; 798pp; French.

XX CC This sequence represents an isolated nucleic acid sequence ass

XX CC with tumour suppression or regression, apoptosis or virus resi

XX CC invention relates to these sequences or sequences having at le

XX CC identity to them, and polypeptides encoded by the sequences or

XX CC polypeptides having 80% identity to the polypeptide sequences.

XX CC invention is used to diagnose or treat viral disease or diseas

XX CC characterized by development of tumour cells or cellular degen

XX SQ Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 7; Length 17;

Best Local Similarity 87.5%; Pred. No. 2.2e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 4 CTTGTCTCTCCACGGT 19

Db 17 CTTGTCTCTCCACAGAT 2

Search completed: February 29, 2004, 09:03:07  
 Job time : 201.649 secs



GenCore version 5.1.6  
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cleic search, using sw model

February 29, 2004, 08:44:24 ; Search time 37.6623 Seconds  
(without alignments)  
294.698 Million cell updates/sec

US-10-090-326-7

20  
1 atccctgtctccacgggtt 20

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

682709 seqs, 277475446 residues

hits satisfying chosen parameters: 874574

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Issued Patents NA: \*  
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5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

Query Match	Length	DB	ID	Description
74.0	20	3	US-09-118-408-12	Sequence 12, Appl
74.0	20	3	US-09-118-408-15	Sequence 15, Appl
74.0	20	4	US-09-506-855-12	Sequence 12, Appl
74.0	20	4	US-09-506-855-15	Sequence 15, Appl
74.0	20	4	US-09-911-176B-12	Sequence 12, Appl
74.0	20	4	US-09-911-176B-15	Sequence 15, Appl
74.0	20	4	US-09-619-740-12	Sequence 12, Appl
74.0	20	4	US-09-619-740-15	Sequence 15, Appl
74.0	20	4	US-09-506-852-12	Sequence 12, Appl
74.0	20	4	US-09-506-852-15	Sequence 15, Appl
72.0	38	4	US-09-268-544B-2	Sequence 2, Appl
70.0	33	1	US-08-138-608-44	Sequence 44, Appl
67.0	29	4	US-08-891-292A-5	Sequence 5, Appl
67.0	29	4	US-08-891-292A-7	Sequence 7, Appl
67.0	29	4	US-09-927-737C-5	Sequence 5, Appl
67.0	29	4	US-09-927-737C-7	Sequence 7, Appl
66.0	30	3	US-08-860-165-8	Sequence 8, Appl
66.0	30	4	US-09-358-645-8	Sequence 8, Appl
66.0	30	4	US-09-359-382-8	Sequence 8, Appl
66.0	32	1	US-08-239-889A-2	Sequence 2, Appl
66.0	32	5	PCT-US95-05659-2	Sequence 2, Appl
66.0	47	4	US-09-422-978-1000	Sequence 1000, Ap
66.0	55	4	US-09-621-976-13666	Sequence 13666, A
64.0	28	2	US-08-859-998-991	Sequence 991, App
64.0	28	4	US-09-225-928-991	Sequence 991, App
64.0	28	4	US-09-225-201B-991	Sequence 991, App
64.0	45	1	US-08-440-103-12	Sequence 12, Appl

28	12.8	64.0	45	1	US-08-440-542-12	Sequence
29	12.8	64.0	45	1	US-08-231-368-12	Sequence
30	12.8	64.0	45	1	US-08-440-210-12	Sequence
31	12.8	64.0	45	4	US-09-046-604-12	Sequence
C 32	12.8	64.0	57	4	US-09-313-294A-4232	Sequence
C 33	12.6	63.0	27	1	US-08-758-306-1196	Sequence
C 34	12.6	63.0	41	1	US-08-356-405-12	Sequence
35	12.6	63.0	45	1	US-08-162-597-6	Sequence
36	12.6	63.0	45	4	US-09-770-949-6	Sequence
37	12.6	63.0	52	2	US-08-883-795A-21	Sequence
C 38	12.4	62.0	36	4	US-09-769-863-4	Sequence
C 39	12.2	61.0	21	4	US-09-079-812E-8	Sequence
C 40	12.2	61.0	31	1	US-08-477-877B-3	Sequence
C 41	12.2	61.0	31	1	US-08-472-281A-3	Sequence
C 42	12.2	61.0	31	2	US-08-477-988B-3	Sequence
C 43	12.2	61.0	32	1	US-08-347-792-23	Sequence
C 44	12.2	61.0	32	1	US-08-431-357-23	Sequence
C 45	12.2	61.0	32	5	PCT-US95-15353-23	Sequence
C 46	12.2	61.0	37	1	US-08-273-362-1	Sequence
C 47	12.2	61.0	45	1	US-08-484-686B-63	Sequence
C 48	12.2	61.0	45	3	US-08-463-160B-63	Sequence
C 49	12.2	61.0	45	5	PCT-US91-02568-4	Sequence
C 50	12.2	61.0	51	4	US-09-529-279-44	Sequence
C 51	12.2	61.0	51	4	US-10-158-895-44	Sequence
52	12.2	61.0	51	4	US-09-443-199C-957	Sequence
C 53	12.2	61.0	51	4	US-09-443-199C-1042	Sequence
C 54	12.2	61.0	56	2	US-08-883-795A-5	Sequence
55	12	60.0	24	1	US-08-095-162-14	Sequence
56	12	60.0	24	1	US-08-294-434-15	Sequence
57	12	60.0	24	1	US-08-457-166-15	Sequence
58	12	60.0	24	1	US-08-470-220A-14	Sequence
59	12	60.0	24	2	US-08-595-868C-19	Sequence
60	12	60.0	24	3	US-08-967-374-14	Sequence
61	12	60.0	24	3	US-08-927-128-11	Sequence
62	12	60.0	24	3	US-09-139-819A-19	Sequence
63	12	60.0	24	4	US-09-505-991-14	Sequence
64	12	60.0	24	4	PCT-US93-06591-15	Sequence
65	12	60.0	24	5	PCT-US95-15800-5	Sequence
66	12	60.0	27	3	US-08-513-974B-186	Sequence
67	12	60.0	28	1	US-08-328-314-8	Sequence
68	12	60.0	28	1	US-08-731-045-8	Sequence
69	12	60.0	28	4	US-09-475-947A-111	Sequence
70	12	60.0	38	4	US-09-367-777-15	Sequence
C 71	12	60.0	38	4	US-09-367-777-19	Sequence
C 72	12	60.0	38	4	US-09-097-055B-12	Sequence
73	12	60.0	57	4	US-09-097-055B-60	Sequence
74	12	60.0	57	4	US-08-488-145-11	Sequence
75	11.8	59.0	20	3	US-08-475-470A-20	Sequence
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78	11.8	59.0	20	4	US-08-723-303-20	Sequence
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C 80	11.8	59.0	25	4	US-09-130-663-9	Sequence
81	11.8	59.0	30	3	US-08-913-842-37	Sequence
82	11.8	59.0	30	3	US-09-432-335-9	Sequence
83	11.8	59.0	30	4	US-09-614-022-9	Sequence
84	11.8	59.0	30	4	US-08-306-546C-9	Sequence
C 85	11.8	59.0	44	1	US-08-530-524A-9	Sequence
86	11.8	59.0	44	2	US-08-761-277A-73	Sequence
87	11.8	59.0	45	2	US-09-641-638-898	Sequence
88	11.8	59.0	47	4	US-09-422-978-2678	Sequence
C 89	11.8	59.0	47	4	US-08-424-788-14	Sequence
C 90	11.8	59.0	60	1	US-09-658-688A-18	Sequence
91	11.6	58.0	20	4	US-09-182-024A-3	Sequence
92	11.6	58.0	21	4	US-09-257-369A-9	Sequence
C 93	11.6	58.0	22	4	US-08-859-998-1145	Sequence
94	11.6	58.0	27	2	US-08-856-331-18	Sequence
C 95	11.6	58.0	27	3	US-09-225-928-1145	Sequence
96	11.6	58.0	27	4	US-09-225-201B-1145	Sequence
97	11.6	58.0	27	4	US-09-418-830-6	Sequence
C 98	11.6	58.0	27	4	US-09-622-166A-6	Sequence
99	11.6	58.0	27	4	US-07-780-973-2	Sequence
100	11.6	58.0	28	1		

58.0	28	2	US-08-899-324-14	Sequence 14, Appl	c 174	11.2	56.0	20	1	US-08-714-626-8	Sequenc
58.0	28	3	US-08-852-824-11	Sequence 11, Appl	175	11.2	56.0	20	2	US-08-478-178A-67	Sequenc
58.0	28	3	US-08-329-892B-14	Sequence 14, Appl	176	11.2	56.0	20	2	US-08-488-177-67	Sequenc
58.0	30	4	US-09-402-317-5	Sequence 5, Appl	177	11.2	56.0	20	2	US-08-481-072A-67	Sequenc
58.0	32	1	US-07-780-973-12	Sequence 12, Appl	178	11.2	56.0	20	2	US-08-664-336-67	Sequenc
58.0	32	1	US-07-780-973-13	Sequence 13, Appl	c 179	11.2	56.0	20	2	US-08-922-169-8	Sequenc
58.0	33	1	US-08-461-731-4	Sequence 4, Appl	180	11.2	56.0	20	2	US-08-481-066A-67	Sequenc
58.0	33	2	US-09-002-072B-4	Sequence 4, Appl	181	11.2	56.0	20	3	US-09-313-930-7	Sequenc
58.0	33	2	US-09-314-199-4	Sequence 4, Appl	182	11.2	56.0	20	3	US-08-829-637A-67	Sequenc
58.0	33	4	US-08-361-337-33	Sequence 33, Appl	183	11.2	56.0	20	4	US-10-025-139-67	Sequenc
58.0	35	1	US-07-780-973-3	Sequence 3, Appl	c 184	11.2	56.0	20	4	US-09-747-391-94	Sequenc
58.0	37	1	US-09-050-739-25	Sequence 25, Appl	c 185	11.2	56.0	20	5	PCT-US95-04852-8	Sequenc
58.0	43	1	US-07-780-973-8	Sequence 8, Appl	186	11.2	56.0	21	1	US-08-219-842-53	Sequenc
58.0	47	1	US-09-422-978-3710	Sequence 3710, Ap	c 187	11.2	56.0	21	1	US-08-219-842-86	Sequenc
58.0	48	1	US-08-753-054-10	Sequence 10, Appl	188	11.2	56.0	21	1	US-08-451-096-53	Sequenc
58.0	48	4	US-08-720-565-15	Sequence 15, Appl	c 189	11.2	56.0	21	1	US-08-451-096-86	Sequenc
58.0	51	3	US-08-785-247-17	Sequence 17, Appl	190	11.2	56.0	21	3	US-08-413-740A-14	Sequenc
58.0	51	4	US-09-443-199C-831	Sequence 831, App	191	11.2	56.0	21	4	US-09-382-552-227	Sequenc
58.0	57	3	US-09-470-618-5	Sequence 5, Appl	192	11.2	56.0	21	5	PCT-US95-04063-14	Sequenc
58.0	57	3	US-09-364-862-5	Sequence 5, Appl	193	11.2	56.0	24	1	US-08-411-913-3	Sequenc
58.0	57	4	US-09-724-916A-25	Sequence 25, Appl	c 194	11.2	56.0	24	2	US-08-031-538-35	Sequenc
58.0	57	4	US-09-724-916A-26	Sequence 26, Appl	c 195	11.2	56.0	25	4	US-09-946-678-14	Sequenc
58.0	60	4	US-08-172-332-3	Sequence 3, Appl	c 196	11.2	56.0	25	4	US-09-946-678-21	Sequenc
57.0	16	4	US-09-531-000-24	Sequence 24, Appl	c 197	11.2	56.0	25	4	US-09-866-108A-13448	Sequenc
57.0	18	4	US-07-758-282B-191	Sequence 191, App	c 198	11.2	56.0	25	4	US-09-866-108A-13449	Sequenc
57.0	18	4	US-09-758-282B-196	Sequence 196, App	c 199	11.2	56.0	25	4	US-09-866-108A-13450	Sequenc
57.0	20	3	US-09-280-799-60	Sequence 60, Appl	c 200	11.2	56.0	25	4	US-09-866-108A-13451	Sequenc
57.0	20	4	US-09-658-688A-19	Sequence 19, Appl	c 201	11.2	56.0	25	4	US-09-866-108A-13452	Sequenc
57.0	21	4	US-09-216-393B-255	Sequence 255, App	c 202	11.2	56.0	25	4	US-09-866-108A-13453	Sequenc
57.0	24	3	US-08-150-900-33	Sequence 33, Appl	c 203	11.2	56.0	25	4	US-09-866-108A-13454	Sequenc
57.0	26	3	US-08-702-665A-17	Sequence 17, Appl	c 204	11.2	56.0	25	4	US-09-866-108A-13455	Sequenc
57.0	28	3	US-09-150-900-34	Sequence 34, Appl	c 205	11.2	56.0	25	4	US-09-866-108A-13456	Sequenc
57.0	30	1	US-09-150-900-35	Sequence 35, Appl	c 206	11.2	56.0	25	4	US-09-866-108A-13457	Sequenc
57.0	30	3	US-08-321-613-3	Sequence 3, Appl	c 207	11.2	56.0	28	2	US-08-859-998-742	Sequenc
57.0	30	3	US-09-150-900-36	Sequence 36, Appl	c 208	11.2	56.0	28	4	US-09-225-928-742	Sequenc
57.0	30	4	US-09-170-496D-116	Sequence 116, App	c 209	11.2	56.0	28	4	US-09-225-201B-742	Sequenc
57.0	30	4	US-09-364-425B-25	Sequence 25, Appl	c 210	11.2	56.0	28	4	US-08-846-012A-6	Sequenc
57.0	31	4	US-09-635-872A-49	Sequence 49, Appl	c 211	11.2	56.0	29	1	US-09-100-297-6	Sequenc
57.0	31	4	US-09-636-077A-49	Sequence 49, Appl	c 212	11.2	56.0	29	2	US-09-794-529B-23	Sequenc
57.0	31	4	US-09-636-060C-49	Sequence 49, Appl	c 213	11.2	56.0	30	4	US-09-794-517A-23	Sequenc
57.0	31	4	US-09-986-552-49	Sequence 49, Appl	c 214	11.2	56.0	30	4	US-09-011-645B-23	Sequenc
57.0	32	3	US-09-150-900-37	Sequence 37, Appl	c 215	11.2	56.0	30	4	US-09-794-832-23	Sequenc
57.0	32	3	US-08-343-923-11	Sequence 11, Appl	c 216	11.2	56.0	31	2	US-08-942-423-54	Sequenc
57.0	36	1	US-08-021-623C-1	Sequence 1, Appl	c 217	11.2	56.0	31	2	US-08-694-869-8	Sequenc
57.0	36	1	US-08-021-623C-14	Sequence 14, Appl	c 218	11.2	56.0	31	3	US-09-349-546-8	Sequenc
57.0	36	1	US-08-021-623C-16	Sequence 16, Appl	c 219	11.2	56.0	31	4	US-09-502-831-8	Sequenc
57.0	36	4	US-09-403-752A-14	Sequence 14, Appl	c 220	11.2	56.0	31	4	US-09-889-914B-5	Sequenc
57.0	39	1	US-08-225-989-10	Sequence 10, Appl	c 221	11.2	56.0	32	3	US-08-606-505B-40	Sequenc
57.0	39	1	US-08-570-923-10	Sequence 10, Appl	c 222	11.2	56.0	32	3	US-09-616-990-40	Sequenc
57.0	39	3	US-09-079-785-10	Sequence 10, Appl	c 223	11.2	56.0	32	4	US-09-479-479-14	Sequenc
57.0	39	4	US-09-628-126-10	Sequence 10, Appl	c 224	11.2	56.0	32	4	US-09-297-851-14	Sequenc
57.0	42	1	US-08-753-054-12	Sequence 12, Appl	c 225	11.2	56.0	33	3	US-08-884-324-24	Sequenc
57.0	47	4	US-09-641-638-900	Sequence 900, App	c 226	11.2	56.0	34	4	US-09-718-034-5	Sequenc
57.0	47	4	US-09-422-978-3692	Sequence 3692, Ap	c 227	11.2	56.0	38	1	US-07-829-954-3	Sequenc
57.0	49	1	US-08-014-723-8	Sequence 8, Appl	c 228	11.2	56.0	39	1	PCT-US92-06821A-107	Sequenc
57.0	49	1	US-08-110-011A-8	Sequence 8, Appl	c 229	11.2	56.0	39	5	US-09-443-199C-885	Sequenc
57.0	49	1	US-08-361-873A-3	Sequence 3, Appl	c 230	11.2	56.0	41	4	US-09-377-885A-16	Sequenc
57.0	60	4	US-09-339-913B-8	Sequence 8, Appl	c 231	11.2	56.0	46	4	US-09-377-885A-17	Sequenc
57.0	60	4	US-09-339-904A-8	Sequence 8, Appl	c 232	11.2	56.0	46	4	US-09-641-638-921	Sequenc
57.0	60	4	US-08-769-062B-8	Sequence 8, Appl	c 233	11.2	56.0	47	4	US-09-422-978-43	Sequenc
57.0	60	4	US-09-344-002B-8	Sequence 8, Appl	c 234	11.2	56.0	47	4	US-09-422-978-2093	Sequenc
57.0	60	4	US-09-559-565C-8	Sequence 8, Appl	c 235	11.2	56.0	47	4	US-08-891-271-29	Sequenc
57.0	60	4	US-09-693-350-8	Sequence 8, Appl	c 236	11.2	56.0	48	3	US-08-755-587-201	Sequenc
57.0	60	4	US-09-693-389-8	Sequence 8, Appl	c 237	11.2	56.0	50	3	US-09-390-867A-42	Sequenc
57.0	60	4	US-09-559-671A-8	Sequence 8, Appl	c 238	11.2	56.0	50	3	US-09-548-260-42	Sequenc
57.0	60	4	US-09-339-926A-8	Sequence 8, Appl	c 239	11.2	56.0	51	4	US-09-443-199C-974	Sequenc
56.0	17	4	US-09-866-108A-8556	Sequence 8556, Ap	c 240	11.2	56.0	51	4	US-08-390-850-1097	Sequenc
56.0	17	4	US-09-866-108A-8557	Sequence 8557, Ap	c 241	11.2	56.0	54	1	US-08-435-634-1097	Sequenc
56.0	18	3	US-09-339-964-35	Sequence 35, Appl	c 242	11.2	56.0	54	1	US-09-256-000-25	Sequenc
56.0	18	4	US-09-422-978-5304	Sequence 5304, Ap	c 243	11.2	56.0	54	4	US-09-479-645A-179	Sequenc
56.0	19	2	US-08-117-952-533	Sequence 533, App	c 244	11.2	56.0	54	4		
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					c 246	11.2	56.0				

56.0	56	4	US-09-007-288E-133	Sequence 133, App	320	10.8	54.0	17	4	US-09-371-772B-3137	Sequence
56.0	56	4	US-08-893-911A-3	Sequence 3, Appli	321	10.8	54.0	18	2	US-09-205-922-26	Sequence
56.0	58	3	US-08-755-587-202	Sequence 22, App	C 322	10.8	54.0	18	3	US-08-881-450A-12	Sequence
56.0	59	4	US-09-007-288E-84	Sequence 84, Appl	C 323	10.8	54.0	18	4	US-09-475-947A-260	Sequence
56.0	60	2	US-08-372-652-15	Sequence 15, Appl	324	10.8	54.0	19	3	US-09-215-221-43	Sequence
56.0	60	5	PCT-US95-16311-15	Sequence 15, Appl	C 325	10.8	54.0	20	1	US-08-531-556-70	Sequence
55.0	18	2	US-09-205-922-76	Sequence 76, Appl	C 326	10.8	54.0	20	1	US-08-472-416-70	Sequence
55.0	20	3	US-09-428-584-39	Sequence 39, Appl	C 327	10.8	54.0	20	3	US-09-286-904-68	Sequence
55.0	20	4	US-09-702-327-62	Sequence 62, Appl	C 328	10.8	54.0	20	3	US-09-418-640-50	Sequence
55.0	20	4	US-09-198-452A-5351	Sequence 5351, Ap	329	10.8	54.0	20	4	US-09-360-545-71	Sequence
55.0	21	3	US-08-840-767-21	Sequence 21, Appl	330	10.8	54.0	20	4	US-09-640-101-68	Sequence
55.0	22	4	US-09-358-383C-19	Sequence 19, Appl	C 331	10.8	54.0	20	4	US-09-255-154D-21	Sequence
55.0	23	3	US-09-222-817-17	Sequence 17, Appl	332	10.8	54.0	20	4	US-09-780-045-33	Sequence
55.0	23	3	US-09-050-559C-28	Sequence 28, Appl	333	10.8	54.0	20	4	US-09-780-045-107	Sequence
55.0	24	3	US-08-041-185-15	Sequence 15, Appl	C 334	10.8	54.0	22	4	US-09-363-243-13	Sequence
55.0	27	1	US-08-758-306-822	Sequence 822, App	C 335	10.8	54.0	23	1	US-08-741-406-13	Sequence
55.0	27	1	US-08-758-306-940	Sequence 940, App	C 336	10.8	54.0	23	3	US-08-544-381B-233	Sequence
55.0	27	3	US-09-023-731-20	Sequence 20, Appl	C 337	10.8	54.0	23	3	US-08-544-381B-234	Sequence
55.0	27	4	US-08-851-062-6	Sequence 6, Appli	C 338	10.8	54.0	23	3	US-09-024-472-13	Sequence
55.0	30	1	US-08-219-012-31	Sequence 31, Appl	C 339	10.8	54.0	25	1	US-08-362-706A-9	Sequence
55.0	30	3	US-08-687-421-219	Sequence 219, App	C 340	10.8	54.0	25	2	US-08-859-998-687	Sequence
55.0	31	4	US-08-793-381A-4	Sequence 4, Appli	341	10.8	54.0	25	3	US-09-522-494-39	Sequence
55.0	31	1	US-08-480-525-10	Sequence 10, Appl	342	10.8	54.0	25	3	US-09-522-494-40	Sequence
55.0	31	5	PCT-US94-06422-10	Sequence 10, Appl	C 343	10.8	54.0	25	4	US-09-549-808-9	Sequence
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55.0	33	1	US-08-138-608-38	Sequence 38, Appl	C 345	10.8	54.0	25	4	US-09-225-201B-687	Sequence
55.0	35	3	US-08-928-881-23	Sequence 23, Appl	C 346	10.8	54.0	25	4	US-09-306-653-7	Sequence
55.0	35	4	US-09-543-921-23	Sequence 23, Appl	C 347	10.8	54.0	25	4	US-09-621-275-14	Sequence
55.0	35	4	US-09-266-014-10	Sequence 10, Appl	C 348	10.8	54.0	26	2	US-08-859-998-1262	Sequence
55.0	35	4	US-09-491-759-23	Sequence 23, Appl	C 349	10.8	54.0	26	4	US-09-225-928-1262	Sequence
55.0	36	1	US-08-466-033-261	Sequence 261, App	C 350	10.8	54.0	26	4	US-09-225-201B-1262	Sequence
55.0	36	1	US-08-444-733-261	Sequence 261, App	C 351	10.8	54.0	26	4	US-09-602-586-8	Sequence
55.0	36	2	US-08-464-134-261	Sequence 261, App	C 352	10.8	54.0	26	4	US-09-602-586-15	Sequence
55.0	36	2	US-08-461-361-261	Sequence 261, App	C 353	10.8	54.0	26	4	US-09-602-586-30	Sequence
55.0	36	2	US-08-485-910-261	Sequence 261, App	354	10.8	54.0	26	4	US-09-602-586-37	Sequence
55.0	39	1	US-08-066-961-22	Sequence 22, Appl	C 355	10.8	54.0	26	4	US-09-561-579A-8	Sequence
55.0	39	1	US-08-034-153D-9	Sequence 9, Appli	C 356	10.8	54.0	26	4	US-09-561-579A-15	Sequence
55.0	40	2	US-08-628-422-36	Sequence 36, Appl	357	10.8	54.0	26	4	US-09-561-579A-30	Sequence
55.0	44	3	US-08-666-354A-5	Sequence 5, Appli	358	10.8	54.0	26	4	US-09-561-579A-37	Sequence
55.0	47	4	US-09-422-978-2917	Sequence 2917, Ap	359	10.8	54.0	27	2	US-08-389-423-6	Sequence
55.0	51	4	US-09-443-199C-963	Sequence 963, App	C 360	10.8	54.0	27	3	US-08-776-251-8	Sequence
55.0	53	1	US-08-429-181-43	Sequence 43, Appl	361	10.8	54.0	27	4	US-09-189-028-6	Sequence
55.0	53	1	US-08-164-388-43	Sequence 43, Appl	C 362	10.8	54.0	28	3	US-08-993-008A-1	Sequence
55.0	58	3	US-09-061-702-12	Sequence 12, Appl	C 363	10.8	54.0	28	4	US-09-534-407-40	Sequence
55.0	58	3	US-08-860-038-15	Sequence 15, Appl	C 364	10.8	54.0	28	4	US-09-999-201B-40	Sequence
55.0	58	4	US-09-580-923-15	Sequence 15, Appl	365	10.8	54.0	28	4	US-09-698-154-5	Sequence
55.0	59	4	US-09-424-712-3	Sequence 3, Appli	C 366	10.8	54.0	31	3	US-08-544-381B-167	Sequence
55.0	60	3	US-07-602-848E-12	Sequence 12, Appl	C 367	10.8	54.0	32	1	US-08-619-724-4	Sequence
54.0	14	3	US-08-544-361B-235	Sequence 235, App	368	10.8	54.0	32	1	US-08-619-724-6	Sequence
54.0	15	1	US-08-311-462-3	Sequence 3, Appli	C 369	10.8	54.0	32	3	US-09-522-494-55	Sequence
54.0	15	1	US-08-311-462-12	Sequence 12, Appl	370	10.8	54.0	32	5	PCT-US95-04094-11	Sequence
54.0	15	2	US-08-434-354-3	Sequence 3, Appli	C 371	10.8	54.0	35	1	US-08-530-492-94	Sequence
54.0	15	2	US-08-434-354-12	Sequence 12, Appl	C 372	10.8	54.0	35	3	US-08-906-517-94	Sequence
54.0	17	1	US-08-179-738-23	Sequence 23, Appl	C 373	10.8	54.0	36	3	US-09-440-001-3	Sequence
54.0	17	1	US-08-281-940-4	Sequence 4, Appli	C 374	10.8	54.0	36	4	US-08-993-035A-20	Sequence
54.0	17	1	US-08-281-940-35	Sequence 35, Appl	375	10.8	54.0	36	4	US-08-993-035A-23	Sequence
54.0	17	1	US-08-308-638-3	Sequence 3, Appli	C 376	10.8	54.0	36	4	US-09-605-685-3	Sequence
54.0	17	1	US-08-373-124A-182	Sequence 182, App	C 377	10.8	54.0	38	4	US-09-564-805-156	Sequence
54.0	17	1	US-08-373-124A-184	Sequence 184, App	378	10.8	54.0	39	1	US-08-066-961-27	Sequence
54.0	17	1	US-08-435-628-182	Sequence 182, App	C 379	10.8	54.0	40	1	US-08-443-957-11	Sequence
54.0	17	2	US-08-435-628-184	Sequence 184, App	C 380	10.8	54.0	40	2	US-08-628-422-35	Sequence
54.0	17	2	US-08-710-134-4	Sequence 4, Appli	C 381	10.8	54.0	42	3	US-08-908-643C-30	Sequence
54.0	17	2	US-08-710-134-35	Sequence 35, Appl	382	10.8	54.0	43	1	US-08-437-538-11	Sequence
54.0	17	2	US-08-485-885-4	Sequence 4, Appli	C 383	10.8	54.0	45	1	US-08-443-957-34	Sequence
54.0	17	2	US-08-485-885-35	Sequence 35, Appl	C 384	10.8	54.0	45	2	US-08-470-939-25	Sequence
54.0	17	2	US-08-628-145-23	Sequence 23, Appl	C 385	10.8	54.0	45	2	US-08-356-786-13	Sequence
54.0	17	3	US-08-544-361B-243	Sequence 243, App	C 386	10.8	54.0	45	5	PCT-US96-09452-25	Sequence
54.0	17	3	US-09-215-221-41	Sequence 41, Appl	C 387	10.8	54.0	47	4	US-09-345-882-41	Sequence
54.0	17	4	US-08-584-040-7327	Sequence 7327, Ap	C 388	10.8	54.0	47	4	US-09-345-882-62	Sequence
54.0	17	4	US-08-584-040-7328	Sequence 7328, Ap	C 389	10.8	54.0	47	4	US-09-422-978-690	Sequence
54.0	17	4	US-09-270-140A-46	Sequence 46, Appl	390	10.8	54.0	47	4	US-09-422-978-919	Sequence
54.0	17	4	US-09-270-140A-47	Sequence 47, Appl	391	10.8	54.0	47	4	US-09-422-978-3644	Sequence
54.0	17	4	US-09-371-772B-3136	Sequence 3136, Ap	C 392	10.8	54.0	47	6	5510256-6	Patent No

54.0	49	4	US-09-306-653-1	Sequence 1, Appli	C 466	10.6	53.0	28	1	US-08-434-823-4	Sequenc
54.0	49	4	US-09-621-275-8	Sequence 8, Appli	C 467	10.6	53.0	28	1	US-08-457-366-4	Sequenc
54.0	49	5	PCT-US91-02568-35	Sequence 35, Appl	C 468	10.6	53.0	28	1	US-07-695-472B-22	Sequenc
54.0	50	1	US-08-171-389-511	Sequence 511, App	C 469	10.6	53.0	28	2	US-08-465-609-1	Sequenc
54.0	50	1	US-08-123-936-511	Sequence 511, App	C 470	10.6	53.0	28	3	US-08-646-861-28	Sequenc
54.0	50	2	US-08-475-228A-511	Sequence 511, App	C 471	10.6	53.0	28	3	US-09-176-320-3	Sequenc
54.0	50	3	US-08-482-080A-511	Sequence 511, App	C 472	10.6	53.0	28	4	US-09-106-375-22	Sequenc
54.0	50	4	US-09-357-487B-29	Sequence 29, Appl	C 473	10.6	53.0	29	4	US-09-562-069-3	Sequenc
54.0	50	4	US-09-354-947-511	Sequence 511, App	C 474	10.6	53.0	30	1	US-08-219-012-35	Sequenc
54.0	50	5	PCT-US93-12388-511	Sequence 511, App	C 475	10.6	53.0	30	1	US-08-186-229-24	Sequenc
54.0	54	1	US-08-390-850-1045	Sequence 1045, Ap	C 476	10.6	53.0	30	2	US-08-470-124-24	Sequenc
54.0	54	1	US-08-435-634-1045	Sequence 1045, Ap	C 477	10.6	53.0	30	3	US-08-467-023-198	Sequenc
54.0	55	1	US-08-484-686B-24	Sequence 24, Appl	C 478	10.6	53.0	30	3	US-08-687-421-223	Sequenc
54.0	55	3	US-08-463-160B-24	Sequence 8, Appli	C 479	10.6	53.0	30	3	US-08-658-034-4	Sequenc
54.0	55	4	US-09-698-154-8	Sequence 27, Appl	C 480	10.6	53.0	30	4	US-09-123-030-6	Sequenc
54.0	56	2	US-08-537-811-27	Sequence 126, App	C 481	10.6	53.0	30	4	US-09-358-052-4	Sequenc
54.0	57	1	US-08-530-492-126	Sequence 126, App	C 482	10.6	53.0	32	1	US-08-445-050-19	Sequenc
54.0	57	3	US-08-906-517-126	Sequence 126, App	C 483	10.6	53.0	32	1	US-08-204-691-19	Sequenc
54.0	57	4	US-09-306-653-18	Sequence 18, Appl	C 484	10.6	53.0	32	3	US-08-875-509-6	Sequenc
54.0	57	4	US-09-621-275-25	Sequence 25, Appl	C 485	10.6	53.0	32	4	US-09-619-334-1	Sequenc
54.0	57	5	PCT-US91-02568-33	Sequence 33, Appl	C 486	10.6	53.0	33	3	US-08-875-509-2	Sequenc
54.0	60	2	US-08-828-008-10	Sequence 10, Appl	C 487	10.6	53.0	33	3	US-07-987-264-19	Sequenc
53.0	17	2	US-08-232-620A-1831	Sequence 1831, Ap	C 488	10.6	53.0	33	4	US-09-472-065A-16	Sequenc
53.0	17	3	US-09-071-845-1831	Sequence 1831, Ap	C 489	10.6	53.0	33	4	US-09-818-780-56	Sequenc
53.0	18	1	US-08-050-073-190	Sequence 190, App	C 490	10.6	53.0	34	1	US-08-271-880A-40	Sequenc
53.0	19	3	US-08-369-822C-17	Sequence 17, Appl	C 491	10.6	53.0	34	2	US-08-910-408-40	Sequenc
53.0	19	3	US-08-582-776C-17	Sequence 17, Appl	C 492	10.6	53.0	34	3	US-09-249-215-40	Sequenc
53.0	20	3	US-09-167-921-41	Sequence 41, Appl	C 493	10.6	53.0	34	3	US-09-091-305-4	Sequenc
53.0	20	3	US-08-822-516-12	Sequence 12, Appl	C 494	10.6	53.0	35	1	US-08-753-054-5	Sequenc
53.0	20	3	US-08-515-495-8	Sequence 8, Appli	C 495	10.6	53.0	35	1	US-08-235-836C-81	Sequenc
53.0	20	3	US-09-323-743-41	Sequence 41, Appl	C 496	10.6	53.0	36	1	US-08-482-882-57	Sequenc
53.0	20	3	US-03-657-481A-53	Sequence 53, Appl	C 497	10.6	53.0	36	2	US-08-483-389-57	Sequenc
53.0	20	3	US-09-593-711A-141	Sequence 141, App	C 498	10.6	53.0	36	2	US-08-487-113D-57	Sequenc
53.0	20	3	US-09-593-711A-142	Sequence 142, App	C 499	10.6	53.0	36	2	US-08-473-503-57	Sequenc
53.0	20	3	US-09-109-663-68	Sequence 68, Appl	C 500	10.6	53.0	36	2	US-08-483-932-57	Sequenc
53.0	20	4	US-09-131-684-12	Sequence 12, Appl	C 501	10.6	53.0	36	2	US-08-954-333-4	Sequenc
53.0	20	4	US-09-142-623-9	Sequence 9, Appli	C 502	10.6	53.0	36	2	US-08-720-420A-57	Sequenc
53.0	20	4	US-09-198-452A-2507	Sequence 2507, Ap	C 503	10.6	53.0	36	3	US-08-714-017-57	Sequenc
53.0	21	1	US-08-823-549-69	Sequence 69, Appl	C 504	10.6	53.0	36	4	US-08-475-680-57	Sequenc
53.0	21	1	US-08-379-078-584	Sequence 584, App	C 505	10.6	53.0	36	4	US-09-147-208-17	Sequenc
53.0	21	4	US-07-974-409C-207	Sequence 207, App	C 506	10.6	53.0	36	4	US-09-550-117A-17	Sequenc
53.0	21	4	US-09-194-842A-33	Sequence 33, Appl	C 507	10.6	53.0	38	2	US-08-464-257-7	Sequenc
53.0	21	4	US-09-380-836-51	Sequence 51, Appl	C 508	10.6	53.0	38	2	US-08-715-341-10	Sequenc
53.0	21	5	PCT-US93-00377-207	Sequence 207, App	C 509	10.6	53.0	38	2	US-09-062-375-7	Sequenc
53.0	22	1	US-08-118-441-22	Sequence 22, Appl	C 510	10.6	53.0	38	3	US-09-203-796A-7	Sequenc
53.0	22	3	US-08-338-579A-22	Sequence 22, Appl	C 511	10.6	53.0	39	2	US-08-254-354-11	Sequenc
53.0	22	3	US-09-092-314-7	Sequence 7, Appli	C 512	10.6	53.0	39	2	US-08-453-024-4	Sequenc
53.0	22	5	PCT-US94-09851-22	Sequence 22, Appl	C 513	10.6	53.0	39	3	US-08-070-162-4	Sequenc
53.0	25	4	US-08-462-509B-8	Sequence 8, Appli	C 514	10.6	53.0	39	5	US-09-475-947A-344	Sequenc
53.0	25	4	US-08-462-509B-10	Sequence 10, Appl	C 515	10.6	53.0	39	5	PCT-US95-06137-11	Sequenc
53.0	25	4	US-08-462-509B-12	Sequence 12, Appl	C 516	10.6	53.0	40	4	US-08-911-393-10	Sequenc
53.0	25	4	US-09-350-969-36	Sequence 36, Appl	C 517	10.6	53.0	41	3	US-08-480-640A-187	Sequenc
53.0	25	5	PCT-US95-05616-8	Sequence 8, Appli	C 518	10.6	53.0	41	3	US-08-295-802-187	Sequenc
53.0	25	5	PCT-US95-05616-10	Sequence 10, Appl	C 519	10.6	53.0	41	3	US-08-686-968C-75	Sequenc
53.0	26	1	US-07-832-905B-65	Sequence 65, Appl	C 520	10.6	53.0	41	3	US-08-488-237A-187	Sequenc
53.0	26	2	US-08-700-757-65	Sequence 65, Appl	C 521	10.6	53.0	41	4	US-08-375-992A-187	Sequenc
53.0	26	2	US-08-996-306-6	Sequence 6, Appli	C 522	10.6	53.0	41	4	US-08-472-679H-187	Sequenc
53.0	26	2	US-08-747-536-17	Sequence 17, Appl	C 523	10.6	53.0	42	1	US-08-225-224-47	Sequenc
53.0	26	2	US-08-859-998-556	Sequence 556, App	C 524	10.6	53.0	42	1	US-08-445-050-14	Sequenc
53.0	26	3	US-09-338-907-6	Sequence 6, Appli	C 525	10.6	53.0	42	1	US-08-204-691-14	Sequenc
53.0	26	4	US-09-218-207-6	Sequence 556, App	C 526	10.6	53.0	42	2	US-08-438-257A-55	Sequenc
53.0	26	4	US-09-225-928-556	Sequence 556, App	C 527	10.6	53.0	42	3	US-08-722-258-47	Sequenc
53.0	27	3	US-08-985-162-1301	Sequence 1301, Ap	C 528	10.6	53.0	42	3	US-08-724-586-5	Sequenc
53.0	27	3	US-08-985-162-1583	Sequence 1583, Ap	C 529	10.6	53.0	42	3	US-09-421-632-5	Sequenc
53.0	27	3	US-08-998-099-267	Sequence 267, App	C 530	10.6	53.0	42	4	US-09-932-190-5	Sequenc
53.0	27	4	US-08-584-040-6561	Sequence 6561, Ap	C 531	10.6	53.0	43	5	PCT-US95-04468-47	Sequenc
53.0	27	4	US-09-585-228-25	Sequence 25, Appl	C 532	10.6	53.0	43	1	US-08-116-388-8	Sequenc
53.0	27	4	US-09-401-063-1301	Sequence 1301, Ap	C 533	10.6	53.0	43	1	US-08-445-050-15	Sequenc
53.0	27	4	US-09-401-063-1583	Sequence 1583, Ap	C 534	10.6	53.0	43	1	US-08-204-691-15	Sequenc
53.0	27	4	US-08-250-740-16	Sequence 16, Appl	C 535	10.6	53.0	44	1	PCT-US94-09318-8	Sequenc
53.0	28	1			C 536	10.6	53.0	44	1	US-08-375-116A-42	Sequenc
53.0	28	1			C 537	10.6	53.0	47	4	US-09-422-978-191	Sequenc
53.0	28	1			C 538	10.6	53.0	47	4	US-09-422-978-2656	Sequenc

53.0	47	4	US-09-422-978-2725	Sequence 2725, Ap	612	10.4	52.0	20	4	US-09-997-579-34	Sequence
53.0	47	4	US-09-422-978-3806	Sequence 3806, Ap	c 613	10.4	52.0	21	4	US-08-977-378-18	Sequence
53.0	49	1	US-08-530-492-89	Sequence 89, Appl	614	10.4	52.0	22	1	US-08-379-078-418	Sequence
53.0	49	1	US-08-482-862-72	Sequence 72, Appl	615	10.4	52.0	22	1	US-08-379-078-419	Sequence
53.0	49	1	US-08-483-389-72	Sequence 72, Appl	c 616	10.4	52.0	22	1	US-08-223-902-12	Sequence
53.0	49	1	US-08-487-113D-72	Sequence 72, Appl	617	10.4	52.0	22	1	US-09-101-886B-8	Sequence
53.0	49	2	US-08-473-503-72	Sequence 72, Appl	618	10.4	52.0	22	3	US-09-101-886B-16	Sequence
53.0	49	2	US-08-483-932-72	Sequence 72, Appl	619	10.4	52.0	22	3	US-09-101-886B-26	Sequence
53.0	49	2	US-08-720-420A-72	Sequence 72, Appl	c 620	10.4	52.0	22	3	US-09-101-886B-27	Sequence
53.0	49	3	US-08-714-017-72	Sequence 72, Appl	621	10.4	52.0	22	4	US-07-974-409C-31	Sequence
53.0	49	3	US-08-475-680-72	Sequence 72, Appl	622	10.4	52.0	22	4	US-07-974-409C-32	Sequence
53.0	49	3	US-08-475-680-72	Sequence 72, Appl	623	10.4	52.0	22	5	PCT-US93-00977-31	Sequence
53.0	50	1	US-08-906-517-89	Sequence 89, Appl	624	10.4	52.0	22	5	PCT-US93-00977-32	Sequence
53.0	50	1	US-08-171-389-571	Sequence 34, Appl	625	10.4	52.0	23	1	US-07-722-798A-95	Sequence
53.0	50	1	US-08-207-901-34	Sequence 571, Appl	c 626	10.4	52.0	23	3	US-09-456-830-68	Sequence
53.0	50	1	US-08-123-936-571	Sequence 571, Appl	c 627	10.4	52.0	23	4	US-09-589-477-68	Sequence
53.0	50	2	US-08-475-228A-571	Sequence 12, Appl	c 628	10.4	52.0	24	3	US-09-474-922A-8	Sequence
53.0	50	2	US-08-999-811-12	Sequence 12, Appl	c 629	10.4	52.0	25	1	US-07-722-798A-96	Sequence
53.0	50	3	US-08-482-080A-571	Sequence 571, Appl	c 630	10.4	52.0	25	1	US-08-049-061-36	Sequence
53.0	50	4	US-09-354-947-571	Sequence 571, Appl	631	10.4	52.0	25	1	US-08-049-061-38	Sequence
53.0	50	4	US-08-465-968-7	Sequence 7, Appl	c 632	10.4	52.0	25	1	US-08-374-144-5	Sequence
53.0	50	5	PCT-US93-12388-571	Sequence 571, Appl	c 633	10.4	52.0	25	1	US-08-374-144-21	Sequence
53.0	50	5	US-09-648-667-10	Sequence 4, Appl	634	10.4	52.0	25	1	US-08-775-164-5	Sequence
53.0	51	4	US-09-443-199C-58	Sequence 10, Appl	c 635	10.4	52.0	25	1	US-08-775-164-21	Sequence
53.0	51	4	US-09-443-199C-147	Sequence 58, Appl	636	10.4	52.0	25	2	US-08-775-609-5	Sequence
53.0	51	4	US-09-443-199C-148	Sequence 147, Appl	c 637	10.4	52.0	25	2	US-08-775-609-21	Sequence
53.0	51	4	US-09-443-199C-636	Sequence 148, Appl	c 638	10.4	52.0	25	2	US-08-775-607-5	Sequence
53.0	51	4	US-09-443-199C-958	Sequence 636, Appl	c 639	10.4	52.0	25	2	US-08-775-607-21	Sequence
53.0	51	4	US-09-443-199C-958	Sequence 958, Appl	640	10.4	52.0	25	2	US-08-775-607-21	Sequence
53.0	51	4	US-09-443-199C-1041	Sequence 1041, Ap	c 641	10.4	52.0	25	4	US-09-866-108A-13458	Sequence
53.0	53	1	US-08-429-181-48	Sequence 48, Appl	c 642	10.4	52.0	25	4	US-09-866-108A-13459	Sequence
53.0	53	1	US-08-164-388-48	Sequence 48, Appl	c 643	10.4	52.0	25	4	US-09-866-108A-13460	Sequence
53.0	54	4	US-09-315-926A-31	Sequence 31, Appl	c 644	10.4	52.0	25	4	US-09-866-108A-13461	Sequence
53.0	54	4	US-09-315-926A-65	Sequence 65, Appl	c 645	10.4	52.0	25	5	PCT-US93-06828-5	Sequence
53.0	55	1	US-08-445-050-18	Sequence 18, Appl	646	10.4	52.0	26	2	US-08-852-806-4	Sequence
53.0	55	1	US-08-204-691-18	Sequence 18, Appl	647	10.4	52.0	26	3	US-09-163-669-4	Sequence
53.0	55	2	US-08-715-941-11	Sequence 11, Appl	c 648	10.4	52.0	26	4	US-09-043-646-5	Sequence
53.0	55	2	US-08-715-941-14	Sequence 14, Appl	649	10.4	52.0	27	2	US-08-853-998-844	Sequence
53.0	56	3	US-08-307-896-8	Sequence 8, Appl	650	10.4	52.0	27	3	US-08-513-974B-187	Sequence
53.0	60	1	US-08-424-788-15	Sequence 15, Appl	651	10.4	52.0	27	3	US-09-242-948-7	Sequence
53.0	60	2	US-08-743-130A-25	Sequence 25, Appl	652	10.4	52.0	27	4	US-08-891-292A-2	Sequence
52.0	16	4	US-09-308-683-3	Sequence 3, Appl	653	10.4	52.0	27	4	US-09-225-928-844	Sequence
52.0	17	1	US-08-373-124A-180	Sequence 180, Appl	654	10.4	52.0	27	4	US-09-225-201B-844	Sequence
52.0	17	1	US-08-435-628-180	Sequence 180, Appl	655	10.4	52.0	27	4	US-09-921-737C-2	Sequence
52.0	17	2	US-08-292-620A-1881	Sequence 1881, Ap	656	10.4	52.0	28	2	US-08-981-663-7	Sequence
52.0	17	3	US-09-071-845-1881	Sequence 1881, Ap	657	10.4	52.0	28	2	US-08-859-998-373	Sequence
52.0	17	4	US-08-679-645-680	Sequence 680, Appl	658	10.4	52.0	28	4	US-09-225-928-373	Sequence
52.0	17	4	US-09-866-108A-8558	Sequence 8558, Ap	659	10.4	52.0	28	4	US-09-225-201B-373	Sequence
52.0	17	4	US-09-866-108A-8559	Sequence 8559, Ap	660	10.4	52.0	29	2	US-08-467-603-83	Sequence
52.0	17	4	US-09-866-108A-8560	Sequence 8560, Ap	661	10.4	52.0	29	2	US-08-467-603-83	Sequence
52.0	17	4	US-09-866-108A-8561	Sequence 8561, Ap	662	10.4	52.0	29	2	US-08-467-603-83	Sequence
52.0	18	1	US-08-369-282-2	Sequence 2, Appl	663	10.4	52.0	29	3	US-08-544-381B-166	Sequence
52.0	18	2	US-09-205-922-85	Sequence 85, Appl	c 664	10.4	52.0	29	3	US-08-920-919A-20	Sequence
52.0	18	3	US-09-474-922A-77	Sequence 77, Appl	c 665	10.4	52.0	29	3	US-09-324-910-10	Sequence
52.0	18	4	US-09-422-978-8353	Sequence 8353, Ap	666	10.4	52.0	29	3	US-09-275-850-160	Sequence
52.0	18	4	US-09-422-978-8862	Sequence 8862, Ap	c 667	10.4	52.0	29	3	US-09-374-671A-83	Sequence
52.0	18	5	PCT-US92-00626-2	Sequence 2, Appl	668	10.4	52.0	30	1	US-08-303-162A-9	Sequence
52.0	20	1	US-08-044-618-2	Sequence 32, Appl	669	10.4	52.0	30	1	US-08-123-702-36	Sequence
52.0	20	1	US-08-148-058A-32	Sequence 32, Appl	670	10.4	52.0	30	1	US-08-634-060-9	Sequence
52.0	20	1	US-08-478-042-32	Sequence 32, Appl	671	10.4	52.0	30	1	US-08-634-060-9	Sequence
52.0	20	1	US-08-645-215-32	Sequence 32, Appl	672	10.4	52.0	30	1	US-08-709-515-9	Sequence
52.0	20	2	US-08-466-604-32	Sequence 47, Appl	673	10.4	52.0	30	1	US-08-078-090-14	Sequence
52.0	20	2	US-08-810-599-47	Sequence 38, Appl	c 674	10.4	52.0	30	3	US-08-544-381B-161	Sequence
52.0	20	3	US-08-757-438-38	Sequence 3, Appl	675	10.4	52.0	30	3	US-08-544-381B-163	Sequence
52.0	20	3	US-09-416-756A-3	Sequence 31, Appl	c 676	10.4	52.0	30	3	US-08-544-381B-164	Sequence
52.0	20	3	US-09-435-296-31	Sequence 84, Appl	c 677	10.4	52.0	30	3	US-08-544-381B-165	Sequence
52.0	20	3	US-09-428-583-84	Sequence 40, Appl	c 678	10.4	52.0	30	4	US-09-342-143-12	Sequence
52.0	20	4	US-09-336-643A-40	Sequence 63, Appl	c 679	10.4	52.0	30	4	US-09-549-564-1	Sequence
52.0	20	4	US-09-702-327-63	Sequence 39, Appl	c 680	10.4	52.0	30	4	US-09-236-268-4	Sequence
52.0	20	4	US-09-302-681-39	Sequence 36, Appl	c 681	10.4	52.0	30	4	US-09-236-268-5	Sequence
52.0	20	4	US-08-626-285-36	Sequence 2, Appl	c 682	10.4	52.0	30	4	US-09-924-439-12	Sequence
52.0	20	4	US-09-425-233-2	Sequence 7954, Ap	c 683	10.4	52.0	30	4	US-09-390-134B-2	Sequence
52.0	20	4	US-09-422-978-7954		684	10.4	52.0	30	4		

52.0	31	2	US-08-649-619B-3	Sequence 3, Appli	C 758	10.4	52.0	50	4	US-09-443-199C-632	Sequenc
52.0	32	3	US-08-446-909-4	Sequence 4, Appli	C 759	10.4	52.0	50	4	US-09-443-199C-633	Sequenc
52.0	33	4	US-08-446-911-4	Sequence 4, Appli	C 760	10.4	52.0	51	4	US-09-443-199C-257	Sequenc
52.0	34	5	US-09-420-861-4	Sequence 4, Appli	C 761	10.4	52.0	51	4	US-09-443-199C-258	Sequenc
52.0	35	6	US-09-374-669-4	Sequence 4, Appli	C 762	10.4	52.0	51	4	US-09-443-199C-259	Sequenc
52.0	36	7	US-09-552-709-4	Sequence 4, Appli	C 763	10.4	52.0	51	4	US-09-443-199C-261	Sequenc
52.0	37	8	US-08-102-567-13	Sequence 13, Appl	C 764	10.4	52.0	51	4	US-09-443-199C-631	Sequenc
52.0	38	9	US-08-462-947-13	Sequence 13, Appl	C 765	10.4	52.0	51	4	US-09-443-199C-634	Sequenc
52.0	39	10	US-08-379-452-32	Sequence 32, Appl	C 766	10.4	52.0	52	5	PCT-US91-02568-34	Sequenc
52.0	40	11	US-08-379-452-33	Sequence 33, Appl	C 767	10.4	52.0	53	2	US-08-771-624B-7	Sequenc
52.0	41	12	US-09-409-670-32	Sequence 32, Appl	C 768	10.4	52.0	54	1	US-08-311-486C-1037	Sequenc
52.0	42	13	US-09-409-670-33	Sequence 33, Appl	C 769	10.4	52.0	54	1	US-08-484-686B-12	Sequenc
52.0	43	14	US-08-021-623C-11	Sequence 11, Appl	C 770	10.4	52.0	54	2	US-08-771-624B-5	Sequenc
52.0	44	15	US-09-367-777-9	Sequence 9, Appli	C 771	10.4	52.0	54	2	US-08-771-624B-9	Sequenc
52.0	45	16	US-09-367-777-25	Sequence 25, Appl	C 772	10.4	52.0	54	3	US-08-463-160B-12	Sequenc
52.0	46	17	US-09-367-777-29	Sequence 29, Appl	C 773	10.4	52.0	55	1	US-08-160-670A-11	Sequenc
52.0	47	18	US-09-367-777-33	Sequence 33, Appl	C 774	10.4	52.0	55	4	US-08-956-171B-2854	Sequenc
52.0	48	19	US-08-771-624B-11	Sequence 11, Appl	C 775	10.4	52.0	56	5	PCT-US91-02568-3	Sequenc
52.0	49	20	US-09-052-995-3	Sequence 3, Appli	C 776	10.4	52.0	57	4	US-09-097-055B-48	Sequenc
52.0	50	21	US-09-318-786-4	Sequence 4, Appli	C 777	10.4	52.0	58	3	US-09-097-055B-54	Sequenc
52.0	51	22	US-09-952-572-5	Sequence 5, Appli	C 778	10.4	52.0	58	3	US-09-275-850-263	Sequenc
52.0	52	23	US-08-443-957-24	Sequence 24, Appl	C 779	10.4	52.0	58	4	US-08-956-171B-2914	Sequenc
52.0	53	24	US-08-857-946-80	Sequence 80, Appl	C 780	10.4	52.0	60	3	US-08-870-930-29	Sequenc
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## ALIGNMENTS

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MATION:

heppard, Paul O.

ENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

CE: 97-30

ICATION NUMBER: US/09/118,408A

NG DATE: 1998-07-17

ICATION NUMBER: 60/053,154

NG DATE: 1997-07-18

Q ID NOS: 47

stSEQ for Windows Version 3.0

rtificial Sequence

MATION: Oligonucleotide ZC13651

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Application US/09118408A

65544

MATION:

heppard, Paul O.

ENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

CE: 97-30

ICATION NUMBER: US/09/118,408A

NG DATE: 1998-07-17

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NG DATE: 1997-07-18

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; Patent No. 6448221

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Lasser, Gerald W.

; APPLICANT: Bishop, Paul D.

; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND

; TITLE OF INVENTION: IMMUNE FUNCTION

; FILE REFERENCE: 99-12

; CURRENT APPLICATION NUMBER: US/09/506,855

; CURRENT FILING DATE: 2000-02-17

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; Sequence 15, Application US/09506855

; Patent No. 6448221

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Lasser, Gerald W.

; APPLICANT: Bishop, Paul D.

; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND

; TITLE OF INVENTION: IMMUNE FUNCTION

; FILE REFERENCE: 99-12

; CURRENT APPLICATION NUMBER: US/09/506,855

; CURRENT FILING DATE: 2000-02-17

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 15

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide ZC13650

US-09-506-855-15



74.0%; Score 14.8; DB 4; Length 20;  
ilarity 88.9%; Pred. No. 1.7e+02;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCCACGGGTT 20  
|||||  
TTGTCTCCACGGTTT 3

2  
pplication US/09911176B  
8403

ATION:  
eppard, Paul O.  
NTION: ANTIBODIES THAT BIND AN  
NTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG

IE: 97-30D1

ICATION NUMBER: US/09/911,176B

IG DATE: 2001-07-23

ATION NUMBER: 09/118,408

DATE: 1998-07-17

ATION NUMBER: 60/053,154

DATE: 1997-07-18

ID NOS: 52

tsEQ for Windows Version 3.0

tificial Sequence

ATION: Oligonucleotide ZC13651

2

74.0%; Score 14.8; DB 4; Length 20;  
ilarity 88.9%; Pred. No. 1.7e+02;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCCACGGGTT 20  
|||||  
TTGTCTCCACGGTTT 18

15/c  
pplication US/09911176B  
18403

ATION:

eppard, Paul O.

NTION: ANTIBODIES THAT BIND AN

NTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG

IE: 97-30D1

ICATION NUMBER: US/09/911,176B

IG DATE: 2001-07-23

ATION NUMBER: 09/118,408

DATE: 1998-07-17

ATION NUMBER: 60/053,154

DATE: 1997-07-18

ID NOS: 52

tsEQ for Windows Version 3.0

rtificial Sequence

ATION: Oligonucleotide ZC13650

15

74.0%; Score 14.8; DB 4; Length 20;  
ilarity 88.9%; Pred. No. 1.7e+02;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTGTCTCCACGGGTT 20

Db 20 CTTGTCTCCACGGTTT 3  
|||||

## RESULT 7

US-09-619-740-12  
; Sequence 12, Application US/09619740  
; Patent No. 6544946  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lasser, Gerald W.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE

; FILE REFERENCE: 99-12C3

; CURRENT APPLICATION NUMBER: US/09/619,740

; CURRENT FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/253,604

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: 09/444,794

; PRIOR FILING DATE: 1999-11-22

; PRIOR APPLICATION NUMBER: 09/506,855

; PRIOR FILING DATE: 2000-02-17

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 12

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide ZC13651

US-09-619-740-12

Query Match 74.0%; Score 14.8; DB 4; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CTTGTCTCCACGGGTT 20  
|||||

Db 1 CTTGTCTCCACGGTTT 18  
|||||

## RESULT 8

US-09-619-740-15/c  
; Sequence 15, Application US/09619740  
; Patent No. 6544946  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lasser, Gerald W.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE

; FILE REFERENCE: 99-12C3

; CURRENT APPLICATION NUMBER: US/09/619,740

; CURRENT FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/253,604

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: 09/444,794

; PRIOR FILING DATE: 1999-11-22

; PRIOR APPLICATION NUMBER: 09/506,855

; PRIOR FILING DATE: 2000-02-17

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 15

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Oligonucleotide ZC13650

US-09-619-740-15

Query Match 74.0%; Score 14.8; DB 4; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

CTTGTCCTCCACGGTT 20  
|||||  
TTTGTCCTCCACGGTT 3

2 Application US/09506852  
56499

MATION:

heppard, Paul O.

ENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

CE: 97-30

ICATION NUMBER: US/09/506,852

NG DATE: 2000-02-17

ICATION NUMBER: 60/053,154

NG DATE: 1997-07-18

Q ID NOS: 44

stSEQ for Windows Version 3.0

rtificial Sequence

MATION: Oligonucleotide ZC13651

2

74.0%; Score 14.8; DB 4; Length 20;

milarity 88.9%; Pred. No. 1.7e+02;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTTGTCCTCCACGGTT 20

|||||

TTTGTCCTCCACGGTT 18

5/c

Application US/09506852

66499

MATION:

heppard, Paul O.

ENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

CE: 97-30

ICATION NUMBER: US/09/506,852

NG DATE: 2000-02-17

ICATION NUMBER: 60/053,154

NG DATE: 1997-07-18

Q ID NOS: 44

stSEQ for Windows Version 3.0

rtificial Sequence

MATION: Oligonucleotide ZC13650

5

74.0%; Score 14.8; DB 4; Length 20;

milarity 88.9%; Pred. No. 1.7e+02;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTTGTCCTCCACGGTT 20

|||||

TTTGTCCTCCACGGTT 3

-2/c

Application US/09268544B

110710

MATION:

Jederman, Seth

APPLICANT: van Eyndhoven, Winfried  
TITLE OF INVENTION: TRAF-3 Deletion Isoforms And Uses Thereof  
FILE REFERENCE: 0575-58732  
CURRENT APPLICATION NUMBER: US/09/268,544B  
CURRENT FILING DATE: 1999-03-11  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 38  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Forwar  
OTHER INFORMATION: Primer or Polymerase Chain Reaction.  
US-09-268-544B-2

Query Match 72.0%; Score 14.4; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 2.9e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0;

QY 2 TCCTGTCTCTCCACGG 17

|||||

Db 32 TACTGTCTCTCCACGG 17

RESULT 12

US-08-138-608-44

Sequence 44, Application US/08138608

Patent No. 5407795

GENERAL INFORMATION:

APPLICANT: Kolberg, Janice A.

APPLICANT: Shen, Lu-Ping

APPLICANT: Urdea, Michael S.

TITLE OF INVENTION: CMV PROBES FOR USE IN SOLUTION

TITLE OF INVENTION: PHASE SANDWICH HYBRIDIZATION ASSAYS

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/138,608

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/813,590

FILING DATE: 23-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Thomas E. Clotetti

REGISTRATION NUMBER: 21,013

REFERENCE/DOCKET NUMBER: 22300-20236.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-813-5600

TELEFAX: 415-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-138-608-44

Query Match 70.0%; Score 14; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;

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us-10-090-326-7.max.rni

Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
TTGTCTCCACG 16  
|||||  
TTGTCTCCACG 31

plication US/08891292A  
2892  
ATION:  
arany, Francis  
uo, Jianying  
hanna, Marilyn  
ergstrom, Donald E.  
ATION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFFERENCES BY  
TION: LIGASE DETECTION REACTION  
E: 19603/457  
3 DATE: 1997-07-10  
TION NUMBER: 60/022,535  
DATE: 1996-07-19  
ID NOS: 96  
tentIn Ver. 2.1

tificial Sequence

ATION: Description of Artificial Sequence: Primer for  
ATION: PCR or LDR

67.0%; Score 13.4; DB 4; Length 29;  
ilarity 93.3%; Pred. No. 8.6e+02;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
TTGTCTCCACG 17  
|||||  
TTGTCTCCACG 28

plication US/08891292A  
2892  
ATION:  
arany, Francis  
uo, Jianying  
hanna, Marilyn  
ergstrom, Donald E.  
ATION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFFERENCES BY  
TION: LIGASE DETECTION REACTION  
E: 19603/457  
ATION NUMBER: US/08/891,292A  
G DATE: 1997-07-10  
TION NUMBER: 60/022,535  
DATE: 1996-07-19  
ID NOS: 96  
tentIn Ver. 2.1

tificial Sequence

ATION: Description of Artificial Sequence: Primer for  
ATION: PCR or LDR  
asure  
10)  
ATION: N at position 10 is either A, C, G, or T

Query Match 67.0%; Score 13.4; DB 4; Length 29;  
Best Local Similarity 93.3%; Pred. No. 8.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;  
QY 3 CCTGTCTCCACGG 17  
|||||  
Db 14 CCTGTCTCCACGG 28

RESULT 15  
US-09-927-737C-5  
; Sequence 5, Application US/09927737C  
; Patent No. 6576453  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Luo, Jianying  
; APPLICANT: Khanna, Marilyn  
; APPLICANT: Bergstrom, Donald E.  
; TITLE OF INVENTION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFFE  
; FILE REFERENCE: 19603/459  
; CURRENT APPLICATION NUMBER: US/09/927,737C  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/022,535  
; PRIOR FILING DATE: 1996-07-19  
; PRIOR APPLICATION NUMBER: 08/891,292  
; PRIOR FILING DATE: 1997-07-19  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer f  
; OTHER INFORMATION: PCR or LDR  
US-09-927-737C-5

Query Match 67.0%; Score 13.4; DB 4; Length 29;  
Best Local Similarity 93.3%; Pred. No. 8.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;  
QY 3 CCTGTCTCCACGG 17  
|||||  
Db 14 CCTGTCTCCACGG 28

RESULT 16  
US-09-927-737C-7  
; Sequence 7, Application US/09927737C  
; Patent No. 6576453  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Luo, Jianying  
; APPLICANT: Khanna, Marilyn  
; APPLICANT: Bergstrom, Donald E.  
; TITLE OF INVENTION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFFE  
; FILE REFERENCE: 19603/459  
; CURRENT APPLICATION NUMBER: US/09/927,737C  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/022,535  
; PRIOR FILING DATE: 1996-07-19  
; PRIOR APPLICATION NUMBER: 08/891,292  
; PRIOR FILING DATE: 1997-07-19  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer :

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ATTENTION: PCR or LDR

asure

10)

ATTENTION: N at position 10 is either A, C, G, or T

67.0%; Score 13.4; DB 4; Length 29;

ilarity 93.3%; Pred. No. 8.6e+02;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TTGTGCTCCACGG 17

|||||

TTGTGCTCCACGG 28

/c  
pplication US/08860165A  
34557

ATION:

DWARDS, Stirling John

OX, John Cooper

BBB, Elizabeth Ann

RAZER, Ian

ENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

JE: 17227/130

ICATION NUMBER: US/08/860,165A

NG DATE: 1997-09-22

ICATION NUMBER: PCT/AU95/00868

NG DATE: 1995-12-20

ICATION NUMBER: AU PN0157

NG DATE: 1994-12-20

Q ID NOS: 15

-entIn Ver. 2.0

rtificial Sequence

ATION: Description of Artificial Sequence: Primer

66.0%; Score 13.2; DB 3; Length 30;

ilarity 83.3%; Pred. No. 1.1e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCCTTGCTCTCCACGG 18

|||||

TCCTCTCTCTCCCGGG 3

/c

pplication US/09358645

03128

ATION:

BBB, Elizabeth Ann

DWARDS, Stirling John

ENTION: IMPROVED METHOD FOR PROTEIN EXPRESSION

CE: 017227/0145

ICATION NUMBER: US/09/358,645

NG DATE: 1999-07-23

ICATION NUMBER: US 08/860,165

NG DATE: 1997-09-22

ICATION NUMBER: PCT/AU95/00868

NG DATE: 1995-12-20

ICATION NUMBER: AU PN 0157/94

NG DATE: 1994-12-20

Q ID NOS: 12

-tentIn Ver. 2.0

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide used for PCR amplification  
US-09-358-645-8

Query Match 66.0%; Score 13.2; DB 4; Length 30;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 ATCCTTGCTCTCCACGG 18

|||||

Db 20 ATCCTCTCTCTCCCGGG 3

RESULT 19

US-09-359-382-8/c

; Sequence 8, Application US/09359382

; Patent No. 6306397

; GENERAL INFORMATION:

; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper

; APPLICANT: WEBB, Elizabeth Ann

; APPLICANT: FRAZER, Ian

; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

; FILE REFERENCE: 017227/0148

; CURRENT APPLICATION NUMBER: US/09/359,382

; CURRENT FILING DATE: 1999-07-23

; EARLIER APPLICATION NUMBER: US 08/860,165

; EARLIER FILING DATE: 1997-09-22

; EARLIER APPLICATION NUMBER: PCT/AU95/00868

; EARLIER FILING DATE: 1995-12-20

; EARLIER APPLICATION NUMBER: AU PN0157/94

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 30

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: Oligonucleotide used for PCR amplification

US-09-359-382-8

Query Match 66.0%; Score 13.2; DB 4; Length 30;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 ATCCTTGCTCTCCACGG 18

|||||

Db 20 ATCCTCTCTCTCCCGGG 3

RESULT 20

US-08-239-889A-2

; Sequence 2, Application US/08239889A

; Patent No. 5677277

; GENERAL INFORMATION:

; APPLICANT: Yatsu, Frank M., Alam, Nargis A.; and Alam, Syed S

; TITLE OF INVENTION: A No. 5677277el Brain Endothelial Cell Pr

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dr. Benjamin A. Adler

; STREET: 8011 Candle Lane

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

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SYSTEM: Macintosh  
Microsoft Word for Macintosh  
LOCATION DATA:  
ON NUMBER: US/08/239,889A  
TE: May 9, 1994  
ACTION: 514  
ENT INFORMATION:  
ler, Dr. Benjamin A.  
ION NUMBER: 35,423  
/DOCKET NUMBER: D5707  
CATION INFORMATION:  
: 713-777-2321  
713-777-6908  
OR SEQ ID NO: 2:  
ARACTERISTICS:  
32  
cleic acid  
SS: double  
linear  
PE: other nucleic acid  
L: No  
No  
URCE:  
L ISOLATE:  
NTAL STAGE:  
PE:  
:  
:  
ilarity 66.0%; Score 13.2; DB 1; Length 32;  
ilarity 83.3%; Pred. No. 1.1e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
CCTTGTCTCTCCACGGG 18  
|||||  
CCTTCTCTCCACGGG 32  
plication PC/TUS9505659  
MATION:  
Yatsu, Frank M.; Alam, Nargis A.; and  
Alam, Syed S.  
VENTION: A Novel Brain Endothelial Cell  
VENTION: Protein And Methods For Its Use  
SEQUENCES: 5  
NCE ADDRESS:  
: James F. Weiler, Attorney-at-Law  
One Riverway, Suite 1560  
uston  
exas  
USA  
56  
ADABLE FORM:  
PE: DS, HD 1.44 Mb/1.44 Mo  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
WordPerfect 6.0  
LOCATION DATA:  
ON NUMBER: PCT/US95/05659  
TE: 08.05.95 (8 May 1995)  
ACTION:  
ENT INFORMATION:  
iler, James F.  
ION NUMBER: 16,040  
/DOCKET NUMBER: D-5707 PCT  
CATION INFORMATION:  
: 713-626-9646  
713-963-5833

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: other nucleic acid  
HYPOTHETICAL: No  
ANTI-SENSE: No  
ORIGINAL SOURCE:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
PCT-US95-05659-2  
Query Match 66.0%; Score 13.2; DB 5; Length 32;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
Qy 1 ATCCTTGTCTCTCCACGGG 18  
|||||  
Db 15 ATCCTTGTCTCTCCACGGG 32  
RESULT 22  
US-09-422-978-1000  
; Sequence 1000, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Coher, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a b  
; FILE REFERENCE: GENSET.020CEI  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 1000  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 99-18777-130 : polymorphic base C or T  
US-09-422-978-1000  
Query Match 66.0%; Score 13.2; DB 4; Length 47;  
Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
Qy 2 TCCTTGTCTCTCCACGGGT 19  
|||||  
Db 2 TCCTTGTCTCTCGAAGGT 19  
RESULT 23  
US-09-621-976-13666/c  
; Sequence 13666, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.

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Siordano, J.Y.  
ENTION: ESTs and Encoded Human Proteins.  
TE: GENSET.054PR2  
ICATION NUMBER: US/09/621,976  
NG DATE: 2000-07-21  
2 ID NOS: 19335  
tent.pm  
66

omo sapiens  
3666

66.0%; Score 13.2; DB 4; Length 55;  
ilarity 83.3%; Pred. No. 1.2e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CCTTGCTCTCCACGGGT 19  
|||||  
CCTCCTCTCCACGGGT 1

91 Application US/08859998  
94076

RMATION:  
Chenchik, Alex  
Jokhadze, George  
Bibilashvilli, Robert  
NVENTION: METHOD OF ASSAYING DIFFERENTIAL  
NVENTION: EXPRESSION  
SEQUENCES: 1375  
ENCE ADDRESS:  
E: Fish & Richardson, P.C.  
2200 Sand Hill Road, Suite 100  
enlo Park  
CA

US  
025  
EADABLE FORM:  
YPE: Diskette  
: IBM Compatible  
3 SYSTEM: Windows95  
PLICATION DATA:  
ION NUMBER: US/08/859,998  
ATE: 21-MAY-1997  
ATION: 435  
ICATION DATA:  
ION NUMBER:  
ENT INFORMATION:  
ield, Bret E.  
ION NUMBER: 37,620  
E/DOCKET NUMBER: 09096/002001  
ICATION INFORMATION:  
E: 415-322-5070  
415-854-0875  
FOR SEQ ID NO: 991:  
HARACTERISTICS:  
28 base pairs  
ucleic acid  
NESS: single  
: linear  
YPE: DNA

FORMATION: oligonucleotide primer  
91

64.0%; Score 12.8; DB 2; Length 28;  
ilarity 87.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCCTTGCTCTCCACGG 17  
|||||  
DB 9 TCCTTGACCTCCACGG 24  
|||||

RESULT 25

US-09-225-928-991  
; Sequence 991, Application US/09225928  
; Patent No. 6352829  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; Jokhadze, George  
; Bibilashvilli, Robert  
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
; EXPRESSION  
; NUMBER OF SEQUENCES: 1375  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94025

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,928  
FILING DATE: 05-Jan-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/859,998  
FILING DATE: 21-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Field, Bret E.  
REGISTRATION NUMBER: 37,620  
REFERENCE/DOCKET NUMBER: 09096/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-322-5070  
TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 991:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
OTHER INFORMATION: oligonucleotide primer  
SEQUENCE DESCRIPTION: SEQ ID NO: 991:  
US-09-225-928-991

Query Match 64.0%; Score 12.8; DB 4; Length 28;  
Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 2 TCCTTGCTCTCCACGG 17  
|||||  
DB 9 TCCTTGACCTCCACGG 24  
|||||

RESULT 26

US-09-225-201B-991  
; Sequence 991, Application US/09225201B  
; Patent No. 6489455  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; Jokhadze, George  
; Bibilashvilli, Robert  
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL

64.0%; Score 12.8; DB 2; Length 28;  
ilarity 87.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

EXPRESSION

OF SEQUENCES: 1375  
 ONDENSE ADDRESS:  
 DRESSEE: Fish & Richardson, P.C.  
 RET: 2200 Sand Hill Road, Suite 100  
 TY: Menlo Park  
 ATE: CA  
 UNTRY: US  
 P: 94025  
 R READABLE FORM:  
 DIUM TYPE: Diskette  
 MPUTER: IBM Compatible  
 ERATING SYSTEM: Windows95  
 FTWARE: FastSeq for Windows Version 2.0  
 APPLICATION DATA:  
 APPLICATION NUMBER: US/09/225,201B  
 LING DATE: 05-Jan-1999  
 ASSIFICATION: <Unknown>  
 APPLICATION DATA:  
 APPLICATION NUMBER: US/08/859,998  
 LING DATE: 21-MAY-1997  
 Y/AGENT INFORMATION:  
 ME: Field, Bret E.  
 GISTRATION NUMBER: 37,620  
 REFERENCE/DOCKET NUMBER: 09096/002001  
 MUNICATION INFORMATION:  
 TELEPHONE: 415-322-5070  
 LEFAX: 415-854-0875  
 FOR SEQ ID NO: 991:  
 E CHARACTERISTICS:  
 NGTH: 28 base pairs  
 PE: nucleic acid  
 RANDEDNESS: single  
 POLOGY: linear  
 E TYPE: DNA  
 HER INFORMATION: oligonucleotide primer  
 E DESCRIPTION: SEQ ID NO: 991:  
 91

ilarity 64.0%; Score 12.8; DB 4; Length 28;  
 Conservativity 87.5%; Pred. No. 1.7e+03;  
 Mismatches 0; Indels 3; Gaps 0;

CTTGCTCTCCACG 17  
 |||||  
 CTTGACCTCCACG 24

application US/08440103

0152  
 MATION:  
 Weiner, Amy J.  
 Houghton, Michael  
 VENTION: Immunoreactive Polypeptide Compositions  
 SEQUENCES: 45  
 NCE ADDRESS:  
 Chiron Corporation  
 4560 Horton Street  
 uryville  
 A  
 USA  
 08  
 ADABLE FORM:  
 PE: Floppy disk  
 IBM PC compatible  
 SYSTEM: PC-DOS/MS-DOS  
 Patent In Release #1.0, Version #1.25  
 LICATION DATA:  
 ON NUMBER: US/08/440,103  
 TE: 12-MAY-1995

CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/231,368  
 FILING DATE:  
 APPLICATION NUMBER: US 07/759,575  
 FILING DATE: 13-SEP-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McClung, Barbara G.  
 REGISTRATION NUMBER: 33,113  
 REFERENCE/DOCKET NUMBER: 0205.001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (510) 601-2708  
 TELEFAX: (510) 655-3542  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 45 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-440-103-12  
 Query Match 64.0%; Score 12.8; DB 1; Length 45;  
 Best Local Similarity 87.5%; Pred. No. 1.8e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0;  
 QY 1 ATCCCTGTCTCTCCACG 16  
 |||||  
 Db 28 ATCCCTGTCTCTCCACG 43  
 RESULT 28  
 US-08-440-542-12  
 Sequence 12, Application US/08440542  
 Patent No. 5670153  
 GENERAL INFORMATION:  
 APPLICANT: Weiner, Amy J.  
 APPLICANT: Houghton, Michael  
 TITLE OF INVENTION: Immunoreactive Polypeptide Compositions  
 NUMBER OF SEQUENCES: 45  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Chiron Corporation  
 STREET: 4560 Horton Street  
 CITY: Emeryville  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94608  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/440,542  
 FILING DATE: 12-MAY-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/231,368  
 FILING DATE:  
 APPLICATION NUMBER: US 07/759,575  
 FILING DATE: 13-SEP-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McClung, Barbara G.  
 REGISTRATION NUMBER: 33,113  
 REFERENCE/DOCKET NUMBER: 0205.001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (510) 601-2708  
 TELEFAX: (510) 655-3542  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 45 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single





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us-10-090-326-7.max.rni

CATION DATA:  
ON NUMBER: US/08/231,368  
TE: 13-SEP-1991  
ON NUMBER: US 07/759,575  
TE: 13-SEP-1991  
ENT INFORMATION:  
Clung, Barbara G.  
ION NUMBER: 33,113  
/DOCKET NUMBER: 0205.001  
CATION INFORMATION:  
: (510) 601-2708  
: (510) 655-3542  
OR SEQ ID NO: 12:  
ARACTERISTICS:  
45 base pairs  
cleic acid  
ESS: single  
linear  
PE: DNA (genomic)

64.0%; Score 12.8; DB 4; Length 45;  
ilarity 87.5%; Pred. No. 1.8e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

'CCTTGTCCTCCAG 16  
||| |||||  
'CCCTGTCCTCCAG 43

232/c  
Application US/09313294A  
'6212  
ATION:  
to, Laura Y.  
herman, Bradley K.  
ENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
E: PL-0017 US  
CATION NUMBER: US/09/313,294A  
G DATE: 1999-05-14  
ID NOS: 7600  
RL Program

a may

sc feature  
ATION: Incyte ID No. 6476212 700348015H1  
sure  
, 40, 47, 54-55  
ATION: a, t, c, g, or other  
.232

64.0%; Score 12.8; DB 4; Length 57;  
ilarity 82.4%; Pred. No. 1.8e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

'CCTTGTCCTCCAGG 17  
||| |||||  
'CAATGTCCTCCAGG 16

.96/c  
Application US/08758306  
17743  
INATION:  
Stinchcomb, Dan T.  
McSwiggen, James A.  
VENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: TREATMENT OF DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH  
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
NUMBER OF SEQUENCES: 1379  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,306  
FILING DATE: December 3, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/132  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1196:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: The letter "N" stands for the stem II  
OTHER INFORMATION: region of a HH ribozyme.  
US-08-758-306-1196

Query Match 63.0%; Score 12.6; DB 1; Length 27;  
Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0;

Oy 1 ATCCTTGTCCTCCAGGGTT 20  
||| |||||  
Db 25 ATCCTTTTCATCAGGTT 6

RESULT 34  
US-08-356-405-12/c  
Sequence 12, Application US/08356405  
Patent No. 5807691  
GENERAL INFORMATION:  
APPLICANT: Amlaiky, No. 5807691rdine  
APPLICANT: Boschert, Ursula  
APPLICANT: Hen, Rene  
APPLICANT: Flasseat, Jean-Luc  
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor  
TITLE OF INVENTION: Activity (5HT5A), Nucleic Acids Coding for  
TITLE OF INVENTION: Polypeptides and Uses Thereof  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3043  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA

126-0107  
READABLE FORM:  
TYPE: Floppy disk  
: IBM PC compatible  
3 SYSTEM: PC-DOS/MS-DOS  
: PatentIn Release #1.0, Version #1.25  
PLICATION DATA:  
ION NUMBER: US/08/356,405  
ATE:  
CATION: 435  
ICATION DATA:  
ION NUMBER: WO PCT/FR93/00650  
ATE: 29-JUN-1992  
ICATION DATA:  
ION NUMBER: FR 92/08081  
ATE: 01-JUL-1992  
GENT INFORMATION:  
mith, Julie K  
TION NUMBER: 38,619  
E/DOCKET NUMBER: EX92004-US  
ICATION INFORMATION:  
E: (610)454-3839  
FOR SEQ ID NO: 12:  
HARACTERISTICS:  
41 base pairs  
nucleic acid  
NESS: single  
: linear  
YPE: other nucleic acid  
: NO  
2  
63.0%; Score 12.6; DB 1; Length 41;  
milarity 78.9%; Pred. No. 2.2e+03;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
CCTTGCTCCTCCACGGGTT 20  
|||||  
CCTTCACCTCCACAGCTT 11  
plication US/08162597  
53225  
RMATION:  
CLARY, Douglas O.  
WESKAMP, Gisela  
AUSTIN, LeeAnn R.  
REICHARDT, Louis F.  
VENTION: ANTIBODIES THAT MIMIC ACTIONS OF  
SEQUENCES: 6  
ENCE ADDRESS:  
E: Townsend and Townsend Kourie and Crew  
Stewart Street Tower, One Market Plaza  
an Francisco  
California  
US  
105-1493  
READABLE FORM:  
TYPE: Floppy disk  
: IBM PC compatible  
3 SYSTEM: PC-DOS/MS-DOS  
: PatentIn Release #1.0, Version #1.25  
PLICATION DATA:  
ION NUMBER: US/08/162,597  
ATE: 03-DEC-1993  
CATION: 424  
GENT INFORMATION:  
eber, Ellen L.  
TION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 2307G-541  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-162-597-6  
Query Match 63.0%; Score 12.6; DB 1; Length 45;  
Best Local Similarity 78.9%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;  
QY 2 TCCTTGCTCCTCCACGGGTT 20  
|||||  
Db 24 TCCTTGCTCCTCCACGGGT 42  
RESULT 36  
US-09-770-949-6  
Sequence 6, Application US/09770949  
Patent No. 6656465  
GENERAL INFORMATION:  
APPLICANT: CLARY, Douglas O.  
WESKAMP, Gisela  
AUSTIN, LeeAnn R.  
REICHARDT, Louis F.  
TITLE OF INVENTION: ANTIBODIES THAT MIMIC ACTIONS OF  
NEUROTROPHINS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/770,949  
FILING DATE: 26-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,597  
FILING DATE: 03-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 2307G-541  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-770-949-6  
Query Match 63.0%; Score 12.6; DB 4; Length 45;  
Best Local Similarity 78.9%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0;

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us-10-090-326-7.max.rni

```
; FILE REFERENCE: 6763.US.01
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer R0838
US-09-769-863-4

Query Match      62.0%; Score 12.4; DB 4; Length 36;
Best Local Similarity 55.6%; Pred. No. 2.7e+03;
Matches 10; Conservative 6; Mismatches 2; Indels 0;

Qy      3 CCTGTCTCTCCACGGGT 20
        |||||:|:|:|:|:|:|
Db      28 CYTTCYACACAGT 11

RESULT 39
US-09-079-812E-8/C
; Sequence 8, Application US/09079812E
; Patent No. 6340575
; GENERAL INFORMATION:
; APPLICANT: Hollag, Gideon
; APPLICANT: Crompton, Anne
; APPLICANT: No. 6340575th, Anne
; APPLICANT: Sharma, Sanju
; APPLICANT: Roscoe, William
; TITLE OF INVENTION: Methods and Compositions for Treating Abnormal
; TITLE OF INVENTION: Growth Related to Unwanted Guanine Nucleotide
; TITLE OF INVENTION: Factor Activity
; FILE REFERENCE: 1028-US
; CURRENT APPLICATION NUMBER: US/09/079,812E
; CURRENT FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/049,879
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Oligonucleotide
US-09-079-812E-8

Query Match      61.0%; Score 12.2; DB 4; Length 21;
Best Local Similarity 82.4%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy      1 ATCCTGTCTCTCCACGG 17
        |||||:|:|:|:|:|
Db      21 ATCCTGTCTCTCCGCG 5

RESULT 40
US-08-477-877B-3/c
; Sequence 3, Application US/08477877B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latime, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhi
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
```

```
pplication US/08883795A
5607
NATION:
Delcuve, Genevieve
Awang, Gregor
VENTION: Recombinant DNA Molecules and Expression
VENTION: Vectors for Tissue Plasminogen Activator
SEQUENCES: 39
NCE ADDRESS:
: BERESKIN & PARR
40 King Street West
ronto
ntario
Canada
3Y2
ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
LICATON DATA:
ON NUMBER: US/08/883,795A
TE: 27-JUN-1997
ATION: 435
ENT INFORMATION:
avelle, Micheline
ION NUMBER: 40,261
/DOCKET NUMBER: 7841-062
CATION INFORMATION:
: (416) 364-7311
(416) 361-1398
OR SEQ ID NO: 21:
ABACTERISTICS:
52 base pairs
cleic acid
ESS: single
linear
PE: cDNA
URCE:
Homo sapiens
OURCE:
POS alpha
1

63.0%; Score 12.6; DB 2; Length 52;
ilarity 78.9%; Pred. No. 2.3e+03;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CTGTCTCTCCACGGGT 20
|||||:|:|:|:|:|
CTGGCTCCAGAGGT 50

plication US/09769863
5451
ATION:
bott Laboratories
tucker], Pradip
uang, Yung-Sheng
as, Tapas
hurmond, Jennifer
ereira, Suzette L.
ENTION: DESATURASE GENES AND USES THEREOF
```

368  
 SADBABLE FORM:  
 YPE: 3.5 inch diskette  
 : IBM PS/2  
 3 SYSTEM: MS-DOS  
 : WordPerfect 5.1  
 PLICATION DATA:  
 ION NUMBER: US/08/477,877B  
 ATE: 07-JUN-1995  
 CATION: 424  
 ION NUMBER: 08/407,009  
 ATE: 29-MAR-1995  
 ION NUMBER: 08/119,032  
 ATE: 09-SEP-1993  
 ION NUMBER: 08/027,008  
 ATE: 05-MAR-1993  
 GENT INFORMATION:  
 lstein, Elliot M.  
 TION NUMBER: 24,025  
 E/DOCKET NUMBER: 61750-146  
 ION INFORMATION:  
 E: 201-994-1700  
 201-994-1744  
 FOR SEQ ID NO: 3:  
 CHARACTERISTICS:  
 31 bases  
 ucleic acid  
 NESS: single  
 : linear  
 YPE: oligonucleotide  
 : PCR primer  
 3

milarity 61.0%; Score 12.2; DB 1; Length 31;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTCTCCACGGGTT 20  
 |||||  
 TGGACCTCCCGGGTT 1

3/c  
 plication US/08472281A  
 17311

RMATION:  
 Bazin, Herv  
 Latine, Dominique  
 NVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa  
 SEQUENCES: 96  
 ENCE ADDRESS:  
 E: Carella, Byrne, Bain, Gilfillan,  
 E: Cecchi, Stewart & Olstein  
 6 Becker Farm Road  
 Oseland  
 New Jersey  
 U.S.A.  
 068  
 RADABLE FORM:  
 YPE: 3.5 inch diskette  
 : IBM PS/2  
 G SYSTEM: MS-DOS  
 : WordPerfect 5.1  
 PLICATION DATA:  
 ION NUMBER: US/08/472,281A  
 ATE: 07-JUN-1995  
 ION INFORMATION:  
 ION NUMBER: 08/407,009  
 ATE: 29-MAR-1995

APPLICATION NUMBER: 08/119,032  
 FILING DATE: 09-SEP-1993  
 APPLICATION NUMBER: 08/027,008  
 FILING DATE: 05-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Olstein, Elliot M.  
 REGISTRATION NUMBER: 24,025  
 REFERENCE/DOCKET NUMBER: 61750-142  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: oligonucleotide  
 FEATURE:  
 NAME/KEY: PCR primer  
 US-08-472-281A-3

Query Match 61.0%; Score 12.2; DB 1; Length 31;  
 Best Local Similarity 82.4%; Pred. No. 3.3e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 4 CTTGTCTCCACGGGTT 20  
 |||||  
 Db 17 CTGGACCTCCCGGGTT 1

## RESULT 42

US-08-477-989B-3/c  
 ; Sequence 3, Application US/08477989B  
 ; Patent No. 5951983  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bazin, Herv  
 ; APPLICANT: Latine, Dominique  
 ; APPLICANT: Kaplan, Ruth  
 ; APPLICANT: Kieber-Emmons, Thomas  
 ; APPLICANT: Postema, Christina E.  
 ; APPLICANT: White-Scharf, Mary  
 ; TITLE OF INVENTION: LO-CD2a Antibody and Uses  
 ; TITLE OF INVENTION: Thereof for Inhibiting  
 ; TITLE OF INVENTION: T-Cell Activation and  
 ; TITLE OF INVENTION: Proliferation  
 ; NUMBER OF SEQUENCES: 96  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
 ; ADDRESSEE: Cecchi, Stewart & Olstein  
 ; STREET: 6 Becker Farm Road  
 ; CITY: Roseland  
 ; STATE: New Jersey  
 ; COUNTRY: U.S.A.  
 ; ZIP: 07068  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch diskette  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/477,989B  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/407,009  
 ; FILING DATE: 29-MAR-1995  
 ; APPLICATION NUMBER: 08/119,032  
 ; FILING DATE: 09-SEP-1993  
 ; APPLICATION NUMBER: 08/027,008  
 ; FILING DATE: 05-MAR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Olstein, Elliot M.

ION NUMBER: 24,025  
/DOCKET NUMBER: 61750-147  
CATION INFORMATION:  
: 201-994-1700  
: 201-994-1744

OR SEQ ID NO: 3:  
ARACTERISTICS:  
31 bases  
cleic acid  
ESS: single  
linear  
PE: oligonucleotide

PCR primer

61.0%; Score 12.2; DB 2; Length 31;  
ilarity 82.4%; Pred. No. 3.3e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TGTCCTCCACGGTT 20  
GGACCTCCCGGTT 1

/c  
application US/08347792  
3925

ATION:  
Halazonetis, Thanos D.  
VENTION: p53 Proteins With Altered  
VENTION: Tetramerization Domains  
SEQUENCES: 37  
NCE ADDRESS:  
: Howson and Howson  
Spring House Corporate Cntr., PO Box 457  
ring House  
ennsylvania  
USA  
77

ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patent In Release #1.0, Version #1.25  
PLICATION DATA:  
ION NUMBER: US/08/347,792  
ATE: 530  
ENT INFORMATION:  
k, Mary E.  
ION NUMBER: 31,215  
/DOCKET NUMBER: WST58USA  
CATION INFORMATION:  
: 215-540-9206  
215-540-5818  
OR SEQ ID NO: 23:  
ARACTERISTICS:  
32 base pairs  
cleic acid  
ESS: single  
PE: DNA (genomic)

61.0%; Score 12.2; DB 1; Length 32;  
ilarity 82.4%; Pred. No. 3.4e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCCTTGCTCCACGG 17  
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ACCTTGCTCCACGG 7

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US-08-431-357-23/C  
; Sequence 23, Application US/08431357  
; Patent No. 5721340  
; GENERAL INFORMATION:  
; APPLICANT: Halazonetis, Thanos D.  
; TITLE OF INVENTION: p53 Proteins With Altered  
; TITLE OF INVENTION: Tetramerization Domains  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr., PO Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/431,357  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/347,792  
; FILING DATE: 28-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: WST58USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-540-9206  
; TELEFAX: 215-540-5818  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-431-357-23  
Query Match 61.0%; Score 12.2; DB 1; Length 32;  
Best Local Similarity 82.4%; Pred. No. 3.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

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Db 23 AACCTTGCTCCACGG 7

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; Sequence 23, Application PC/TUS9515353  
; GENERAL INFORMATION:  
; APPLICANT: The Wistar Institute of Anatomy  
; APPLICANT: and Biology  
; APPLICANT: Halazonetis, Thanos D.  
; TITLE OF INVENTION: p53 Proteins With Altered  
; TITLE OF INVENTION: Tetramerization Domains  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: Spring House Corporate Cntr., PO Box 457  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19477  
; COMPUTER READABLE FORM:

09:38:26 2004

us-10-090-326-7.max.rni

PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patent In Release #1.0, Version #1.30  
PLICATION DATA:  
ION NUMBER: PCT/US95/15353  
ATE:  
ATION:  
ICATION DATA:  
ION NUMBER: US 08/347,792  
ATE: 28-NOV-1994  
ICATION DATA:  
ION NUMBER: US 08/431,357  
ATE: 28-APR-1995  
ICATION DATA:  
ION NUMBER: US 08/456,623  
ATE: 01-JUN-1995  
ENT INFORMATION:  
ak, Mary E.  
ION NUMBER: 31,215  
3/DOCKET NUMBER: WST58CPCT  
ICATION INFORMATION:  
3: 215-540-9206  
FOR SEQ ID NO: 23:  
CHARACTERISTICS:  
32 base pairs  
nucleic acid  
NESS: single  
: linear  
YPE: DNA (genomic)  
23

61.0%; Score 12.2; DB 5; Length 32;  
ilarity 82.4%; Pred. No. 3.4e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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623 secs

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56.0	25	14	US-10-098-263B-32561	Sequence 32561, A	C 468	11.2	56.0	60	10	US-09-908-975-16166	Sequen
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56.0	25	14	US-10-098-263B-44881	Sequence 44881, A	C 470	11.2	56.0	60	10	US-09-908-975-19221	Sequen
56.0	25	14	US-10-098-263B-60390	Sequence 60390, A	C 471	11.2	56.0	60	10	US-09-908-975-19877	Sequen
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56.0	25	14	US-10-098-263B-83942	Sequence 83942, A	C 473	11	55.0	18	10	US-09-944-049-43	Sequen
56.0	25	14	US-10-098-263B-84773	Sequence 84773, A	C 474	11	55.0	18	15	US-10-388-263-317	Sequen
56.0	25	14	US-10-098-263B-84774	Sequence 84774, A	C 475	11	55.0	20	9	US-09-791-406-62	Sequen
56.0	25	14	US-10-098-263B-95670	Sequence 95670, A	C 476	11	55.0	20	10	US-09-850-948-15	Sequen
56.0	25	14	US-10-098-263B-96767	Sequence 96767, A	C 477	11	55.0	20	10	US-09-954-556-71	Sequen
56.0	25	14	US-10-098-263B-103242	Sequence 103242, A	C 478	11	55.0	20	10	US-09-954-679-64	Sequen
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56.0	25	14	US-10-098-263B-106205	Sequence 106205, A	C 481	11	55.0	20	14	US-10-128-714-4014	Sequen
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56.0	25	14	US-10-098-263B-119858	Sequence 119858, A	C 483	11	55.0	20	15	US-10-283-762-5351	Sequen
56.0	25	14	US-10-061-201-3153	Sequence 3153, Ap	C 484	11	55.0	21	15	US-10-085-198-461	Sequen
56.0	25	14	US-10-023-634-104	Sequence 332, App	C 485	11	55.0	22	9	US-09-956-636A-4	Sequen
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56.0	25	14	US-09-814-786-40	Sequence 40, Appl	C 494	11	55.0	25	14	US-10-215-112-2600	Sequen
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56.0	25	14	US-10-315-515-162	Sequence 162, App	C 496	11	55.0	25	14	US-10-098-263B-2700	Sequen
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56.0	25	14	US-10-422-934-32	Sequence 949, App	C 498	11	55.0	25	14	US-10-098-263B-51731	Sequen
56.0	25	14	US-09-377-885A-16	Sequence 16, Appl	C 499	11	55.0	25	14	US-10-098-263B-51732	Sequen
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## ALIGNMENTS

58079  
 '9, Application US/10098263B  
 Co. US20030104410A1  
 INVENTOR: Michael  
 Hittman, Michael  
 TITLE: Human Microarray  
 DATE: 2001-03-16  
 FILING DATE: 2003-01-08  
 PUBLICATION NUMBER: US/10/098,263B  
 NG DATE: 2003-01-08  
 APPLICATION NUMBER: 09/276,759  
 DATE: 2001-03-16  
 Q ID NOS: 131066  
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ATCCTGTCCTCCAC 15  
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 Application US/0991176B

; Patent No. US20020156243A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; TITLE OF INVENTION: ANTIBODIES THAT BIND AN  
 ; FILE REFERENCE: 97-30D1  
 ; CURRENT APPLICATION NUMBER: US/09/911,176B  
 ; CURRENT FILING DATE: 2001-07-23  
 ; PRIOR FILING DATE: 1998-07-17  
 ; PRIOR APPLICATION NUMBER: 09/118,408  
 ; PRIOR FILING DATE: 1997-07-18  
 ; PRIOR APPLICATION NUMBER: 60/053,154  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 12  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Oligonucleotide ZC13651  
 US-09-911-176B-12  
 Query Match 74.0%; Score 14.8; DB 9; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0;  
 Qy 3 CCTGTGCTCCACGGTT 20  
 Db 1 CTTGTCTCCACGGTT 18  
 RESULT 3  
 US-09-911-176B-15/c  
 ; Sequence 15, Application US/09911176B  
 ; Patent No. US20020156243A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; TITLE OF INVENTION: ANTIBODIES THAT BIND AN  
 ; FILE REFERENCE: 97-30D1  
 ; CURRENT APPLICATION NUMBER: US/09/911,176B  
 ; CURRENT FILING DATE: 2001-07-23  
 ; PRIOR FILING DATE: 1998-07-17  
 ; PRIOR APPLICATION NUMBER: 60/053,154  
 ; PRIOR FILING DATE: 1997-07-18  
 ; NUMBER OF SEQ ID NOS: 52  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 15  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Oligonucleotide ZC13650  
 US-09-911-176B-15  
 Query Match 74.0%; Score 14.8; DB 9; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0;  
 Qy 3 CCTGTGCTCCACGGTT 20  
 Db 20 CTTGTCTCCACGGTT 3

RESULT 4  
 US-10-180-762-12  
 ; Sequence 12, Application US/10180762  
 ; Publication No. US20030022838A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Lasser, Gerald W.  
 ; APPLICANT: Bishop, Paul D.

L 09:38:26 2004

us-10-090-326-7.max.rnpb

NTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION  
E: 99-12C3  
CATION NUMBER: US/10/180,762  
IG DATE: 2002-06-25  
TION NUMBER: 09/253,604  
DATE: 1999-02-19  
TION NUMBER: 09/444,794  
DATE: 1999-11-22  
TION NUMBER: 09/506,855  
DATE: 2000-02-17  
ID NOS: 55  
tSEQ for Windows Version 3.0

tificial Sequence

ATION: Oligonucleotide ZC13651

74.0%; Score 14.8; DB 14; Length 20;  
ilarity 88.9%; Pred. No. 1.6e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCTCCACGGTT 20  
|||||  
TTGTCTCTCCACGGTT 18

/c  
pplication US/10180762  
US2003002838A1  
ATION:  
eppard, Paul O.  
isher, Gerald W.  
ishop, Paul D.  
NTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION  
E: 99-12C3

CATION NUMBER: US/10/180,762  
IG DATE: 2002-06-25  
TION NUMBER: 09/253,604  
DATE: 1999-02-19  
TION NUMBER: 09/444,794  
DATE: 1999-11-22  
TION NUMBER: 09/506,855  
DATE: 2000-02-17  
ID NOS: 55  
tSEQ for Windows Version 3.0

tificial Sequence

ATION: Oligonucleotide ZC13650

74.0%; Score 14.8; DB 14; Length 20;  
ilarity 88.9%; Pred. No. 1.6e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCTCCACGGTT 20  
|||||  
TTGTCTCTCCACGGTT 3

pplication US/10241258  
US20030078206A1  
ATION:  
eppard, Paul O.  
asser, Gerald W.

; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
; FILE REFERENCE: 99-12  
; CURRENT APPLICATION NUMBER: US/10/241,258  
; CURRENT FILING DATE: 2002-09-10  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC13651  
US-10-241-258-12

Query Match 74.0%; Score 14.8; DB 14; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CTTGTCTCTCCACGGTT 20  
|||||  
DB 1 CTTGTCTCTCCACGGTT 18

RESULT 7  
US-10-241-258-15/c  
; Sequence 15, Application US/10241258  
; Publication No. US20030078206A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lasser, Gerald W.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
; FILE REFERENCE: 99-12  
; CURRENT APPLICATION NUMBER: US/10/241,258  
; CURRENT FILING DATE: 2002-09-10  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC13650  
US-10-241-258-15

Query Match 74.0%; Score 14.8; DB 14; Length 20;  
Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 3 CTTGTCTCTCCACGGTT 20  
|||||  
DB 20 CTTGTCTCTCCACGGTT 3

RESULT 8  
US-10-194-370-53  
; Sequence 53, Application US/10194370  
; Publication No. US20030096270A1  
; GENERAL INFORMATION:  
; APPLICANT: Paul Andrew Whittaker et al  
; TITLE OF INVENTION: Disease-Associated Gene  
; FILE REFERENCE: Case 4-32067A/HO 41  
; CURRENT APPLICATION NUMBER: US/10/194,370  
; CURRENT FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens

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us-10-090-326-7.max.rnpb

```
3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC13650
US-10-360-186-15

Query Match      74.0%; Score 14.8; DB 14; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

TCCTGTCTCTCCACGGG 18
|||||
TCCTGTCTCTCCACTGG 20

2
Application US/10360186
O. US20030144208A1
MATION:
heppard, Paul O.
Lasser, Gerald W.
Bishop, Paul D.
ENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
CE: 99-12C3
ICATION NUMBER: US/10/360,186
NG DATE: 2003-02-07
ATION NUMBER: US/09/619,740
DATE: 2000-07-19
ATION NUMBER: 09/253,604
DATE: 1999-02-19
ATION NUMBER: 09/444,794
DATE: 1999-11-22
ATION NUMBER: 09/506,855
DATE: 2000-02-17
Q ID NOS: 55
stSEQ for Windows Version 3.0

rtificial Sequence
MATION: Oligonucleotide ZC13651
2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC13651
US-10-392-531-12

Query Match      74.0%; Score 14.8; DB 14; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

CTTGTCCTCTCCACGGGTT 20
|||||
TTTGTCCTCTCCACGGTTT 18

5/c
Application US/10360186
O. US20030144208A1
MATION:
heppard, Paul O.
Lasser, Gerald W.
Bishop, Paul D.
ENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
CE: 99-12C3
ICATION NUMBER: US/10/360,186
NG DATE: 2003-02-07
ATION NUMBER: US/09/619,740
DATE: 2000-07-19
ATION NUMBER: 09/253,604
DATE: 1999-02-19
ATION NUMBER: 09/444,794
DATE: 1999-11-22
ATION NUMBER: 09/506,855
DATE: 2000-02-17
Q ID NOS: 55
stSEQ for Windows Version 3.0
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC13650
US-10-360-186-15

Query Match      74.0%; Score 14.8; DB 14; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY      3 CCTTGTCCTCTCCACGGGTT 20
Db      20 CTTGTCTCTCCACGGTTT 3

RESULT 11
US-10-392-531-12
; Sequence 12, Application US/10392531
; Publication No. US20030176658A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-30
; CURRENT APPLICATION NUMBER: US/10/392,531
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US/09/506,852
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/053,154
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC13651
US-10-392-531-12

Query Match      74.0%; Score 14.8; DB 14; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY      3 CCTTGTCCTCTCCACGGGTT 20
Db      1 CTTGTCTCTCCACGGTTT 18

RESULT 12
US-10-392-531-15/c
; Sequence 15, Application US/10392531
; Publication No. US20030176658A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-30
; CURRENT APPLICATION NUMBER: US/10/392,531
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US/09/506,852
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/053,154
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC13650
US-10-392-531-15
```



74.0%; Score 14.8; DB 14; Length 20;  
 ilarity 88.9%; Pred. No. 1.6e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCCACGGTT 20  
 |||||  
 TTGTCTCCACGGTTT 3

pplication US/10392706  
 . US2003017659A1

epard, Paul O.  
 NITION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
 E: 97-30  
 CATION NUMBER: US/10/392,706  
 G DATE: 2003-03-20  
 TION NUMBER: US/09/506,852  
 DATE: 2000-02-17  
 TION NUMBER: EARLIER APPLICATION NUMBER: 60/053,154  
 DATE: EARLIER FILING DATE: 1997-07-18  
 ID NOS: 44  
 tSEQ for Windows Version 3.0

tificial Sequence

ATION: Oligonucleotide ZC13651

74.0%; Score 14.8; DB 14; Length 20;  
 ilarity 88.9%; Pred. No. 1.6e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCCACGGTT 20  
 |||||  
 TTGTCTCCACGGTTT 18

/c  
 pplication US/10392706  
 . US2003017659A1

ATION:  
 epard, Paul O.  
 NITION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
 E: 97-30  
 CATION NUMBER: US/10/392,706  
 G DATE: 2003-03-20  
 TION NUMBER: US/09/506,852  
 DATE: 2000-02-17  
 TION NUMBER: EARLIER APPLICATION NUMBER: 60/053,154  
 DATE: EARLIER FILING DATE: 1997-07-18  
 ID NOS: 44  
 tSEQ for Windows Version 3.0

tificial Sequence

ATION: Oligonucleotide ZC13650

74.0%; Score 14.8; DB 14; Length 20;  
 ilarity 88.9%; Pred. No. 1.6e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTGTCTCCACGGTT 20  
 |||||  
 TTGTCTCCACGGTTT 3

RESULT 15  
 US-10-198-695-12  
 ; Sequence 12, Application US/10198695  
 ; Publication No. US20040014650A1  
 ; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Lasser, Gerald W.  
 ; APPLICANT: Bishop, Paul D.  
 ; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
 ; TITLE OF INVENTION: IMMUNE FUNCTION

; FILE REFERENCE: 99-12  
 ; CURRENT APPLICATION NUMBER: US/10/198,695  
 ; CURRENT FILING DATE: 2002-07-17  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 12  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Oligonucleotide ZC13651  
 US-10-198-695-12

Query Match 74.0%; Score 14.8; DB 15; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0;

Qy 3 CCITGTCTCCACGGTT 20  
 |||||  
 Db 1 CTTTGTCTCCACGGTTT 18

RESULT 16

US-10-198-695-15/c  
 ; Sequence 15, Application US/10198695  
 ; Publication No. US20040014650A1  
 ; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.  
 ; APPLICANT: Lasser, Gerald W.  
 ; APPLICANT: Bishop, Paul D.  
 ; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
 ; TITLE OF INVENTION: IMMUNE FUNCTION

; FILE REFERENCE: 99-12  
 ; CURRENT APPLICATION NUMBER: US/10/198,695  
 ; CURRENT FILING DATE: 2002-07-17  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 15  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Oligonucleotide ZC13650  
 US-10-198-695-15

Query Match 74.0%; Score 14.8; DB 15; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0;

Qy 3 CCITGTCTCCACGGTT 20  
 |||||  
 Db 20 CTTTGTCTCCACGGTTT 3

RESULT 17

US-10-098-263B-119019  
 ; Sequence 119019, Application US/10098263B  
 ; Publication No. US20030104410A1  
 ; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael  
 ; TITLE OF INVENTION: Human Microarray

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sox18 B primer
US-09-814-777A-70

Query Match      71.0%; Score 14.2; DB 9; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTGTGCTCTCCACGGGT 20
Db 19 TCCGTGCTCTCCACGGCT 1

RESULT 20
US-10-098-263B-76558/c
; Sequence 76558, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 76558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-76558

Query Match      71.0%; Score 14.2; DB 14; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTGTGCTCTCCACGGGT 20
Db 25 TCCGTGCTCTCCACGGCT 7

RESULT 21
US-10-098-263B-54313
; Sequence 54313, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 54313
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-54313

Query Match      69.0%; Score 13.8; DB 14; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 4 CTGTGCTCTCCACGGGT 20
Db 1 CTGTGCTCTCCACGGGT 17

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sox18 B primer
US-09-814-777A-70

Query Match      74.0%; Score 14.8; DB 14; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTCTGCTCTCCACGGGT 19
|||||
CTCTGCTCTCCACGGGT 24

/c
pplication US/09950902
20020127615A1
NATION:
ne Trustees of Columbia University in the City of
ENTION: TRAP-3 DELETION ISOFORMS AND USES THEREOF
TE: 58732-A-PCT
ICATION NUMBER: US/09/950,902
NG DATE: 2001-09-10
ATION NUMBER: PCT/US00/06503
DATE: 2000-03-10
ATION NUMBER: 03/268,544
DATE: 1999-03-11
ID NOS: 14
tentIn ver. 2.1

rtificial Sequence
NATION: Description of Artificial Sequence:forward primer
NATION: ZnRING

milarity 72.0%; Score 14.4; DB 9; Length 38;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CCTGTGCTCTCCACGG 17
ACTGTGCTCTCCACGG 17

70/c
Application US/09814777A
20020142415A1
NATION:
OPMAN, Peter Anthony
MUSCAT, George Eugene Orlando
ENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES AND METHODS OF USING THEM
CE: 21415-0003
ICATION NUMBER: US/09/814,777A
NG DATE: 2001-03-23
ATION NUMBER: AU P06457
DATE: 2000-03-24
Q ID NOS: 128
tentIn version 3.0
```

342  
Application US/09908975  
US20030165843A1  
ATION: JOSHAN, Avi  
VASSERMAN, Alon  
INTZ, Eli  
INTZ, Liat  
AIGLER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
TION: THAT POPULATE A TRANSCRIPTOME  
E: 36688-0005  
G DATE: 2001-07-20  
TION NUMBER: US 60/287,724  
DATE: 2001-05-02  
TION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
entIn version 3.0

mo sapiens  
342  
69.0%; Score 13.8; DB 10; Length 60;  
ilarity 88.2%; Pred. No. 4.5e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CCTTGCTCTCCACGG 17  
|||||  
CCTTGCTCTCTGG 36

/c  
Application US/09110716A  
0020034739A1

ATION: hrer, Robert I.  
hao, Chengquan  
asgow, Benjamin J.  
TION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS  
E: 22000-20596.00  
ATION NUMBER: US/09/110,716A  
G DATE: 1998-07-07  
ID NOS: 41  
entIn Ver. 2.0

tificial Sequence

ATION: Description of Artificial Sequence: primer

ilarity 68.0%; Score 13.6; DB 9; Length 24;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CCTTGCTCTCCACGGTT 20  
|||||  
ACCATGCTCTCCAGAGTT 2

38080  
Application US/10098263B  
US20030104410A1  
ATION: itzman, Michael

; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 58080  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-58080

Query Match 67.0%; Score 13.4; DB 14; Length 25;  
Best Local Similarity 93.3%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 1 ATCCTTGCTCTCCAC 15  
|||||  
Db 3 ATCCTTGCTCCACC 17

RESULT 25

US-09-927-737-5  
; Sequence 5, Application US/09927737  
; Publication No. US20030082545A1  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Luo, Jianying  
; APPLICANT: Khanna, Marilyn  
; APPLICANT: Bergstrom, Donald E.  
; TITLE OF INVENTION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFF  
; TITLE OF INVENTION: LIGASE DETECTION REACTION  
; FILE REFERENCE: 19603/457  
; CURRENT APPLICATION NUMBER: US/09/927,737  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 08/891,292  
; PRIOR FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
; OTHER INFORMATION: PCR or LDR  
US-09-927-737-5

Query Match 67.0%; Score 13.4; DB 10; Length 29;  
Best Local Similarity 93.3%; Pred. No. 7.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 3 CCTTGCTCTCCACGG 17  
|||||  
Db 14 CCTTGCTCTCCACGG 28

RESULT 26

US-09-927-737-7  
; Sequence 7, Application US/09927737  
; Publication No. US20030082545A1  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Luo, Jianying  
; APPLICANT: Khanna, Marilyn  
; APPLICANT: Bergstrom, Donald E.  
; TITLE OF INVENTION: HIGH FIDELITY DETECTION OF NUCLEIC ACID DIFF  
; TITLE OF INVENTION: LIGASE DETECTION REACTION  
; FILE REFERENCE: 19603/457  
; CURRENT APPLICATION NUMBER: US/09/927,737  
; CURRENT FILING DATE: 2001-08-10

ATION NUMBER: 08/891,292  
DATE: 1997-07-10  
Q ID NOS: 96  
tentIn Ver. 2.1

## rtificial Sequence

MATION: Description of Artificial Sequence: Primer for  
MATION: PCR or LDR

10)  
MATION: N at position 10 is either A, C, G, or T

67.0%; Score 13.4; DB 10; Length 29;  
milarity 93.3%; Pred. No. 7.3e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CTGTGCTCCACGG 17  
|||||  
CTGTGCTCCACGG 28

451  
Application US/10131827  
o. US20040009479A1

MATION:  
ohlgenuth, Jay

Fry, Kirk  
Woodward, Robert

Ly, Ngoc

ENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

ENTON: CHRONIC INFLAMMATORY DISEASES

CE: 50661200120

ICATION NUMBER: US/10/131,827

NG DATE: 2002-09-06

ATION NUMBER: US 10/006,290

DATE: 2001-10-22

ATION NUMBER: US 60/296,764

DATE: 2001-06-08

Q ID NOS: 9090

tentIn version 3.1

1

omo sapiens

451

67.0%; Score 13.4; DB 15; Length 50;  
milarity 93.3%; Pred. No. 7e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGTCTCCACGGGT 19  
|||||  
TGTCTCCACGGGT 25

.03/c

Application US/10148835

o. US20030207380A1

MATION:

AITO et al.

ENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION

ICE: 2185-0648P

ICATION NUMBER: US/10/148,835

NG DATE: 2002-10-11

Q ID NOS: 213

tentIn Ver. 2.0

1

LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Designed  
OTHER INFORMATION: oligonucleotide primer for PCR  
US-10-148-835-103

Query Match 66.0%; Score 13.2; DB 15; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTTGCTCTCCACGGGT 19  
|||||  
DB 20 TCCGTCTCTCCACGGAT 3

## RESULT 29

US-10-098-263B-119020

Sequence 119020, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 119020

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-119020

Query Match 66.0%; Score 13.2; DB 14; Length 25;  
Best Local Similarity 83.3%; Pred. No. 9.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCCTTGCTCTCCACGGGT 19  
|||||  
DB 7 TCCTTGACTCCACGGGT 24

## RESULT 30

US-10-349-143-1000

Sequence 1000, Application US/10349143

Publication No. US20040005584A1

GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Biallelic markers for use in constructing a

FILE REFERENCE: GENSET-020CP1

CURRENT APPLICATION NUMBER: US/10/349,143

CURRENT FILING DATE: 2003-01-21

PRIOR APPLICATION NUMBER: US/09/422,978

PRIOR FILING DATE: 1999-10-20

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,

PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,

PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 1000

LENGTH: 47

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: allele

ATION: 99-18777-130 : polymorphic base C or T  
00

66.0%; Score 13.2; DB 15; Length 47;  
ilarity 83.3%; Pred. No. 8.6e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
CTTGCTCCTCCACGGGT 19  
|||||  
CTTCTCCTCGAGGGT 19

59/c  
Application US/09908975  
. US20030165843A1  
ATION:  
OSHAN, Avi  
ASSERMAN, Alon  
INTZ, Eli  
INTZ, Liat  
AIGLER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
TION: THAT POPULATE A TRANSCRIPTOME  
E: 36688-0005  
CATION NUMBER: US/09/908,975  
G DATE: 2001-07-20  
TION NUMBER: US 60/287,724  
DATE: 2001-05-02  
TION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
entIn version 3.0

mo sapiens  
59

66.0%; Score 13.2; DB 10; Length 60;  
ilarity 83.3%; Pred. No. 8.6e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
CTTGCTCCTCCACGGGT 19  
|||||  
CTTGCTCCTCACTGGT 3

055/c  
Application US/09908975  
. US20030165843A1  
ATION:  
OSHAN, Avi  
ASSERMAN, Alon  
INTZ, Eli  
INTZ, Liat  
AIGLER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
TION: THAT POPULATE A TRANSCRIPTOME  
E: 36688-0005  
CATION NUMBER: US/09/908,975  
G DATE: 2001-07-20  
TION NUMBER: US 60/287,724  
DATE: 2001-05-02  
TION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
entIn version 3.0  
5

ORGANISM: Homo sapiens  
US-09-908-975-10055

Query Match 66.0%; Score 13.2; DB 10; Length 60;  
Best Local Similarity 83.3%; Pred. No. 8.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
QY 3 CTTGCTCCTCCACGGGT 20  
|||||  
Db 23 CTTGCTCCTCAAGGGT 6

RESULT 33  
US-09-908-975-16879/c  
Sequence 16879, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Liat  
APPLICANT: FAIGLER, Simchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRP  
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 16879  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-16875

Query Match 66.0%; Score 13.2; DB 10; Length 60;  
Best Local Similarity 83.3%; Pred. No. 8.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
QY 2 TCCTGTCTCCTCCACGGGT 19  
|||||  
Db 33 TCCTGTCTCTATGGGT 16

RESULT 34  
US-801-274-949/c  
Sequence 949, Application US/09801274  
Patent No. US20020032319A1  
GENERAL INFORMATION:  
APPLICANT: Cargill, Michele  
APPLICANT: Ireland, James S.  
APPLICANT: Lander, Eric S.  
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
FILE REFERENCE: 2825.2009-001  
CURRENT APPLICATION NUMBER: US/09/801,274  
CURRENT FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: US 60/187,510  
PRIOR FILING DATE: 2000-03-07  
PRIOR APPLICATION NUMBER: US 60/206,129  
PRIOR FILING DATE: 2000-05-22  
NUMBER OF SEQ ID NOS: 1802  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 949  
LENGTH: 31  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-801-274-949

Query Match 65.0%; Score 13; DB 9; Length 31;

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us-10-090-326-7.max.rnpb

milarity 86.7%; Pred. No. 1.1e+04; Indels 0; Gaps 0;  
Conservative 1; Mismatches 1;

CTTGCTCCACGG 17  
||||| : |||||  
CTTGTCWCACGG 10

640/c  
, Application US/10215112  
O. US20030082596A1  
MATION: Mittmann

ENTION: Method of Genetic Analysis of Probes:  
ENTION: Test3  
CE: 3119

ICATION NUMBER: US/10/215,112  
NG DATE: 2002-08-08  
Q ID NOS: 14936  
stSEQ for Windows Version 4.0  
0

rtificial Sequence

MATION: Synthetic Oligonucleotide  
640

milarity 86.7%; Pred. No. 1.1e+04; Indels 0; Gaps 0;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TGCTCTCCACGGTT 20  
||||| : |||||  
TGCTCTCCACGGTTT 7

83941/c  
1, Application US/10098263B  
O. US2003010410A1  
MATION: Michael

ENTION: Human Microarray  
CE: 3118.1  
ICATION NUMBER: US/10/098,263B  
NG DATE: 2003-01-08  
ATION NUMBER: 60/276,759  
DATE: 2001-03-16  
Q ID NOS: 131066

croarray Probe Sequence Listing Generator V 1.1  
41

omo sapien  
83941

milarity 86.7%; Pred. No. 1.1e+04; Indels 0; Gaps 0;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CCTTGCTCCACGG 17  
||||| : |||||  
TCTCGTCTCCACGG 9

105401/c  
01, Application US/10098263B  
O. US2003010410A1  
MATION: Michael

; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 105401  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; US-10-098-263B-105401

Query Match 64.0%; Score 12.8; DB 14; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 1 ATCCTTGCTCCACG 16  
||||| : |||||  
Db 21 AACCTTGCTCTACG 6

RESULT 38

US-10-131-827-830  
; Sequence 830, Application US/10131827  
; Publication No. US20040009479A1  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 830  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-830

Query Match 64.0%; Score 12.8; DB 15; Length 50;  
Best Local Similarity 87.5%; Pred. No. 1.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 3 CCTTGCTCTCCACGG 18  
||||| : |||||  
Db 22 CCTTGCTCTCTGGG 37

RESULT 39

US-10-305-555-20  
; Sequence 20, Application US/10305555  
; Publication No. US20030157525A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPR  
; FILE REFERENCE: D0196 NP  
; CURRENT APPLICATION NUMBER: US/10/305,555  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: U.S. 60/333,337  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: U.S. 60/355,619  
; PRIOR FILING DATE: 2002-02-06

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} ID NOS: 42
.entin version 3.1

pmo sapiens
)

      64.0%; Score 12.8; DB 14; Length 53;
ilarity 87.5%; Pred. No. 1.3e+04;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTGTGTCCTCCACGG 17
|||||
CTGTGTCCTCCACGG 39

;0174/c
; Application US/10098263B
; US20030104410A1
tman, Michael
NTION: Human Microarray
E: 3118.1
CATION NUMBER: US/10/098,263B
G DATE: 2003-01-08
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
roarray Probe Sequence Listing Generator V 1.1
'4

pmo sapien
;0174

      63.0%; Score 12.6; DB 14; Length 25;
ilarity 78.9%; Pred. No. 1.8e+04;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CTGTGTCCTCCACGGTT 20
|||||
CTGTGTCCTCAGAGTT 1

2313
; Application US/10098263B
; US20030104410A1
tman, Michael
NTION: Human Microarray
E: 3118.1
CATION NUMBER: US/10/098,263B
G DATE: 2003-01-08
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
roarray Probe Sequence Listing Generator V 1.1
3

pmo sapien
2313

      63.0%; Score 12.6; DB 14; Length 25;
ilarity 78.9%; Pred. No. 1.8e+04;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CTGTGTCCTCCACGGTT 19
|||||
GTTTGTATCCACGTGT 24

RESULT 42
US-10-098-263B-66128
; Sequence 66128, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 66128
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-66128

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 14; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 2 TCCTGTCTCTCCACGGTT 20
|||||
Db 2 TCCTGTCTCTCAGAGTT 20

RESULT 43
US-10-098-263B-72882/c
; Sequence 72882, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 72882
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-72882

Query Match
Best Local Similarity 63.0%; Score 12.6; DB 14; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0;

QY 2 TCCTGTCTCTCCACGGTT 20
|||||
Db 2 TCCTGTCTCTCAGAGTT 2

RESULT 44
US-10-098-263B-76557/c
; Sequence 76557, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
```

1 09:38:26 2004

us-10-090-326-7.max.rnpb

croarray Probe Sequence Listing Generator V 1.1  
57

omo sapien  
76557

63.0%; Score 12.6; DB 14; Length 25;  
milarity 78.9%; Pred.No. 1.8e+04;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
CCTTGTCCTCCACGGGTT 20  
|||||  
CCGTGTCCTCGTCGGCTT 7

104826/c  
26, Application US/10098263B  
O. US20030104410A1  
MATION:  
ittman, Michael  
ENTION: Human Microarray  
CE: 3118.1  
ICATION NUMBER: US/10/098,263B  
NG DATE: 2003-01-08  
ACTION NUMBER: 60/276,759  
DATE: 2001-03-16  
Q ID NOS: 131066  
croarray Probe Sequence Listing Generator V 1.1  
826

omo sapien  
104826

63.0%; Score 12.6; DB 14; Length 25;  
milarity 78.9%; Pred.No. 1.8e+04;  
Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
CCTTGTCCTCCACGGGTT 20  
|||||  
CCGTGTCCTCCACGAGAT 7

d: February 29, 2004, 13:42:44  
857 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

February 29, 2004, 08:43:19 ; Search time 1501.3 Seconds  
(without alignments)  
397.818 Million cell updates/sec

US-10-090-326-7

20  
1 atccttgctcccaagggtt 20

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 203984

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
71.0	54	14	CA797539		CA797539 Cac BL_46
69.0	59	14	CF298713		CF298713 7LEAF--02
68.0	55	14	T70039		T70039 vcl7b01.s1
66.0	35	10	AW140195		AW140195 SWACAC44

57.0	49	9	AU243854	151	11	55.0	54	9	AA190045
57.0	51	28	AZ495072	c 152	11	55.0	56	9	AU258629
57.0	52	28	BH897343	153	11	55.0	56	14	H69956
57.0	55	14	CA397523	154	11	55.0	57	28	AI905179
56.0	35	28	AZ421500	c 155	11	55.0	58	9	AZ454242
56.0	37	28	BZ763407	c 156	11	55.0	58	9	AI656273
56.0	39	28	BZ665246	c 157	11	55.0	58	12	BM534325
56.0	40	9	AI813961	c 158	11	55.0	59	9	AI246100
56.0	40	28	BH128122	c 159	11	55.0	60	14	CD288877
56.0	43	9	AA181395	c 160	11	55.0	60	14	H55293
56.0	45	9	AI559917	c 161	10.8	54.0	19	28	AZ783569
56.0	45	12	BI754711	c 162	10.8	54.0	25	14	L32062
56.0	45	28	BH855442	c 163	10.8	54.0	26	28	BZ660808
56.0	47	28	BH856951	c 164	10.8	54.0	27	28	AZ835139
56.0	50	9	AU105489	c 165	10.8	54.0	31	28	AZ816189
56.0	50	9	AU105492	c 166	10.8	54.0	31	29	AG256531
56.0	50	9	AU107202	c 167	10.8	54.0	32	29	CG708456
56.0	50	9	AU107203	c 168	10.8	54.0	34	28	AZ485756
56.0	50	9	AU107206	c 169	10.8	54.0	37	9	AA992758
56.0	50	9	AU107207	c 170	10.8	54.0	38	28	AZ821943
56.0	50	9	AU107210	c 171	10.8	54.0	39	28	AZ852950
56.0	50	9	AU107213	c 172	10.8	54.0	40	9	AA018337
56.0	50	9	AU107214	c 173	10.8	54.0	40	9	AI073810
56.0	50	9	AU107216	c 174	10.8	54.0	41	29	BI150554
56.0	50	28	CC024195	c 175	10.8	54.0	42	28	AZ814453
56.0	51	28	AZ761115	c 176	10.8	54.0	42	28	BH905673
56.0	52	9	AA929522	c 177	10.8	54.0	43	9	AA193759
56.0	55	9	AI224478	c 178	10.8	54.0	43	28	BZ288372
56.0	55	13	BQ289498	c 179	10.8	54.0	44	28	BH910443
56.0	56	14	CF857035	c 180	10.8	54.0	46	9	AI282441
56.0	58	29	BX891429	c 181	10.8	54.0	46	9	AI631068
56.0	59	12	BI669126	c 182	10.8	54.0	46	14	W30168
56.0	59	14	T61794	c 183	10.8	54.0	46	29	CC886211
56.0	59	28	BH848880	c 184	10.8	54.0	47	28	AZ860255
56.0	60	28	BQ3761	c 185	10.8	54.0	47	28	BX661317
56.0	60	28	BZ290591	c 186	10.8	54.0	49	9	AA804906
55.0	27	28	AZ307201	c 187	10.8	54.0	49	28	AZ964781
55.0	28	9	AA905471	c 188	10.8	54.0	50	9	AU102994
55.0	28	28	AZ633359	c 189	10.8	54.0	50	9	AU107902
55.0	35	28	AZ657249	c 190	10.8	54.0	50	28	AZ807846
55.0	36	12	BQ041351	c 191	10.8	54.0	51	28	BH640903
55.0	36	29	TA362C11P	c 192	10.8	54.0	52	10	BF645565
55.0	37	28	AZ832358	c 193	10.8	54.0	52	10	BE315620
55.0	38	28	BH851440	c 194	10.8	54.0	52	28	BH225527
55.0	38	29	BX896340	c 195	10.8	54.0	52	29	BX219012
55.0	41	28	AZ663826	c 196	10.8	54.0	53	28	AQ025275
55.0	41	28	BH625409	c 197	10.8	54.0	53	28	AZ356283
55.0	41	29	BX162572	c 198	10.8	54.0	55	9	AA872208
55.0	43	9	AI477210	c 199	10.8	54.0	55	28	CC325110
55.0	43	14	W86565	c 200	10.8	54.0	56	10	BF026677
55.0	43	29	DME545852	c 201	10.8	54.0	56	28	AZ865094
55.0	44	28	AZ801644	c 202	10.8	54.0	58	9	AA663265
55.0	46	29	AL952906	c 203	10.8	54.0	58	9	AI327266
55.0	47	12	BI685348	c 204	10.8	54.0	58	14	CF863585
55.0	49	9	AA854556	c 205	10.8	54.0	59	12	BI760827
55.0	49	9	AI744869	c 206	10.8	54.0	59	29	CG672163
55.0	49	28	AZ805592	c 207	10.8	54.0	60	28	AZ603495
55.0	49	28	BZ381817	c 208	10.8	54.0	60	29	DR42K185
55.0	49	29	AI771128	c 209	10.8	54.0	60	29	AI017105
55.0	50	9	AU104312	c 210	10.6	53.0	25	9	AA006896
55.0	50	9	AU104314	c 211	10.6	53.0	33	9	AA006896
55.0	50	9	AU104316	c 212	10.6	53.0	33	10	BF184963
55.0	50	12	BG526086	c 213	10.6	53.0	33	28	CC182131
55.0	50	28	AZ922086	c 214	10.6	53.0	37	28	AZ660325
55.0	50	28	BZ357218	c 215	10.6	53.0	37	29	BX293466
55.0	50	29	BX654687	c 216	10.6	53.0	39	9	AU256556
55.0	51	13	BQ627447	c 217	10.6	53.0	39	28	AZ499899
55.0	51	29	BX662722	c 218	10.6	53.0	42	12	BI668257
55.0	52	9	AI098966	c 219	10.6	53.0	42	28	BH864588
55.0	52	9	AI343111	c 220	10.6	53.0	42	28	BZ584441
55.0	52	28	AZ647203	c 221	10.6	53.0	43	9	AA931447
55.0	52	28	BX002086	c 222	10.6	53.0	43	12	BG244016
55.0	53	29	BX002086	c 223	10.6	53.0	44	28	BH854174

53.0	46	9	AI191806	AI191806 qd47e10.x	297	10.6	53.0	50	9	AUI07816	AUI07816
53.0	46	14	D67712	D67712 CELK076HZF	298	10.6	53.0	50	9	AUI07817	AUI07817
53.0	48	28	BH637902	BH637902 1008019D0	299	10.6	53.0	50	9	AUI07819	AUI07819
53.0	48	29	CG732540	CG732540 1119149C0	300	10.6	53.0	50	9	AUI07820	AUI07820
53.0	48	29	AG216175	AG216175 Drosophil	301	10.6	53.0	50	9	AUI07821	AUI07821
53.0	49	9	AI095125	AI095125 qai9c03.x	302	10.6	53.0	50	9	AUI07822	AUI07822
53.0	49	9	AV856631	AV856631 AV856631	303	10.6	53.0	50	9	AUI07823	AUI07823
53.0	49	12	BM021294	BM021294 1e75c11.y	304	10.6	53.0	50	9	AUI07825	AUI07825
53.0	49	29	CG721821	CG721821 1119069B0	305	10.6	53.0	50	9	AUI07826	AUI07826
53.0	50	9	AI042693	AI042693 uc76e08.x	306	10.6	53.0	50	9	AUI07827	AUI07827
53.0	50	9	AUI02256	AUI02256	307	10.6	53.0	50	28	AZ875367	AZ875367
53.0	50	9	AUI04315	AUI04315	308	10.6	53.0	50	28	BH890468	BH890468
53.0	50	9	AUI07747	AUI07747	309	10.6	53.0	51	28	AZ621614	AZ621614
53.0	50	9	AUI07748	AUI07748	310	10.6	53.0	52	9	AA638823	AA638823
53.0	50	9	AUI07749	AUI07749	311	10.6	53.0	52	9	AI504673	AI504673
53.0	50	9	AUI07750	AUI07750	312	10.6	53.0	52	28	BH790794	BH790794
53.0	50	9	AUI07751	AUI07751	313	10.6	53.0	52	28	CC248941	CC248941
53.0	50	9	AUI07753	AUI07753	314	10.6	53.0	54	9	AI930813	AI930813
53.0	50	9	AUI07754	AUI07754	315	10.6	53.0	54	9	AI786998	AI786998
53.0	50	9	AUI07755	AUI07755	316	10.6	53.0	54	12	BG526210	BG526210
53.0	50	9	AUI07756	AUI07756	317	10.6	53.0	54	28	AZ815205	AZ815205
53.0	50	9	AUI07757	AUI07757	318	10.6	53.0	54	28	BZ358880	BZ358880
53.0	50	9	AUI07759	AUI07759	319	10.6	53.0	55	9	AA434258	AA434258
53.0	50	9	AUI07760	AUI07760	320	10.6	53.0	55	28	BH415675	BH415675
53.0	50	9	AUI07761	AUI07761	321	10.6	53.0	55	28	BZ581514	BZ581514
53.0	50	9	AUI07764	AUI07764	322	10.6	53.0	56	9	AL847510	AL847510
53.0	50	9	AUI07765	AUI07765	323	10.6	53.0	56	28	AZ492220	AZ492220
53.0	50	9	AUI07766	AUI07766	324	10.6	53.0	56	28	B44818	B44818
53.0	50	9	AUI07767	AUI07767	325	10.6	53.0	56	28	CC022423	CC022423
53.0	50	9	AUI07768	AUI07768	326	10.6	53.0	56	28	CNS02BNW	CNS02BNW
53.0	50	9	AUI07769	AUI07769	327	10.6	53.0	57	28	AZ660093	AZ660093
53.0	50	9	AUI07774	AUI07774	328	10.6	53.0	57	28	BH233365	BH233365
53.0	50	9	AUI07775	AUI07775	329	10.6	53.0	57	28	BH635027	BH635027
53.0	50	9	AUI07776	AUI07776	330	10.6	53.0	58	13	BQ626004	BQ626004
53.0	50	9	AUI07777	AUI07777	331	10.6	53.0	58	14	W74798	W74798
53.0	50	9	AUI07778	AUI07778	332	10.6	53.0	58	28	BZ766894	BZ766894
53.0	50	9	AUI07779	AUI07779	333	10.6	53.0	58	29	AL757800	AL757800
53.0	50	9	AUI07780	AUI07780	334	10.6	53.0	59	10	AW248773	AW248773
53.0	50	9	AUI07781	AUI07781	335	10.6	53.0	59	28	AZ351787	AZ351787
53.0	50	9	AUI07782	AUI07782	336	10.6	53.0	60	13	BQ473102	BQ473102
53.0	50	9	AUI07783	AUI07783	337	10.6	53.0	60	14	CA851565	CA851565
53.0	50	9	AUI07784	AUI07784	338	10.6	53.0	60	14	CD525559	CD525559
53.0	50	9	AUI07785	AUI07785	339	10.4	52.0	22	12	BG926061	BG926061
53.0	50	9	AUI07786	AUI07786	340	10.4	52.0	22	28	AZ762378	AZ762378
53.0	50	9	AUI07787	AUI07787	341	10.4	52.0	26	28	AZ825865	AZ825865
53.0	50	9	AUI07788	AUI07788	342	10.4	52.0	30	28	AZ783604	AZ783604
53.0	50	9	AUI07789	AUI07789	343	10.4	52.0	33	10	BE739126	BE739126
53.0	50	9	AUI07790	AUI07790	344	10.4	52.0	37	14	H69029	H69029
53.0	50	9	AUI07791	AUI07791	345	10.4	52.0	37	29	CG707299	CG707299
53.0	50	9	AUI07792	AUI07792	346	10.4	52.0	38	29	AL767019	AL767019
53.0	50	9	AUI07793	AUI07793	347	10.4	52.0	39	29	CL002872	CL002872
53.0	50	9	AUI07794	AUI07794	348	10.4	52.0	40	9	AA811470	AA811470
53.0	50	9	AUI07795	AUI07795	349	10.4	52.0	40	9	AL933274	AL933274
53.0	50	9	AUI07796	AUI07796	350	10.4	52.0	40	28	BZ767501	BZ767501
53.0	50	9	AUI07797	AUI07797	351	10.4	52.0	41	28	BH849731	BH849731
53.0	50	9	AUI07798	AUI07798	352	10.4	52.0	42	28	BZ583894	BZ583894
53.0	50	9	AUI07799	AUI07799	353	10.4	52.0	42	29	CG715948	CG715948
53.0	50	9	AUI07800	AUI07800	354	10.4	52.0	43	12	BG745981	BG745981
53.0	50	9	AUI07801	AUI07801	355	10.4	52.0	43	14	CF292564	CF292564
53.0	50	9	AUI07802	AUI07802	356	10.4	52.0	44	14	H64101	H64101
53.0	50	9	AUI07803	AUI07803	357	10.4	52.0	45	28	AZ817198	AZ817198
53.0	50	9	AUI07804	AUI07804	358	10.4	52.0	45	28	AZ820873	AZ820873
53.0	50	9	AUI07805	AUI07805	359	10.4	52.0	45	28	BH802881	BH802881
53.0	50	9	AUI07806	AUI07806	360	10.4	52.0	45	29	CC888123	CC888123
53.0	50	9	AUI07807	AUI07807	361	10.4	52.0	45	29	CG711564	CG711564
53.0	50	9	AUI07808	AUI07808	362	10.4	52.0	46	9	AA869036	AA869036
53.0	50	9	AUI07809	AUI07809	363	10.4	52.0	46	9	AA877316	AA877316
53.0	50	9	AUI07810	AUI07810	364	10.4	52.0	46	9	AA244435	AA244435
53.0	50	9	AUI07811	AUI07811	365	10.4	52.0	46	28	AZ585571	AZ585571
53.0	50	9	AUI07812	AUI07812	366	10.4	52.0	46	29	TA316B04Q	TA316B04Q
53.0	50	9	AUI07813	AUI07813	367	10.4	52.0	47	28	BH804707	BH804707
53.0	50	9	AUI07814	AUI07814	368	10.4	52.0	47	28	BH866277	BH866277
53.0	50	9	AUI07815	AUI07815	369	10.4	52.0	48	28	BH803091	BH803091













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69.0%; Score 13.8; DB 14; Length 59;
ilarity 88.2%; Pred. No. 1e+05;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTTGTCCTCCACGGG 18
|||||
CTCTCTCCTCCACGGG 42

39 55 bp mRNA linear EST 23-FEB-1995
b01.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
E:80905 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR
NUCLEOPROTEINS C1/C2 (HUMAN); mRNA sequence.
39
39.1 GI:681187
sapiens (human)
sapiens
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
bases 1 to 55)
ier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
soe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
ins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
is, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
fing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
askis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
Marra, M.
ration and analysis of 280,000 human expressed sequence tags
me Res. 6 (9), 807-828 (1996)
4478
549
act: Wilson RK
ington University School of Medicine
Forest Park Parkway, Box 8501, St. Louis, MO 63108
314 286 1800
314 286 1810
l: est@watson.wustl.edu
quality sequence starts: 1
quality sequence stops: 1
ce: IMAGE Consortium, LLNL
clone is available royalty-free through LLNL; contact the
E Consortium (info@image.llnl.gov) for further information.
e considered overall poor quality
primer: -21ml3
quality sequence stop: 1.
Location/Qualifiers
1. .55
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:484522"
/db_xref="taxon:9606"
/clone="IMAGE:80905"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene lung (#937210)"
/notes="Organ: lung; Vector: pBluescript SK-; Site: 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. normal lung. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

68.0%; Score 13.6; DB 14; Length 55;
ilarity 80.0%; Pred. No. 1.2e+05;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CTTGTCCTCCACGGGTT 20
|||||

36 ATCCTGTGCTTCCCATGTT 17
|||||

RESULT 4
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
/organism="Brugia malayi"
/mol_type="mRNA"
/strain="TR5 Labs"
/db_xref="taxon:6279"
/clone="SWAMC44A12"
/lab_host="XLI-Blue MRF"
/clone_lib="Brugia malayi adult male cDNA (SAW9
/notes="Vector: lambda Unizap XR; Site 1: EcoR I
Xho I; Lymphatic filarial nematode parasite of
Brugia was prepared from adult males of Brugia ma
isolated from jirds and converted to double str
using reverse transcriptase and oligo(dT) foll
RNase H and DNase I. The library had 4.6 x 10E
independent recombinants and average insert siz
base pairs. The library was constructed by Noe
The library is available from Dr. S.A. Williams
genome@smith.edu."
ORIGIN
Query Match 66.0%; Score 13.2; DB 10; Length 35;
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 3 CCTGTGCTCCTCCACGGGTT 20
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Db 13 CGTGTGCTCCTCCACTGGTT 30
|||||

RESULT 5
BH851251/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
BH851251
SALK_072736.23.80.x Arabidopsis thaliana TDNA insertion
Arabidopsis thaliana genomic clone SALK_072736.23.80.x,
survey sequence.
BH851251
BH851251.1 GI:21422122
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
rosids; eurosids II; Brassicales; Brassicaceae; Arabidop
1 (bases 1 to 45)

```

iso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
cinab,C., Jeske,A., Karnea,M., Kim,C.J., Parker,H., Prednis,L.,  
m,P., Zimmerman,J. and Ecker,J.R.  
Sequence-Indexed Library of Insertion Mutations in the  
Bidopsis Genome  
Published (2001)

act: Joseph R. Ecker  
c Institute Genomic Analysis Laboratory (SIGNAL)  
Salk Institute for Biological Studies  
10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
858 453 4100 x1752  
858 538 6379  
il: ecker@salk.edu

s is single pass sequence recovered from the left border of

ts: TDNA tagged.

Location/Qualifiers

1. 45

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK 072736.23.80.x"

/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

66.0%; Score 13.2; DB 28; Length 45;

Similarity 83.3%; Pred. No. 1.7e+05;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTTGTCTCCACCGGGT 19

|||||

CTTATCCACCGCGT 27

1234 49 bp mRNA linear EST 30-AUG-1996  
#06.r1 Soares\_fetal heart NBH19W Homo sapiens cDNA clone  
HE:376259 5' similar to PIR:A54211 A54211 H+transporting ATP  
base ; mRNA sequence.

1234

1234.1 GI:1517468

sapiens (human)

sapiens

ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
(bases 1 to 49)

ier.L., Clark.N., Dubuque.T., Elliston.K., Hawkins.M.,

ian.M., Hultman.M., Kucaba.T., Le.M., Lennon.G., Marra.M.,

sons.J., Rafkin.L., Rohlfing.T., Soares.M., Tan.F.,

askis.B., Waterston.R., Williamson.A., Woldmann.P., and

son.R.

WashU-Merck EST Project

ublished (1995)

act: Wilson RK

ington University School of Medicine

Forest Park Parkway, Box 8501, St. Louis, MO 63108

314 286 1800

314 286 1810

il: est@wustl.edu

s clone is available royalty-free through LNL ; contact the

SE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

re considered overall poor quality

ible reversed clone; similarity on wrong strand

primer: -28M13 rev2 from Amerham

High quality sequence stop: 1.

Location/Qualifiers

1. 49

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:1284515"

/db\_xref="taxon:9606"

/clone="IMAGE:376259"

/sex="unknown"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares\_fetal heart NBH19W"

/note="Organ: heart; Vector: pT73D (Pharmacia;  
modified polylinker; Site 1: Not I; Site 2: Eco  
strand cDNA was primed with a Not I - oligo(dT)  
TGTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTT  
double-stranded cDNA was size selected, ligated  
adapters (Pharmacia), digested with Not I and  
the Not I and Eco RI sites of a modified pT73  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed  
M.Fatima Bonaldo. This library was constructed  
same fetus as the fetal lung library, Soares f  
NBH19W."

ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 49;  
Best Local Similarity 83.3%; Pred. No. 1.7e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCTTGTCTCCACCGGT 19

|||||

DB 18 TTCTTGTCTCCACGTGT 1

RESULT 7

AA180620

LOCUS

DEFINITION

malayi cDNA clone AFGC1B10 5', mRNA sequence.

ACCESSION

AA180620

VERSION

AA180620.1 GI:1763812

KEYWORDS

EST.

SOURCE

Brugia malayi

Brugia malayi

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; F;

Onchocercidae; Brugia.

1 (bases 1 to 49)

REFERENCE

AUTHORS

Blaxter,M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,I

Jones,S.J.

Genes expressed in adult female Brugia malayi

Unpublished (1996)

CONTACT: Blaxter ML

Institute of Cell, Animal and Population Biology

University of Edinburgh

Ashtworth Labs, King's Buildings, West Mains Road, Edinbu

3JT, UK.

Tel: +44 131 650 6760

Fax: +44 131 670 5450

Email: mark.blaxter@ed.ac.uk

The ABI trace of this sequence can be viewed at

<http://www.sanger.ac.uk/brugia/AF/MBAFGB1073.html> This

full sequence of the cDNA clone. The polyA tail has been

and is excluded from this sequence

Seq primer: T3.

Location/Qualifiers

1. 49

/organism="Brugia malayi"

/mol\_type="mRNA"

/db\_xref="taxon:6279"

/clone="AFGB10"

/sex="female"

/dev\_stage="adult"

FEATURES

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/lab\_host="XLI-Blue MRF"  
 /clone lib="Brugia malayi adult female cDNA  
 (SAW96MLW-BmaF)"  
 /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
 Xho I; Lymphatic filarial nematode parasite of humans.  
 mRNA was prepared from approximately 50 adult females  
 isolated from the peritoneal cavity of jirds and  
 converted to double-stranded cDNA using reverse  
 transcriptase and oligo(dT) followed by RNase H and DNA  
 pol I. The library has 5 x 10<sup>5</sup> independent recombinants  
 and the average insert size is ~900bp. The library was  
 constructed by Michelle Lizotte-Waniewski. The  
 library is available from Dr.S.A.Williams, email:  
 genome@smith.edu."

66.0%; Score 13.2; DB 9; Length 49;  
 Similarity 83.3%; Pred. No. 1.7e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTCTCCACGGGTT 20  
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 TTGTCTGCACGTGGTT 47

1635 50 bp mRNA linear EST 17-DEC-1996  
 2G0A07T3 Brugia malayi adult female cDNA (SAW96MLW-BmaF) Brugia  
 i cDNA clone AFCG0A07 5', mRNA sequence.

1635.1 GI:1737665

ia malayi  
 ia malayi  
 cyota: Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 cericiidae; Brugia.  
 ases 1 to 50)  
 er.M.L., Waterfall,M., Daub,J., Lizotte,M., Baron,L. and  
 S.S.J.  
 s expressed in adult female Brugia malayi  
 ublished (1996)  
 ct: Blaxter ML  
 tute of Cell, Animal and Population Biology  
 rsity of Edinburgh  
 irth Labs, King's Buildings, West Mains Road, Edinburgh, EH9  
 UK.

+44 131 650 6760  
 +44 131 670 5450  
 l: mark.blaxter@ed.ac.uk  
 ABI trace of this sequence can be viewed at  
 ://www.sanger.ac.uk/bugia/AFC/MBAFG0A07T3.html  
 primer: T3.

Location/Qualifiers  
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 /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
 Xho I; Lymphatic filarial nematode parasite of humans.  
 mRNA was prepared from approximately 50 adult females  
 isolated from the peritoneal cavity of jirds and  
 converted to double-stranded cDNA using reverse  
 transcriptase and oligo(dT) followed by RNase H and DNA  
 pol I. The library has 5 x 10<sup>5</sup> independent recombinants  
 and the average insert size is ~900bp. The library was  
 constructed by Michelle Lizotte-Waniewski. The

library is available from  
 genome@smith.edu."

Dr.S.A.Williams,

ORIGIN  
 Query Match 66.0%; Score 13.2; DB 9; Length 50;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;  
 QY 3 CCTTGTCTCCACGGGTT 20  
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 Db 31 CGTTGTCTGCACGTGGTT 48

RESULT 9  
 AA406799  
 LOCUS  
 DEFINITION  
 MAFPCZ4G10T3 Brugia malayi adult female cDNA (SAW96MLW-B  
 malayi cDNA clone AFCZ4G10 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Brugia malayi  
 Brugia malayi  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Fi  
 onchocercidae; Brugia.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

1 (bases 1 to 51)  
 Jones,S.J.  
 Genes expressed in adult female Brugia malayi  
 Unpublished (1996)  
 Contact: Blaxter ML  
 Institute of Cell, Animal and Population Biology  
 University of Edinburgh  
 Ashworth Labs, King's Buildings, West Mains Road, Edinbu  
 3JT, UK.

Tel: +44 131 650 6760  
 Fax: +44 131 670 5450  
 Email: mark.blaxter@ed.ac.uk

The ABI trace of this sequence can be viewed at  
 http://www.sanger.ac.uk/bugia/AFC/MAFPCZ4G10T3.html Thi  
 full sequence of the cDNA clone. The polyA tail has been  
 and is excluded from this sequence  
 Seq primer: T3.

FEATURES  
 source  
 Location/Qualifiers

1. .51  
 /organism="Brugia malayi"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6279"  
 /clone="AFCZ4G10"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="XLI-Blue MRF"  
 /clone lib="Brugia malayi adult female cDNA  
 (SAW96MLW-BmaF)"  
 /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco R  
 Xho I; Lymphatic filarial nematode parasite of  
 mRNA was prepared from approximately 50 adult f  
 isolated from the peritoneal cavity of jirds a  
 converted to double-stranded cDNA using  
 transcriptase and oligo(dT) followed by RNase H  
 and the average insert size is ~900bp. The libra  
 constructed by Michelle Lizotte-Waniew  
 library is available from  
 genome@smith.edu."

ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 51;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 3 CCTTGTCTCCACGGGTT 20  
 ||||| |||||

GTGTGCTGCACTGGTT 49

54424 53 bp mRNA linear EST 05-JUN-1997  
 FCX1D10T3 Brugia malayi adult female cDNA (SAW96MLW-Bmaf) Brugia  
 ay1 cDNA clone AFCX1D10 5', mRNA sequence.

54424  
 54424.1 GI:2168093

Gia malayi  
 Gia malayi  
 aryoita; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 hoceridae; Brugia.  
 (bases 1 to 53)  
 xter M.L., Waterfall, M., Daub, J., Lizotte, M., Baron, L. and  
 es, S.J.  
 es expressed in adult female Brugia malayi  
 ublished (1996)  
 tact: Blaxter ML  
 titute of Cell, Animal and Population Biology  
 versity of Edinburgh  
 worth labs, King's Buildings, West Mains Road, Edinburgh, EH9  
 , UK.

: +44 131 650 6760  
 : +44 131 670 5450  
 il: mark.blaxter@ed.ac.uk  
 ABI trace of this sequence can be viewed at  
 p://www.sanger.ac.uk/brugia/AFC/MBFAFCX1D10T3.html  
 primer: T3:  
 Location/Qualifiers

1. .53  
 /organism="Brugia malayi"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6279"  
 /clone="AFCX1D10"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="XLI-Blue MRF"  
 /clone\_lib="Brugia malayi adult female cDNA  
 (SAW96MLW-Bmaf)"  
 /note="Vector: Lambda Uni-ZAP XR; Site\_1: Eco RI; Site\_2:  
 Xho I; Lymphatic filarial nematode parasite of humans.  
 mRNA was prepared from approximately 50 adult females  
 isolated from the peritoneal cavity of jirds and  
 converted to double-stranded cDNA using reverse  
 transcriptase and oligo(dT) followed by RNase H and DNA  
 pol I. The library has 5 x 10E6 independent recombinants  
 and the average insert size is ~900bp. The library was  
 constructed by Michelle Lizotte-Waniewski. The  
 library is available from Dr.S.A.Williams, email:  
 genome@smith.edu."

66.0%; Score 13.2; DB 9; Length 53;  
 nilarity 83.3%; Pred. No. 1.8e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTGCTGCACTGGTT 20  
 |||||  
 GTTGTGCTGCACTGGTT 51

89356 54 bp mRNA linear EST 12-DEC-1996  
 FC45SK Brugia malayi adult female cDNA (SAW96MLW-Bmaf) Brugia  
 ay1 cDNA clone SWAFCA55 5', mRNA sequence.

89356  
 89356.1 GI:1634835

Gia malayi

# ORGANISM

Brugia malayi  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; F  
 Onchocercidae; Brugia.

1 (bases 1 to 54)

## REFERENCE

AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Williams, S.A.  
 Genes expressed in adult females of Brugia malayi  
 Unpublished (1996)  
 Contact: Steven A. Williams  
 Molecular Parasitology  
 Smith College Department of Biological Sciences  
 Department of Biological Sciences, Clark Science Center  
 College, Northampton, MA, 01063, USA  
 Tel: 4135853826  
 Fax: 4135853786  
 Email: genome@smith.edu

Seq primer: pBluescript SK.

## FEATURES

source

1. .54  
 Location/Qualifiers  
 /organism="Brugia malayi"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6279"  
 /clone="SWAFCA55"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="XLI-Blue MRF"  
 /clone\_lib="Brugia malayi adult female cDNA  
 (SAW96MLW-Bmaf)"  
 /note="Vector: Lambda Uni-ZAP XR; Site\_1: Eco  
 Xho I; Lymphatic filarial nematode parasite of  
 mRNA was prepared from approximately 50 adult  
 isolated from the peritoneal cavity of jirds  
 converted to double-stranded cDNA using  
 transcriptase and oligo(dT) followed by RNase  
 pol I. The library has 5 x 10E6 independent re  
 and the average insert size is ~900bp. The libr  
 constructed by Michelle Lizotte-Wanie  
 library is available from Dr.S.A.Williams  
 genome@smith.edu."

## ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 54;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 3 CCTGTGCTGCTCCACGGGTT 20

Db |||||  
 32 CGTGTGCTGCTGCTGTT 49

## RESULT 12

AV955284

LOCUS

DEFINITION

AV955284 54 bp mRNA linear EST  
 Ciona intestinalis cDNA clone c109n01 5', mRNA sequen  
 Ciona intestinalis  
 EST.  
 AV955284.1 GI:19443583

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ciona intestinalis  
 Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; J  
 Phlebobranchia; Cionidae; Ciona.  
 1 (bases 1 to 54)

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-Ku, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.  
 Location/Qualifiers

```

1. .54
/organism="Ciona intestinalis"
/mol_type="mrna"
/db_xref="taxon:7719"
/clone="cic109n01"
/tissue_type="whole animal"
/dev_stage="cleavage stage embryo"
/clone_lib="Nori Satoh unpublished cDNA library, cleavage
stage embryo"

66.0%; Score 13.2; DB 9; Length 54;
ilarity 83.3%; Pred. No. 1.8e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTGTCTCTCCACGGGTT 20
|||||
TTGTCTCTCGACAGGAT 20

7148
35G10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
e UUGC1M0035G10 R, genomic survey sequence.
7148
7148.1 GI:10365669

musculus (house mouse)
musculus
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
bases 1 to 55)
D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
m.H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
ly,M., Rose,M., Stokes,R., Tingley,A., von
erhausen,A. and Wright,D.,Weiss,R.
e whole genome scaffolding with paired end reads from 10kb
mid inserts
ished (2000)
act: Robert B. Weiss
ersity of Utah Genome Center
ersity of Utah
308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
2. USA
801 585 5606
801 585 7177
l: ddum@genetics.utah.edu
rt Length: 10000 Std Error: 0.00
e: 0035 row: G column: 10
primer: CACACAGGAACAGCTATGACC
s: plasmid ends
quality sequence stop: 55.
Location/Qualifiers
1. .55
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0035G10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to

```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from of pWD42 (gi|4732114|gb|AF129072.1), a copy-nu inducible derivative of plasmid R1. The vector with adaptors complementary to the insert adap purified. The sheared, adaptor mouse DNA was adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Strata) and selected for ampicillin resistance."

## ORIGIN

Query Match 66.0%; Score 13.2; DB 28; Length 55;  
Best Local Similarity 83.3%; Pred. No. 1.8e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 3 CCTGTCTCTCCACGGGTT 20  
|||||  
DB 20 CCTTCTCTTCCACTGGTT 3

## RESULT 14

AA406768  
LOCUS MBAPC24B07T3 Brugia malayi adult female cDNA (SAW96MLW-1)  
DEFINITION malayi cDNA clone AFCZ4B07 5', mRNA sequence.  
ACCESSION AA406768  
VERSION AA406768.1 GI:2064734  
KEYWORDS EST.  
SOURCE Brugia malayi  
ORGANISM Brugia malayi  
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; F;  
Onchocercidae; Brugia.  
1 (bases 1 to 60)  
Jones, S.J.  
Genes expressed in adult female Brugia malayi  
Contact: Blaxter ML  
Institute of Cell, Animal and Population Biology  
University of Edinburgh  
Ashworth Labs, King's Buildings, West Mains Road, Edinbu  
3JT, UK.  
Tel: +44 131 650 6760  
Fax: +44 131 670 5450  
Email: mark.blaxter@ed.ac.uk  
The ABI trace of this sequence can be viewed at  
<http://www.sanger.ac.uk/brugia/AFC/MBAPC24B07T3.html>  
Seq primer: T3

## FEATURES

Location/Qualifiers  
1. .60  
/organism="Brugia malayi"  
/mol\_type="mrna"  
/db\_xref="taxon:6279"  
/clone="AFCZ4B07"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="XL1-Blue MRF"  
/clone\_lib="Brugia malayi adult female cDNA  
(SAW96MLW-BmAF)"  
/notes="Vector: Lambda Uni-ZAP XR, Site 1: Eco R  
Xho I; Lymphatic filarial nematode parasite of  
mRNA was prepared from approximately 50 adult f  
isolated from the peritoneal cavity of jirds a  
converted to double-stranded cDNA using  
transcriptase and oligo(dT) followed by RNase H  
pol I. The library has 5 x 10E6 independent rec  
and the average insert size is ~900bp. The libra  
constructed by Michelle Lizotte-Waniew  
library is available from Dr.S.A.Williams,  
genome@smith.edu."

## ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 60;

```

.milarity 83.3%; Pred. No. 1.8e+05; Indels 0; Gaps 0;
Conservative 0; Mismatches 3;

CCTTGTCCTCCACGGGTT 20
|||||
CCTTGTCCTGCACCTGGTT 58

.031 linear EST 01-MAR-1995
:0d12.sl StrataGene liver (#937224) Homo sapiens cDNA clone
AGE:84119 3', similar to gb:X00570 AF01POPROTEIN C-I PRECURSOR
(MAN);, mRNA sequence.
.031
.031.1 GI:685552
.
to sapiens (human)
to sapiens
to sapiens
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 60)
lier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
scoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
kins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le.N.,
ling,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
lfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
vaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.,
Marra,M.
eration and analysis of 280,000 human expressed sequence tags
ome Res. 6 (9), 807-828 (1996)
44478
9549
tact: Wilson RK
hington University School of Medicine
4 Forest Park Parkway, Box 8501, St. Louis, MO 63108
: 314 286 1800
: 314 286 1810
il: est@watson.wustl.edu
ert Size: -19
ert Size: 409
h quality sequence starts: 1
h quality sequence stops: 1
rcb: IMAGE Consortium, LLNL
s clone is available royalty-free through LLNL; contact the
GE Consortium (info@image.llnl.gov) for further information.
primer: -21ml3
h quality sequence stop: 1.
Location/Qualifiers
1. .60
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:501176"
/db_xref="taxon:9606"
/clone="IMAGE:84119"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOIR cells (kanamycin resistant)"
/clone_lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site_1:
ECori; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Hepatotomy from normal male caucasian. Average
insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGGCAG 3' ~3' adaptor sequence: 5'
CTCAGATTTTTTTTTTTTTT 3'"

66.0%; Score 13.2; DB 14; Length 60;
milarity 75.0%; Pred. No. 1.8e+05; Indels 0; Gaps 0;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CCTTGTCCTCCACGGGTT 20

```

38464 40 bp mRNA linear EST 18-AUG-1997  
 5b09.s1 NCI CGAP Pr8 Homo sapiens cDNA clone IMAGE:957305  
 ilar to TR:G547185 G547185 ELFO-ATP SYNTHASE COMPLEX FO MEMBRANE  
 AIN F SUBUNIT. ;, mRNA sequence.

38464 40 bp mRNA linear EST 18-AUG-1997  
 5b09.s1 NCI CGAP Pr8 Homo sapiens cDNA clone IMAGE:957305  
 ilar to TR:G547185 G547185 ELFO-ATP SYNTHASE COMPLEX FO MEMBRANE  
 AIN F SUBUNIT. ;, mRNA sequence.

38464.1 GI:2245967  
 sapiens (human)  
 sapiens  
 anyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 -CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 onal Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 r Gene Index  
 ublished (1997)  
 act: Robert Strausberg, Ph.D.  
 li: cgapbs-r@mail.nih.gov  
 sue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuacui,  
 ., Michael R. Emmert-Buck, M.D., Ph.D.  
 VA Library Preparation: David B. Krizman, Ph.D.  
 VA Library Arrayed by: Greg Lennon, Ph.D.  
 Sequencing by: Washington University Genome Sequencing Center  
 ne distribution: NCI-CGAP clone distribution information can be  
 id through the I.M.A.G.E. Consortium/LLNL at:  
 .bio.llnl.gov/bbrp/image/image.html

re considered overall poor quality  
 rt Length: 520 Std Error: 0.00  
 primer: -40m13 fwd. ET from Amersham  
 i quality sequence stop: 1.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:957305"  
 /sex="male"  
 /tissue\_type="prostate"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Pr8"  
 /note="Vector: pAMP10; mRNA made from invasive prostate  
 tumor, cDNA made by oligo-dT priming. Non-directionally  
 cloned. Size-selected on agarose gel, average insert  
 size 600 bp."

64.0%; Score 12.8; DB 9; Length 40;  
 ilarity 87.5%; Pred. No. 2.4e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 TGTCCTCCACGGGT 19  
 |||||  
 TGTCCTCACTGGT 1

8783 49 bp mRNA linear EST 23-OCT-1998  
 d05.s1 Soares NHMPu S1 Homo sapiens cDNA clone IMAGE:1661769  
 ilar to TR:O14923 O14923 REGULATOR OF G PROTEIN SIGNALING  
 2. ;, mRNA sequence.

8783 49 bp mRNA linear EST 23-OCT-1998  
 d05.s1 Soares NHMPu S1 Homo sapiens cDNA clone IMAGE:1661769  
 ilar to TR:O14923 O14923 REGULATOR OF G PROTEIN SIGNALING  
 2. ;, mRNA sequence.

8783.1 GI:3701953  
 sapiens (human)  
 sapiens  
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 This clone is available royalty-free through LLNL ; con  
 IMAGE Consortium (info@image.llnl.gov) for further info  
 Trace considered overall poor quality  
 Insert Length: 387 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 49  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /tissue\_type="Pooled human melanocyte, fetal h  
 pregnant uterus"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares NHMPu S1"  
 /note="Organ: mixed (see below); Vector: pT7T3;  
 (Pharmacia) with a modified polylinker; Site 1  
 Site 2: Eco RI; Equal amounts of plasmid DNA f  
 normalized libraries (melanocyte 2NBHM, pregna  
 NBHM, and fetal heart NBH19M) were mixed, an  
 were made in vitro. Following HAP purification,  
 was used as tracer in a subtractive hybridizat  
 reaction. The driver was PCR-amplified cDNAs f  
 5,000 clones made from the same 3 libraries. T  
 consisted of I.M.A.G.E. clones 260232-265223,  
 340488-345479, and 484488-489479."

Query Match 64.0%; Score 12.8; DB 9; Length 49;  
 Best Local Similarity 87.5%; Pred. No. 2.5e+05;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0;  
 QY 4 CTGTGCTCCACGGGT 19  
 |||||  
 Db 8 CTGTGCTCTCTCGGGT 23

RESULT 19  
 AA161672  
 LOCUS  
 DEFINITION  
 AA161672  
 malayi cDNA clone AFG0E08 5', mRNA sequence.  
 ACCESSION  
 VERSION  
 AA161672.1 GI:1737702  
 KEYWORDS  
 EST.  
 SOURCE  
 Brugia malayi  
 ORGANISM  
 Brugia malayi  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Fi  
 Onchocercidae; Brugia.  
 1 (bases 1 to 60)  
 Blaxter, M.L., Waterfall, M., Daub, J., Lizotte, M., Baron, I  
 Jones, S.J.  
 Genes expressed in adult female Brugia malayi  
 Unpublished (1996)  
 Contact: Blaxter ML  
 Institute of Cell, Animal and Population Biology  
 University of Edinburgh  
 Ashworth Labs, King's Buildings, West Mains Road, Edinbu  
 3UT, UK.  
 Tel: +44 131 650 6760  
 Fax: +44 131 670 5450  
 Email: mark.blaxter@ed.ac.uk  
 The ABI trace of this sequence can be viewed at  
 http://www.sanger.ac.uk/brugia/AF/MBAPCG0E08T3.html  
 Seq primer: T3.  
 Location/Qualifiers

```

1. .56
/organism="Brugia malayi"
/mol_type="mRNA"
/db_xref="taxon:6279"
/clone="AFG0E08"
/sex="female"
/dev_stage="adult"
/lab_host="XLI-Blue MRF"
/clone_lib="Brugia malayi adult female cDNA
(SAW96MLW-BmaF)"
/notes="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from approximately 50 adult females
isolated from the peritoneal cavity of jirds and
converted to double-stranded cDNA using reverse
transcriptase and oligo(dT) followed by RNase H and DNA
pol I. The library has 5 x 108 independent recombinants
and the average insert size is ~900bp. The library was
constructed by Michelle Lizotte-Waniewski. The
library is available from Dr.S.A.Williams, email:
genome@smith.edu."

```

```

64.0%; Score 12.8; DB 9; Length 60;
milarity 87.5%; Pred. No. 2.7e+05;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

TGTCCTCCACGGGTT 20
||||| ||| |||
TGTCCTGCAGTGGT 16

```

```

395 56 bp mRNA linear EST 22-MAY-1996
1c11.s1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328724 3'
ilar to gb:213009_rnal EPITHELIAL-CADHERIN PRECURSOR (HUMAN);
A sequence.

```

```

395
395.1 GI:1329476

```

```

o sapiens (human)
o sapiens
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 56)
lier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
ssoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
kins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
dis,E., Moore,B., Morris,M., Parsons,J., Frange,C., Rifkin,L.,
ling,T., Schellenberg,K., Soares,M.B., Tan,F., Thierri-Meg,J.,
vaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
Marra,M.
eration and analysis of 280,000 human expressed sequence tags
One Res. 6 (9), 807-828 (1996)

```

```

4478
9549
tact: Wilson RK
ington University School of Medicine
4 Forest Park Parkway, Box 8501, St. Louis, MO 63108
: 314 286 1800
: 314 286 1810

```

```

i: est@wustl.edu
s clone is available royalty-free through LNL ; contact the
GE Consortium (info@image.llnl.gov) for further information.
sible reversed clone: polyT not found
primer: mob REGA+ET.

```

```

Location/Qualifiers
1. .56
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1262928"
/db_xref="taxon:9606"

```

```

/clone="IMAGE:328724"
/tissue type="pancreatic islet"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Pancreatic Islet"
/notes="Organ: pancreas; Vector: pBluescript SK
EcORI; Site 2: XhoI; Reference: Hum Mol Gen 2,
Takeda et al. Cloned unidirectionally. Primer:
-5' adaptor sequence: 5' GAATTCGGCAGG 3' -3'
sequence: 5' CTCGAGTTTITTTTTTTT 3'"

```

## ORIGIN

```

Query Match 63.0%; Score 12.6; DB 14; Length 56;
Best Local Similarity 78.9%; Pred. No. 3.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0;

```

```

QY 1 ATCCTTGTCTCCACGGGT 19
||||| ||| |||
Db 3 AGCCTTGTCTCTCCAGGT 21

```

## RESULT 21

```

AA680800 58 bp mRNA linear EST
LOCUS
DEFINITION
UnfrAm0338 Leishmania major Amastigote Lambda Zap II li
Leishmania major cDNA clone M87 5', mRNA sequence.
AA680800
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Leishmania major
Leishmania major
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae
Leishmania.

```

```

AA680800.1 GI:2662805

```

```

REFERENCE
1 (bases 1 to 58)
AUTHORS
Norrish,A.R., Dyall,S.D., Smith,D.F. and Blackwell,J.M.
TITLE
Analysis of Leishmania Major Amastigote Expressed Sequ
JOURNAL
Unpublished (1997)
COMMENT
Contact: Blackwell JM
Cambridge Institute for Medical Research
Wellcome Trust/MRC Building, Addenbrooke's Hospital, Hi
Cambridge CB2 2XY, UK
Tel: 01223 336 143
Fax: 01223 331 206
Email: jmb37@cus.cam.ac.uk
PCR Primers
FORWARD: GTAAACGACGCGCCAGT
BACKWARD: GGAACAGCTATGACCATG
Seq primer: AATTACCTCTACTAAGGG
High quality sequence stop: 58.

```

```

FEATURES
source
1. .58
/organism="Leishmania major"
/mol_type="mRNA"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="M87"
/cell_type="Amastigote"
/clone_lib="Leishmania major Amastigote Lambda
library"
/notes="Vector: Lambda Zap II; Site 1: XhoI; Si

```

## ORIGIN

```

Query Match 63.0%; Score 12.6; DB 9; Length 58;
Best Local Similarity 78.9%; Pred. No. 3.2e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0;

```

```

QY 2 TCCTTGTCTCTCCACGGGT 20
||||| ||| |||
Db 20 TCCCTCTCTCTGCAGGT 38

```

## RESULT 22

```

H98532/c
LOCUS
H98532 44 bp mRNA linear EST

```



Id03.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone  
 SE:250661 3' similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL  
 FORM (HUMAN); mRNA sequence.

332  
 332.1 GI:1123182

> sapiens (human)  
 > sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 (bases 1 to 44)  
 Lier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Han, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Traskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

WashU-Merck EST Project  
 Published (1995)  
 Contact: Wilson RK  
 Washington University School of Medicine  
 1 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 : 314 286 1800  
 : 314 286 1810

1: est@wustl.wustl.edu  
 1 quality sequence stops: 1  
 1 quality sequence stops: 1  
 Note: IMAGE Consortium, LLNL  
 3E Consortium (info@image.llnl.gov) for further information.  
 The considered overall poor quality  
 cDNA reversed clone: polyT not found

Insert Length: 747 Std Error: 0.00  
 primer: Promega -21m13

1 quality sequence stop: 1.  
 Location/Qualifiers

1..44  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:3868367"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:250661"  
 /sex="Male"

/tissue\_type="melanocyte"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares melanocyte 2NBHM"  
 /note="Vector: pT73D (Pharmacia) with a modified  
 polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5'  
 TGTTCACCATCTGAGTGGGACGGCGCGAGTCTTTTCTTTTCTTTT 3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library constructed by Bento Soares and  
 M. Fatima Bonaldo. RNA from normal foreskin melanocytes  
 (FS374) was kindly provided by Dr. Anthony P. Albino."

62.0%; Score 12.4; DB 14; Length 44;  
 ilarity 81.2%; Pred. No. 3.6e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTGTGCTCTCCACGG 17  
 :|||||  
 :CNTGTCTCTCCACNG 22

13207  
 7b08.s1 NCI CGAP Co9 Homo sapiens cDNA clone IMAGE:1147959 3'  
 lar to SW:AFAR\_RAT P38918 AFLATOXIN B1 ALDEHYDE REDUCTASE ;  
 a sequence.  
 13207

AA633207.1 GI:2556621  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 (bases 1 to 52)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgpbs-remail.nih.gov  
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmer  
 M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequen  
 Clone distribution: NCI-CGAP clone distribution inform  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

1..52  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1147959"  
 /tissue\_type="colon tumor RER+"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Co9"  
 /note="Organ: colon; Vector: pT73D-Pac (Pharm  
 modified polylinker; 1st strand cDNA was prepa  
 RER+ colon tumor, and was then primed with a N  
 oligo(dT) primer. Double-stranded cDNA was lig  
 RI adaptors (Pharmacia), digested with Not I a  
 into the Not I and Eco RI sites of the modified  
 vector. Library is not normalized. Library wa  
 constructed by Bento Soares and M. Fatima Bona  
 (Soares4)."

## ORIGIN

Query Match 62.0%; Score 12.4; DB 9; Length 52;  
 Best Local Similarity 92.9%; Pred. No. 3.8e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 1 ATCCCTGTCTCTCCA 14  
 |||||  
 DB 2 ATCCTGTCTCTCAA 15

## RESULT 24

R95728/c

## LOCUS

R95728 55 bp mRNA linear EST  
 Yq47g09.r1 Soares fetal liver spleen INFLS Homo sapiens  
 IMAGE:198976 5' similar to gb:M91036 rna2 HEMOGLOBIN GA  
 GAMMA-G CHAINS (HUMAN); mRNA sequence.

R95728.1 GI:981388  
 EST.

## ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 55)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Traskis, E., Waterston, R., Williamson, A., Wohlmann, P.,  
 Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

JOURNAL

act: Wilson RK  
 ington University School of Medicine  
 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 314 286 1800  
 314 286 1810  
 rt Size: 1338  
 1: est@watson.wustl.edu  
 1 quality sequence starts: 1  
 1 quality sequence stops: 1  
 ce: IMAGE Consortium, L1NL  
 clone is available royalty-free through L1NL; contact the  
 Consortium (info@image.l1nl.gov) for further information.  
 rt Length: 1338 Std Error: 0.00  
 primer: M13RPI  
 1 quality sequence stop: 1.  
 Location/Qualifiers  
 1..55  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:3768026"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:198976"  
 /sex="male"  
 /dev\_stage="20 week-post conception fetus"  
 /lab\_host="PH108 (ampicillin resistant)"  
 /clone\_lib="Soares fetal liver spleen INFLS"  
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)  
 with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;  
 1st strand cDNA was primed with a Pac I - oligo(dT) primer  
 15' AACGGAGAAATTAATAAGATCTTTTTTTTTTTT 3',  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Pac I and cloned into the Pac I  
 and Eco RI sites of the modified pT7T3 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo."

ilarity 62.0%; Score 12.4; DB 14; Length 55;  
 Conservativity 86.7%; Pred. No. 3.8e+05;  
 Conservativity 0; Mismatches 2; Indels 0; Gaps 0;  
 TTGTCTCCACGG 17  
 |||||  
 TTGTCTCCACGCTG 19

18197 32 bp DNA linear GSS 13-JUN-2002  
 067630.51.80.x Arabidopsis thaliana TDNA insertion lines  
 idopsis thaliana genomic clone SALK\_067630.51.80.x, genomic  
 rey sequence.  
 18197  
 18197.1 GI:21419068  
 idopsis thaliana (thale cress)  
 idopsis thaliana  
 alyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 (bases 1 to 32)  
 nso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 rinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 on,P., Zimmerman,J. and Ecker,J.R.  
 sequence-Indexed Library of Insertion Mutations in the  
 idopsis Genome  
 ublished (2001)  
 tact: Joseph R. Ecker  
 k Institute Genomic Analysis Laboratory (SIGnAL)  
 Salk Institute for Biological Studies  
 10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 : 858 453 4100 x1752

Fax: 858 558 6379  
 Email: ecker@salx.edu  
 This is single pass sequence recovered from the left bot  
 TDNA. This sequence lies within an annotated exon of At1  
 Class: TDNA tagged  
 Location/Qualifiers  
 1..32  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_067630.51.80.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /note="PCR was performed on Arabidopsis thaliana  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic sec  
 the site of insertion. Details of the protocol  
 be found at http://signal.salx.edu/tdna\_protoc

ORIGIN  
 Query Match 61.0%; Score 12.2; DB 28; Length 32;  
 Best Local Similarity 82.4%; Pred. No. 4.1e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;  
 QY 4 CTGTCTCCACGGGTT 20  
 |||||  
 Db 30 CTGTCTCCACGTTGGT 14

RESULT 26  
 CC583588  
 LOCUS  
 DEFINITION  
 CH240 379P17.TARBA13P2 CHORI-240 Bos taurus genomic cl  
 CH240 379P17, genomic survey sequence.

ACCESSION  
 CC583588  
 VERSION  
 CC583588.1 GI:31933404  
 KEYWORDS  
 GSS.  
 SOURCE  
 Bos taurus (cow)  
 ORGANISM  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora,  
 Bovidae; Bovinae; Bos.

REFERENCE  
 AUTHORS  
 Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabl  
 Tsai,M., Cloutier,A., Lee,D., Gryn,N., Olson,T., Mayo,M.  
 Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A  
 Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S  
 Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.  
 Dairympie,B.P. and Tellam,R.  
 Bovine BAC End Sequences from Library CHORI-240, PLATES  
 Unpublished (2003)  
 Other GSSs: CH240 379P17.T7  
 Contac: Rob Holt

Sequencing  
 The British Columbia Cancer Agency Genome Science Centre  
 600 W. 10th Ave, Vancouver, British Columbia, Canada.V5;  
 Tel: 604-877-6085  
 Fax: 604-877-6276  
 Email: rholt@bcgsc.ca  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm). For BAC lib  
 availability, please contact Pieter de Jong (pdejong@ema  
 clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.html).  
 was undertaken as part of the International Bovine BAC  
 Consortium (IBBMC) by CSIRO Livestock Industries, Austri  
 British Columbia Genome Sciences Centre, Canada.  
 Plate: 379 row: P column: 17  
 Seq primer: SP6  
 Class: BAC ends  
 Location/Qualifiers  
 1..53

FEATURES  
 source

```

/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_379P17"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site.1: MboI; Site.2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

61.0%; Score 12.2; DB 29; Length 53;
ilarity 82.4%; Pred. No. 4.6e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTTGTCCTCCACGGG 18
|||||
TTATCTCCACGGG 22

3798 54 bp DNA linear GSS 14-FEB-2002
J24H12.1EL_x1 1008 - RescueMu Grid I Zea mays genomic, genomic
3798 sequence.
3798.1 GI:18663266

nays
nays
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
a; Panicoideae; Andropogoneae; Zea.
oases 1 to 54)
37.V.
a genomic sequences found using engineered RescueMu transposon
sliced (2001)
act: Walbot V
rtment of Biological Sciences
ford University
California Ave, Palo Alto, CA 94304, USA
650 723 2227
650 725 8221
l: walbot@stanford.edu
probable ligation site of ends cut by single endonuclease.
rse complemented post-ligation sequence from source sequence.
a: 1008024 row: 10
s: transposon-tagged.
Location/Qualifiers
1. 54
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev stage="adult"
/lab host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site.1: BamHI; Site.2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmdb.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

```

```

Query Match 61.0%; Score 12.2; DB 28; Length 54;
Best Local Similarity 82.4%; Pred. No. 4.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 3 CTTGTCTCCACGGGT 19
|||||
Db 17 CTTGTCTCTCCGGGT 33

RESULT 28
AA862784/c
LOCUS AA862784 59 bp mRNA linear EST
DEFINITION OH41906.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:14
similar to gb:J04810 DIVERGENT UPSTREAM PROTEIN (HUMAN);
sequence.
ACCESSION AA862784
VERSION AA862784.1 GI:2955263
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Hom
REFERENCE 1 (bases 1 to 59)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequenc
Clone distribution: NCI-CGAP clone distribution informa
found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 872 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.

FEATURES
Location/Qualifiers
1. 59
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="pooled germ cell tumors"
/lab host="DH10B"
/clone_lib="NCI CGAP GC4"
/note="Vector: p77m3D-Pac (Pharmacia) with a mo
polylinker; 1st strand cDNA was prepared from 3
germ cell tumors, and was then primed with a No
oligo(dT) primer. Double-stranded cDNA was ligo
RI adaptors (Pharmacia), digested with Not I an
into the Not I and Eco RI sites of the modified
vector. Library is normalized. Library was con
Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 61.0%; Score 12.2; DB 9; Length 59;
Best Local Similarity 82.4%; Pred. No. 4.7e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 3 CTTGTCTCTCCACGGGT 19
|||||
Db 37 CTTCTCTCTCCACAGGT 21

RESULT 29
CA913675
LOCUS CA913675 59 bp mRNA linear EST
DEFINITION PCSCL8719 Scarlet Runner Bean Suspensor Region TriplEx2
coccineus cDNA 5' similar to sb07g10.y1 Gm-cl004 Glycine

```

## sequence.

3675  
3675.1 GI:27400667

## neolus coccineus

neolus coccineus  
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
neolus.

(bases 1 to 59)

A.Q., Le, B.H., Weterings, K., Bi, Y.-P., Choi, J.-S.,  
Iroy, K.E., Choi, P.-S., Harada, J.U., Fischer, R.L. and  
berg, R.B.

Activity in Different Regions of a Post-Fertilization Plant  
Published (2002)

act: Goldberg, R.B.

artment of Molecular, Cell, & Developmental Biology  
ersity of California, Los Angeles

Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA

: 310 825 3270

: 310 825 8201

il: bob@ucla.edu

primer: 5' Triplex

FA=No.

## Location/Qualifiers

1. .59

/organism="Phaseolus coccineus"

/mol\_type="rRNA"

/cultivar="Hammond's Dwarf Scarlet"

/db\_xref="taxon:3886"

/dev\_stage="6-days post-pollination"

/clone\_lib="Scarlet Runner Bean Suspensor Region Triplex2"

/note="Organ: Suspensor Region of Globular-Stage Embryos;

Vector: Triplex2; Site\_1: SfiIA; Site\_2: SfiIB; Suspensor

regions were micro-dissected from globular-stage embryos

six days after pollination from greenhouse-grown plants

[Weterings et al., Plant Cell 13, 2409-2425 (2001)].

Double-stranded cDNA was synthesized from suspensor mRNA

using the SMART cDNA Library Construction Kit according to

the manufacturer (Clontech). The suspensor cDNA fragments

were directionally ligated into the SfiI restriction site

of the lambda triplex2 vector (Clontech), and the

recombinant cDNAs were transformed into E. coli XL1-Blue

cells (Clontech). Suspensor cDNA plasmids used for

directional sequencing were obtained by in vivo excision

from the lambda Triplex2 recombinants in E. coli BM25.8

cells (Clontech)."

61.0%; Score 12.2; DB 14; Length 59;

ilarity 82.4%; Pred. No. 4.7e+05;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCCTTGCTCCACGG 17

|||||

TCCTTGGCTCCATGG 13

202

8c03.r1 Soares fetal liver spleen INFLS Homo sapiens EST 05-OCT-1995

3E:204676 5' similar to gb:X54150 Inal IMMUNOGLOBULIN ALPHA FC

EPTOR PRECURSOR (HUMAN); mRNA sequence.

202.1

GI:1010034

sapiens (human)

sapiens

aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 60)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, I,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Mar,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Travaskis, E., Waterston, R., Williamson, A., Wohlmann, P.,  
Wilson, R.

TITLE  
JOURNAL

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1551

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; con

IMAGE Consortium (info@image.llnl.gov) for further info:

Trace considered overall poor quality

Insert Length: 1551 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

1. .60

/organism="Homo sapiens"

/mol\_type="rRNA"

/db\_xref="GDB:3773807"

/db\_xref="taxon:9606"

/clone="IMAGE:204676"

/sex="male"

/dev\_stage="20 week-post conception fetus"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal liver spleen INFLS"

/note="Organ: Liver and Spleen; Vector: pT7T3D

with a modified polylinker; Site\_1: Pac I; Site

1st strand cDNA was primed with a Pac I - olig

15' AACGGAAGATTAATAAGATCTTTTCTTTTCTTTT

double-stranded cDNA was ligated to Eco RI ada

(Pharmacia), digested with Pac I and cloned in

and Eco RI sites of the modified pT7T3 vector.

went through one round of normalization. Libra

constructed by Bento Soares and M.Fatima Bonal

## Query Match

Best Local Similarity 61.0%; Score 12.2; DB 14; Length 60;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 4 CTTGTCTCCACGGTT 20

|||||

Db 28 CTTGACCTCCAGGATT 12

## RESULT 31

AU014006

LOCUS

DEFINITION

Schizosaccharomyces pombe cDNA clone spc08993, mRNA seq

Schizosaccharomyces pombe

ACCESSION

AU014006

VERSION

AU014006.1 GI:3368797

EST.

KEYWORDS

Schizosaccharomyces pombe (fission yeast)

Schizosaccharomyces pombe

Schizosaccharomyces pombe

Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomycetes.

1 (bases 1 to 37)

Morimyo, M. and Mita, K.

Identification of expressed sequence tags of Schizosaccl

pombe

Unpublished (1998)

60.0%; Score 12; DB 9; Length 37;  
75.0%; Pred. No. 5.1e+05;  
ilarity

**REFERENCE**  
1. (bases 1 to 46)

**AUTHORS**  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

**TITLE**  
National Cancer Institute, Cancer Genome Anatomy Project  
Tumor Gene Index

```

blished (1997)
act: Robert Strausberg, Ph.D.
l: cgapbs@mail.nih.gov
clone is available royalty-free through LNL; contact the
E Consortium (info@image.lnl.gov) for further information.
e considered overall poor quality
rt Length: 790 Std Error: 0.00
primer: -40UP from Gibco
quality sequence stop: 1.
Location/Qualifiers
1. .46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1723359"
/dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta_8to9weeks_2NBHP8to9W"
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGCGCGCGATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

60.0%; Score 12; DB 9; Length 46;
ilarity 75.0%; Pred. No. 5.4e+05;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

TCTTGTCTCTCCACGGGTT 20
|||||
TCTTATCCACACGTGTT 30

30301 47 bp DNA linear GSS 17-DEC-2002
1_1_27_1_B01_1BL_x_1 3590 - RescueMu Grid M Zea mays genomic,
omic survey sequence.
30301
30301.1 GI:27215362
mays
mays
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; Liliopsida; Poales; PACCAD
le; Panicoideae; Andropogoneae; Zea.
(bases 1 to 47)
ot,V.
ze genomic sequences found using engineered RescueMu transposon
blished (2001)
-act: Walbot V
artment of Biological Sciences
iford University
California Ave, Palo Alto, CA 94304, USA
: 650 723 2227
: 650 725 8221
il: walbot@stanford.edu
y probable ligation site of ends cut by single endonuclease.
erse complemented post-ligation sequence from source sequence.
te: 3590.1-27.1 column: 5
ss: transposon-tagged.
Location/Qualifiers
1. .47
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"

```

```

/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="3590 - RescueMu Grid M"
/note="Organ: leaf; Vector: RescueMu (engineered
pBlueScript backbone); Site 1: BamHI; Site 2:
RescueMu is a 4.9 kb, modified maize Mu transp
designed to allow plasmid rescue from total ge
Mu elements insert preferentially into transcr
units. For more information on RescueMu, go to
site 'www.zmdb.iastate.edu' and follow the lin
'RescueMu.' Grid M was grown at University of
2001. DNA was extracted from leaf punches, dou
using BamHI and BglII, and ligated to form circ
plasmids. DH10B cells were transformed and ther
on LB plates with ampicillin."

Query Match 60.0%; Score 12; DB 28; Length 47;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 1 ATCCTTGTCTCTCCACGGGTT 20
|||||
DB 29 ATCCTTGTCTCTCCACGGGTT 10
|||||

RESULT 36
CG710925
LOCUS 49 bp DNA linear GSS
DEFINITION 1119019D08.2EL_x1 1119 - RescueMu Grid AA Zea mays genom
survey sequence.
ACCESSION CG710925
VERSION CG710925.1 GI:37736831
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tri
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poace
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 49)
Walbot V.
Maize genomic sequences found using engineered RescueMu
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endom
Reverse complemented post-ligation sequence from source
Plate: 1119019 row: 25
Class: transposon-tagged.
Location/Qualifiers
1. .49
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered
pBlueScript backbone); Site 1: BamHI; Site 2:
RescueMu is a 4.9 kb, modified maize Mu transp
designed to allow plasmid rescue from total ge
Mu elements insert preferentially into transcr
units. For more information on RescueMu, go to
site 'www.zmdb.iastate.edu' and follow the lin
'RescueMu.' Grid AA was grown at UC San Diego

```

was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

60.0%; Score 12; DB 29; Length 49;  
 ilarity 75.0%; Pred. No. 5.5e+05;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 CCTGTCTCTCCACGGGTT 20  
 |||||  
 CATTGCTCTGCGAGCTT 37

33694 49 bp DNA linear GSS 03-APR-2001  
 medium chabaudi genome survey sequence, clone PC9h11.pit,  
 nic survey sequence.  
 3694  
 3694.1 GI:11140201  
 genome survey sequence.  
 medium chabaudi  
 medium chabaudi  
 ryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 cases 1 to 49)  
 sen, C.S., Barrett, M.P., Lawson, D., Quail, M.A., Harris, D.,  
 an, S., Phillips, R.S. and Turner, C.M.  
 discovery in Plasmodium chabaudi by genome survey sequencing  
 Biochem. Parasitol. 113 (2), 251-260 (2001)  
 2558  
 5179  
 cases 1 to 49)  
 sen, C.S.  
 ct Submission  
 irted (06-NOV-2000) Division of Infection & Immunity,  
 arcity of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK  
 s 122 to 170 (QL to QR).  
 Location/Qualifiers  
 1. 49  
 /organism="Plasmodium chabaudi"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:5825"  
 /clone="PC9h11.pit"

60.0%; Score 12; DB 29; Length 49;  
 ilarity 75.0%; Pred. No. 5.5e+05;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 CCTGTCTCTCCACGGGTT 20  
 |||||  
 CAGAGTACACACCGGGTT 20

9714 51 bp mRNA linear EST 20-DEC-2001  
 9c06.y1 Gm-cl075 Glycine max cDNA clone SOYBEAN CLONE ID:  
 1075-3563 5', mRNA sequence.  
 9714

9714.1 GI:17962959  
 ine max (soybean)  
 ine max  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 ine.  
 bases 1 to 51)  
 maker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,  
 na, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B.,  
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., B  
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Card  
 McCann, R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project

TITLE  
 JOURNAL  
 COMMENT  
 Unpublished (1999)  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp  
 South Memorial Parkway Huntsville, AL 35801 For further  
 call: (800)-533-4363 or contact: ccu@resgen.com web site  
 www.resgen.com

Putative full length read  
 vector to vector length is 52  
 Seq primer: -40RP from Gibco.  
 Location/Qualifiers

FEATURES  
 source  
 1. 51  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl075-3563"  
 /tissue\_type="differentiating somatic embryos c  
 MSN6AC"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-cl075"  
 /note="Vector: pBluescript II SK+; Site 1: EcoR  
 XhoI; The cDNA library was constructed from mRN  
 from differentiating somatic embryos cultured  
 The library was prepared using the Stratagene  
 II SK(+) library construction kit. Complementary  
 synthesized from mRNA using a primer consisting  
 poly(GT) sequence with an XhoI restriction sit  
 adaptors were ligated to the blunt-ended cDNA  
 followed by XhoI digestion. The cDNA fragments  
 directionally cloned into the EcoRI-XhoI restri  
 of the pBluescript vector. The ligated cDNA fr  
 were transformed into E.coli ElectroMax DH10B h  
 tissue culture and library construction were pe  
 Francoise Thibaud-Nissen and Anu Khana (Lila Vo  
 University of Illinois)."

## ORIGIN

Query Match 60.0%; Score 12; DB 12; Length 51;  
 Best Local Similarity 75.0%; Pred. No. 5.5e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0;

Qy 1 ATCTTGTCTCTCCACGGGTT 20  
 |||||  
 Db 31 ATATTTTCTCTCAATGGGTT 12

## RESULT 39

CE225675/c

LOCUS

DEFINITION

1RT19B10 Bos taurus Reticulum #1 library Bos taurus cDNA

ribosomal protein L21 (EC 2.3.8.-) - GO terms: structura

constituent of ribosome (0003735); mRNA sequence.

CE225675

CE225675.1 GI:28296189

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;

Bovidae; Bovinae; Bos.

1 (bases 1 to 52)

Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,

Gordon, P.M.K. and Moore, S.S.

e Expression Profiling of the Bovine Gastrointestinal Tract  
 ublished (2002)  
 tact: Dr. Stephen Moore  
 f Genomics Laboratory  
 t of AFNS, University of Alberta  
 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada  
 : 780 492 0369  
 : 780 492 4265  
 il: stephen.moore@ualberta.ca  
 ert Length: 52 Std Error: 0.00  
 YA=No.

## Location/Qualifiers

1. .52  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="Smooth muscle"  
 /cell\_type="Stratified squamous epithelial"  
 /dev\_stage="Young adult"  
 /lab\_host="XLI-BlueWRF strain"  
 /clone\_lib="Bos taurus Reticulum #1 library"  
 /note="Organ: Reticulum; Vector: Uni-2ZAPXR; Site\_1:  
 EcoRI; Site\_2: Xho I"

60.0%; Score 12; DB 14; Length 52;  
 nilarity 75.0%; Pred. No. 5.6e+05;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

TCCTTGCTCCTCCACGGTT 20  
 |||||  
 TCATTTTCCTCCACGGTT 2

10472 55 bp DNA linear GSS 01-APR-2003  
 l\_1139\_1\_C11.1BL\_x\_1\_3591 - RescueMu Grid P Zea mays genomic,  
 omic survey sequence.

10472  
 10472.1 GI:29455363

mays  
 mays

ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 rmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 le; Panicoideae; Andropogoneae; Zea.  
 (bases 1 to 55)

ot.V.

ze genomic sequences found using engineered RescueMu transposon

ublished (2001)

-act: Walbot V

artment of Biological Sciences

ford University

California Ave, Palo Alto, CA 94304, USA

: 650 723 2227

: 650 723 8221

li: walbot@stanford.edu

y probable ligation site of ends cut by single endonuclease.

arse complemented post-ligation sequence from source sequence.

-e: 3591.1.139.1 row: 30

as: transposon-tagged:

Location/Qualifiers

1. .55

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="PH10B"

/clone\_lib="3591 - RescueMu Grid P"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site\_1: BamHI; Site\_2:  
 RescueMu is a 4.9 kb, modified maize Mu transp  
 designed to allow plasmid rescue from total ge  
 Mu elements insert preferentially into transcr  
 units. For more information on RescueMu, go to  
 site 'www.zmndb.iastate.edu' and follow the lin  
 'RescueMu.' Grid P was grown at Molokai in 200  
 extracted from leaf strips, double digested us  
 and BglII, and ligated to form circular plasm  
 cells were transformed and then screened on LB  
 ampicillin."

## ORIGIN

Query Match 60.0%; Score 12; DB 28; Length 55;  
 Best Local Similarity 75.0%; Pred. No. 5.6e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0;

QY 1 ATCCTTGCTCCTCCACGGTT 20

|||||

Db 1 ATCCTTTTCCTCTTCCCGTT 20

## RESULT 41

BX661950

LOCUS

DEFINITION

BX661950

Arabisopsis thaliana T-DNA flanking sequence GK-681H02-

genomic survey sequence.

ACCESSION

BX661950

VERSION

BX661950.1 GI:37618372

KEYWORDS

GSS

SOURCE

Arabisopsis thaliana (thale cress)

ORGANISM

Arabisopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr

Spermatophyta; Magnoliophyta; eudicotyledons; core eudi

rosids; eurosids II; Brassicales; Brassicaceae; Arabido

Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K.,

and Weisshaar, B.

A pipeline for automated high-throughput generation of

(flanking sequence tags) from Arabidopsis thaliana T-DN

transformed lines

Unpublished

3 (bases 1 to 57)

Li, Y., Strizhov, N., Rosso, M. and Weisshaar, B.

Direct Submission

Submitted (06-OCT-2003) Weisshaar B., Max-Planck-Instit

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 5082

This sequence is recovered from the left border of the

indicates an insertion close to or within gene At3g0408

sequences are generated at the MPI for Plant Breeding R

the context of the GABI-Kat project. GABI-Kat is part of

Plant Genomics program designated 'GABI'. Information o

availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1. .57

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-681H02-023045"

/note="PCR was performed on DNA from Arabidops

plants (T1) which were transformed with the T-1

vector pAC161. The lines contain one or more T-

insertions. The DNA fragment(s) resulting from

were directly sequenced to determine the genom

flanking the insertion. Sequences displaying s

source



similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

60.0%; Score 12; DB 29; Length 57;  
 ilarity 75.0%; Pred. No. 5.7e+05;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 'CCTGTGCTCCACGGGTT 20  
 |||||  
 'CCTCGCTTCTACTGGTT 54

3UMR 59 bp DNA linear GSS 01-SEP-2000  
 aodon nigroviridis genome survey sequence PUC-ORI end of clone  
 08 of library G from Tetraodon nigroviridis, genomic survey  
 ence.  
 1324

1324.1 GI:7982949  
 genome survey sequence.  
 aodon nigroviridis  
 aodon nigroviridis  
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 noterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 thomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 adontoidea; Tetraodontidae; Tetraodon.

t Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,  
 ot, A., Fizes, C., Wincker, P., Brottier, P., Quetier, F.,  
 in, W., and Weissenbach, J.  
 mate of human gene number provided by genome-wide analysis  
 g Tetraodon nigroviridis DNA sequence  
 Genet. 25 (2), 235-238 (2000)  
 6633  
 5645

t Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,  
 mes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,  
 in, W., Bernot, A., and Weissenbach, J.  
 aoterization and repeat analysis of the compact genome of the  
 water pufferfish Tetraodon nigroviridis  
 me Res. 10 (7), 939-949 (2000)  
 9837

9143  
 bases 1 to 59)  
 scope.  
 ct Submission  
 itted (12-APR-2000) Genoscope - Centre National de Sequencage :  
 91 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 b : www.genoscope.cns.fr)  
 e clone-end sequencing project of the Tetraodon nigroviridis  
 me. For more information, please take a look at  
 ://www.genoscope.cns.fr/Tetraodon.  
 Location/Qualifiers  
 1. .59

/organism="Tetraodon nigroviridis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:99883"  
 /clone="059G08"  
 /clone\_lib="G"  
 /note="Genoscope sequence ID : C0BG059BD04SP1-end :  
 PUC-ORI"

60.0%; Score 12; DB 29; Length 59;  
 ilarity 75.0%; Pred. No. 5.7e+05;  
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 CCTGTGCTCCACGGGTT 20

DB 57 ACCCTGGACCTCCACGGGCT 38

RESULT 43  
 CF296469/c  
 LOCUS  
 DEFINITION  
 30DGS--06-N14.g1 Rice leaf plasmid cDNA library I (30DG;  
 sativa cDNA clone 30DGS--06-N14, mRNA sequence.

ACCESSION  
 CF296469  
 VERSION  
 CF296469.1  
 KEYWORDS  
 EST.  
 SOURCE  
 Oryza sativa

ORGANISM  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 spermatophyta; Magnoliophyta; Liliopsida; Poales; Poace  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 AUTHORS  
 1 (bases 1 to 60)  
 Kim, J.S., Jun, K.W., Cheong, P.J., Kim, M.J., Lee, T.H., Shi  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 COMMENT  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.;  
 of Bioscience and Bioinformatics, Myongui University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bbnahm@bio.com, bbnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1. .60  
 Location/Qualifiers  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="30DGS--06-N14"  
 /tissue\_type="leaf"  
 /dev\_stage="30 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library I (3  
 /note="vector: PCR4-TOBO; Site 1: EcoRI; mRNA &  
 with oligoribonucleotides and then used as temp  
 RT-PCR."

ORIGIN  
 Query Match 60.0%; Score 12; DB 14; Length 60;  
 Best Local Similarity 75.0%; Pred. No. 5.8e+05;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0;  
 Qy 1 ATCCTTCTCCTCCACGGGTT 20  
 |||||  
 Db 40 ATCCTGCTACTCCATGGAT 21

RESULT 44  
 AZ650525  
 LOCUS  
 DEFINITION  
 1M0520F13R Mouse 10kb plasmid UUGCIM library Mus musculus  
 clone UUGCIM0520F13 R, genomic survey sequence.  
 ACCESSION  
 AZ650525  
 VERSION  
 AZ650525.1  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur  
 1 (bases 1 to 22)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ham  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D. Weiss, R.  
 Mouse whole genome scaffolding with paired end reads fro  
 plasmid inserts

ublished (2000)  
 uact: Robert B. Weiss  
 iversity of Utah Genome Center  
 iversity of Utah  
 . 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 112, USA  
 l: 801 585 5606  
 k: 801 585 7177  
 ail: ddm@genetics.utah.edu  
 ert Length: 10000 Std Error: 0.00  
 ate: 0520 row: F column: 13  
 i primer: CACACGAGAAACAGCTATGACC  
 as: plasmid ends  
 th quality sequence stop: 22.

Location/Qualifiers  
 1. .22  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="U06C1M0520F13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid U06C1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 [gil4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ilarity 59.0%; Score 11.8; DB 28; Length 22;  
 milarity 86.7%; Pred. No. 5.4e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TCCTTGTCCTCCAC 15  
 |||||  
 TCTTGTCCTCCAC 20

99801 34 bp mRNA linear EST 05-JUN-1998  
 ic11.s1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1607924 3,  
 liar to TR:Q28298 Q28298 RIBOSOME RECEPTOR. ; mRNA sequence.

99801  
 99801.1 GI:3190356

. sapiens (human)  
 . sapiens  
 ariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 (bases 1 to 34)  
 -CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 ional Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 or Gene Index  
 ublished (1997)  
 act: Robert Strausberg, Ph.D.  
 il: cgapps-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Sequencing by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequ  
 Clone distribution: NCI-CGAP clone distribution infor  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 1.

## FEATURES

## source

1. .34  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1607924"  
 /sex="female, pooled"  
 /tissue\_type="breast"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Br2"  
 /note="Vector: PT73D-Pac (Pharmacia) with a  
 polylinker; 1st strand cDNA was prepared from  
 breast tumor tissue, and was then primed with  
 oligo(dt) primer. Double-stranded cDNA was lig  
 RI adaptors (Pharmacia), digested with Not I &  
 into the Not I and Eco RI sites of the modifie  
 vector. This library is the normalized versio  
 NCI CGAP Br1.1. Library was constructed by Ber  
 and M. Fatima Bonaldo."

## ORIGIN

Query Match 59.0%; Score 11.8; DB 9; Length 34;  
 Best Local Similarity 86.7%; Pred. No. 6.1e+05;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 2 TCCTTGTCCTCCACG 16  
 |||||  
 Db 9 TCTTGTCCTCCACG 23

Search completed: February 29, 2004, 11:20:44  
 Job time : 1545.3 secs

1 09:38:22 2004

us-10-090-326-16.max.rge

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

cleic search, using sw model

February 29, 2004, 08:42:24 ; Search time 561.974 Seconds  
(without alignments)  
1388.275 Million cell updates/sec

US-10-090-326-16

18  
1 ctcatttggaatttggc 18

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

3470272 seqs, 21671516995 residues

hits satisfying chosen parameters: 1685580

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vi:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pla:\*

35: em\_htg\_rod:\*

36: em\_htg\_man:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

score greater than or equal to the score of the result being  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Query %	Describe
C 1	14.8	82.2	52	6	AX802710		AX802710
C 2	14.8	82.2	52	6	AX803056		AX803056
C 3	14	77.8	20	6	AR299374		AR299374
C 4	13.4	74.4	17	6	AR039529		AR039529
C 5	13.4	74.4	21	6	BD223828		BD223828
C 6	13.4	74.4	21	6	BD223838		BD223838
C 7	13.2	73.3	30	6	AR088737		AR088737
C 8	13.2	73.3	30	6	AR095464		AR095464
C 9	13.2	73.3	30	6	AR112465		AR112465
C 10	13.2	73.3	30	6	BD070730		BD070730
C 11	13.2	73.3	30	6	BD070756		BD070756
C 12	13.2	73.3	43	6	AR218439		AR218439
C 13	13.2	73.3	43	6	AR308225		AR308225
C 14	13.2	73.3	53	6	AR360210		AR360210
C 15	13	72.2	24	6	AX487503		AX487503
C 16	13	72.2	25	6	AX115740		AX115740
C 17	13	72.2	50	6	AX165018		AX165018
C 18	13	72.2	51	6	AX115741		AX115741
C 19	13	72.2	51	6	AX203928		AX203928
C 20	12.8	71.1	17	6	AR143576		AR143576
C 21	12.8	71.1	17	6	AR142578		AR142578
C 22	12.8	71.1	17	6	E49169		E49169
C 23	12.8	71.1	17	6	E49171		E49171
C 24	12.8	71.1	19	6	AR212683		AR212683
C 25	12.8	71.1	21	6	AX802543		AX802543
C 26	12.8	71.1	21	6	AX803055		AX803055
C 27	12.8	71.1	21	6	AX803276		AX803276
C 28	12.8	71.1	22	6	AR152786		AR152786
C 29	12.8	71.1	22	6	AX460279		AX460279
C 30	12.8	71.1	22	6	BD134242		BD134242
C 31	12.8	71.1	29	6	BD107065		BD107065
C 32	12.8	71.1	30	6	E49553		E49553
C 33	12.8	71.1	30	6	AX791284		AX791284
C 34	12.8	71.1	30	6	AX792291		AX792291
C 35	12.8	71.1	30	6	BD000721		BD000721
C 36	12.8	71.1	30	6	BD176724		BD176724
C 37	12.8	71.1	44	6	A23713		A23713
C 38	12.8	71.1	51	6	AX161257		AX161257
C 39	12.8	71.1	51	6	AX161258		AX161258
C 40	12.8	71.1	51	6	AX199396		AX199396
C 41	12.8	71.1	60	6	AX612397		AX612397
C 42	12.4	68.9	17	6	AR039527		AR039527
C 43	12.4	68.9	17	6	AX722776		AX722776
C 44	12.4	68.9	27	6	AX197327		AX197327
C 45	12.4	68.9	30	6	AX791288		AX791288
C 46	12.4	68.9	30	6	AX792109		AX792109
C 47	12.4	68.9	30	6	AX792504		AX792504
C 48	12.4	68.9	30	6	AX792638		AX792638
C 49	12.4	68.9	36	6	BD187098		BD187098
C 50	12.4	68.9	36	6	BD187099		BD187099
C 51	12.4	68.9	41	6	AX515933		AX515933
C 52	12.4	68.9	41	6	AX517373		AX517373
C 53	12.4	68.9	60	6	AX612395		AX612395
C 54	12.4	68.9	60	6	AX612396		AX612396
C 55	12.2	67.8	17	6	BD258527		BD258527
C 56	12.2	67.8	20	6	AR158757		AR158757
C 57	12.2	67.8	20	6	AR158758		AR158758
C 58	12.2	67.8	20	6	AR158759		AR158759
C 59	12.2	67.8	20	6	AR158760		AR158760
C 60	12.2	67.8	20	6	BD182366		BD182366
C 61	12.2	67.8	22	6	AR275223		AR275223
C 62	12.2	67.8	22	6	AR339881		AR339881
C 63	12.2	67.8	34	6	AR093100		AR093100
C 64	12.2	67.8	34	6	BD009924		BD009924
C 65	12.2	67.8	36	6	AR026172		AR026172

is the number of results predicted by chance to have a

67.8	36	6	AR026252	Sequence	C 139	11.6	64.4	30	6	E64516	E64516
67.8	36	6	AR026289	Sequence	C 140	11.6	64.4	36	6	AR031680	AR031680
67.8	36	6	AR026293	Sequence	C 141	11.6	64.4	36	6	I90298	I90298
67.8	36	6	I82914	Sequence 16	C 142	11.6	64.4	41	6	A10955	A10955
67.8	36	6	I82994	Sequence 96	C 143	11.6	64.4	43	6	AX483395	AX483395
67.8	36	6	I83031	Sequence 13	C 144	11.6	64.4	46	5	XELBETA6	M3550
67.8	36	6	I83035	Sequence 13	C 145	11.6	64.4	48	6	AR011223	AR011223
67.8	36	6	AR431100	Sequence	C 146	11.6	64.4	48	6	I17861	I17861
67.8	36	6	AR431180	Sequence	C 147	11.6	64.4	50	6	AR103103	AR103103
67.8	36	6	AR431217	Sequence	C 148	11.6	64.4	50	6	AR139719	AR139719
67.8	36	6	AR431221	Sequence	C 149	11.6	64.4	50	6	AR169834	AR169834
67.8	36	6	AX828893	Sequence	C 150	11.6	64.4	50	6	AR391898	AR391898
67.8	36	6	AX828973	Sequence	C 151	11.6	64.4	50	6	AX161129	AX161129
67.8	36	6	AX829010	Sequence	C 152	11.6	64.4	51	6	AX159880	AX159880
67.8	36	6	AX829014	Sequence	C 153	11.6	64.4	51	6	AX161723	AX161723
67.8	39	6	AX024135	Sequence	C 154	11.6	64.4	51	6	AX161724	AX161724
67.8	39	6	AX695305	Sequence	C 155	11.6	64.4	51	6	AX161725	AX161725
67.8	40	6	AR338013	Sequence	C 156	11.6	64.4	51	6	AX161727	AX161727
67.8	42	8	ATH521719	Sequence	C 157	11.6	64.4	52	6	AR360214	AR360214
67.8	43	6	AX683986	Sequence	C 158	11.6	64.4	52	6	AR360214	AR360214
67.8	50	6	AR011756	Sequence	C 159	11.6	64.4	59	9	AB010679	AB010679
67.8	50	6	I15869	Sequence 19	C 160	11.4	63.3	15	6	BD235742	BD235742
67.8	50	9	HUMFIRC	Human nucle	C 161	11.4	63.3	17	6	AX727163	AX727163
67.8	51	6	AX159515	Sequence	C 162	11.4	63.3	17	6	AX739421	AX739421
67.8	51	6	AX159516	Sequence	C 163	11.4	63.3	18	6	AR039705	AR039705
67.8	58	3	DROPRIS7	Sequence	C 164	11.4	63.3	19	6	E51982	E51982
67.8	58	3	AR269015	Sequence	C 165	11.4	63.3	19	6	E51983	E51983
67.8	59	8	ATH52349	Sequence	C 166	11.4	63.3	20	6	AR158761	AR158761
67.8	60	6	AX269016	Sequence	C 167	11.4	63.3	20	6	AR158762	AR158762
66.7	17	6	AR039531	Sequence	C 168	11.4	63.3	20	6	AR158763	AR158763
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66.7	22	6	BD070842	Method to	C 170	11.4	63.3	20	6	BD248791	BD248791
66.7	36	6	AX183680	Sequence	C 171	11.4	63.3	20	6	AR257161	AR257161
66.7	37	6	AX183678	Sequence	C 172	11.4	63.3	20	6	AR313819	AR313819
66.7	53	6	AR356620	Sequence	C 173	11.4	63.3	21	6	A49119	A49119
65.6	17	6	AX673592	Sequence	C 174	11.4	63.3	21	6	AR298039	AR298039
65.6	17	6	AX673601	Sequence	C 175	11.4	63.3	21	6	AX154108	AX154108
65.6	17	6	AX732265	Sequence	C 176	11.4	63.3	22	6	E26542	E26542
65.6	17	6	AX760467	Sequence	C 177	11.4	63.3	23	6	AR049795	AR049795
65.6	20	6	AX154268	Sequence	C 178	11.4	63.3	23	6	AR149689	AR149689
65.6	20	6	E32854	Sequence	C 179	11.4	63.3	24	6	AR404818	AR404818
65.6	21	6	A91603	Sequence 13	C 180	11.4	63.3	24	6	AX488314	AX488314
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65.6	21	6	BD023385	Method fo	C 182	11.4	63.3	25	6	AX114999	AX114999
65.6	22	8	ATH520143	Arabidops	C 183	11.4	63.3	25	6	AX197276	AX197276
65.6	27	6	AX178597	Sequence	C 184	11.4	63.3	25	6	BD133804	BD133804
65.6	27	6	AX117650	Sequence	C 185	11.4	63.3	29	6	AX163906	AX163906
65.6	27	6	AX742001	Sequence	C 186	11.4	63.3	29	6	AX163914	AX163914
65.6	27	6	AX742002	Sequence	C 187	11.4	63.3	29	6	AX163928	AX163928
65.6	27	6	AX742003	Sequence	C 188	11.4	63.3	30	6	A23714	A23714
65.6	28	6	AX236643	Sequence	C 189	11.4	63.3	30	6	A23715	A23715
65.6	38	6	AX222780	Sequence	C 190	11.4	63.3	30	6	AR122678	AR122678
65.6	38	6	AX424219	Sequence	C 191	11.4	63.3	30	6	AX766990	AX766990
65.6	38	6	AX581545	Sequence	C 192	11.4	63.3	30	6	AX792262	AX792262
65.6	51	6	AX160341	Sequence	C 193	11.4	63.3	30	6	AX792836	AX792836
65.6	51	6	AX160342	Sequence	C 194	11.4	63.3	30	6	BD000562	BD000562
65.6	51	6	AX160343	Sequence	C 195	11.4	63.3	31	6	E48925	E48925
65.6	51	6	AX160345	Sequence	C 196	11.4	63.3	31	6	BD094837	BD094837
65.6	51	6	AX160346	Sequence	C 197	11.4	63.3	31	6	AR083987	AR083987
65.6	51	6	AX164861	Sequence	C 198	11.4	63.3	35	6	AX521778	AX521778
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65.6	55	6	I45542	Sequence 15	C 200	11.4	63.3	36	6	AX058129	AX058129
65.6	59	8	ATH522061	Arabidops	C 201	11.4	63.3	37	6	BD131641	BD131641
64.4	20	6	BD090250	Method	C 202	11.4	63.3	38	6	AR118806	AR118806
64.4	20	6	BD176328	A method	C 203	11.4	63.3	38	6	AX766976	AX766976
64.4	23	6	AX802019	Sequence	C 204	11.4	63.3	38	8	AJ595611	AJ595611
64.4	24	6	AX164280	Sequence	C 205	11.4	63.3	41	6	A42975	A42975
64.4	24	6	AX565508	Sequence	C 206	11.4	63.3	41	6	A45521	A45521
64.4	24	6	BD012870	Sequence	C 207	11.4	63.3	41	6	AR030793	AR030793
64.4	25	6	AX467435	Sequence	C 208	11.4	63.3	41	6	AR082130	AR082130
64.4	25	6	AX487091	Sequence	C 209	11.4	63.3	41	6	AX516624	AX516624
64.4	28	6	AX554106	Sequence	C 210	11.4	63.3	41	6	AX518795	AX518795
64.4	28	6			C 211	11.4	63.3	42	6	A97026	A97026

63.3	42	6	A97032	A97032 Sequence 9	C 285	11.2	62.2	40	6	BD177307	BD177307
63.3	42	6	AR166711	AR166711 Sequence	C 286	11.2	62.2	40	8	ATH529715	AJ529715
63.3	42	6	BD086303	BD086303 CD8 as ce	C 287	11.2	62.2	41	6	AR003331	AR003331
63.3	42	6	BD086309	BD086309 CD8 as ce	C 288	11.2	62.2	41	6	AR109119	AR109119
63.3	43	6	AX484594	AX484594 Sequence	C 289	11.2	62.2	41	6	AR200774	AR200774
63.3	47	6	AR289704	AR289704 Sequence	C 290	11.2	62.2	42	6	AR009122	AR009122
63.3	47	6	AR290479	AR290479 Sequence	C 291	11.2	62.2	42	6	AR028096	AR028096
63.3	47	6	AX194770	AX194770 Sequence	C 292	11.2	62.2	42	6	AR031539	AR031539
63.3	48	10	MMCRV83	X79969 M.musculus	C 293	11.2	62.2	42	6	AR052833	AR052833
63.3	51	6	AX115477	AX115477 Sequence	C 294	11.2	62.2	42	6	AR127985	AR127985
63.3	51	6	AX203929	AX203929 Sequence	C 295	11.2	62.2	42	6	AR175210	AR175210
63.3	53	8	AJ589857	AJ589857 Arabidops	C 296	11.2	62.2	42	6	AR267930	AR267930
63.3	56	12	SYNCRPBSA	M33417 Synthetic E	C 297	11.2	62.2	42	6	AR288145	AR288145
63.3	56	12	SYNCRPBSA	M33417 Synthetic E	C 298	11.2	62.2	42	6	AR302754	AR302754
63.3	60	9	S72312	S72312 phosphofruct	C 299	11.2	62.2	42	6	AR408330	AR408330
62.2	17	6	AR142560	AR142560 Sequence	C 300	11.2	62.2	42	6	AX068052	AX068052
62.2	17	6	AR142562	AR142562 Sequence	C 301	11.2	62.2	42	6	AX078773	AX078773
62.2	17	6	AR142572	AR142572 Sequence	C 302	11.2	62.2	42	6	AX328126	AX328126
62.2	17	6	AR142574	AR142574 Sequence	C 303	11.2	62.2	42	6	AX589713	AX589713
62.2	17	6	AR142577	AR142577 Sequence	C 304	11.2	62.2	42	6	AX703578	AX703578
62.2	17	6	AR142579	AR142579 Sequence	C 305	11.2	62.2	42	6	AX838876	AX838876
62.2	17	6	BD258528	BD258528 Regulatio	C 306	11.2	62.2	42	8	AJ587913	AJ587913
62.2	17	6	E49153	E49153 Coccidioidis	C 307	11.2	62.2	44	6	AX463220	AX463220
62.2	17	6	E49155	E49155 Coccidioidis	C 308	11.2	62.2	45	6	AR003330	AR003330
62.2	17	6	E49165	E49165 Coccidioidis	C 309	11.2	62.2	47	6	AR284609	AR284609
62.2	17	6	E49167	E49167 Coccidioidis	C 310	11.2	62.2	47	6	AR284748	AR284748
62.2	17	6	E49170	E49170 Coccidioidis	C 311	11.2	62.2	47	6	AR288602	AR288602
62.2	17	6	E49172	E49172 Coccidioidis	C 312	11.2	62.2	47	6	AR289172	AR289172
62.2	17	6	AR188289	AR188289 Sequence	C 313	11.2	62.2	47	6	AR289329	AR289329
62.2	17	6	AR324142	AR324142 Sequence	C 314	11.2	62.2	47	6	AR289765	AR289765
62.2	17	6	AR328768	AR328768 Sequence	C 315	11.2	62.2	47	6	AR290560	AR290560
62.2	18	6	AR098820	AR098820 Sequence	C 316	11.2	62.2	47	6	AR291008	AR291008
62.2	20	6	AR073972	AR073972 Sequence	C 317	11.2	62.2	47	6	AR291110	AR291110
62.2	20	6	AR158756	AR158756 Sequence	C 318	11.2	62.2	47	6	AR291135	AR291135
62.2	20	6	AR215996	AR215996 Sequence	C 319	11.2	62.2	47	6	AX463213	AX463213
62.2	20	6	AR262268	AR262268 Sequence	C 320	11.2	62.2	48	6	BD002301	BD002301
62.2	20	6	AR275220	AR275220 Sequence	C 321	11.2	62.2	51	6	AX158257	AX158257
62.2	20	6	AR316186	AR316186 Sequence	C 322	11.2	62.2	51	6	AX160095	AX160095
62.2	20	6	AR339878	AR339878 Sequence	C 323	11.2	62.2	51	6	AX160096	AX160096
62.2	20	6	BD090197	BD090197 A method	C 324	11.2	62.2	51	6	AX160259	AX160259
62.2	20	6	BD176275	BD176275 A method	C 325	11.2	62.2	51	6	AX193395	AX193395
62.2	22	6	A99112	A99112 Sequence 16	C 326	11.2	62.2	51	6	AX204267	AX204267
62.2	22	6	BD074921	BD074921 Peroxisom	C 327	11.2	62.2	56	4	AY240935	AY240935
62.2	24	6	AR271760	AR271760 Sequence	C 328	11.2	62.2	56	4	AY240936	AY240936
62.2	24	6	BD253026	BD253026 Sequence 37	C 329	11.2	62.2	56	4	AX011428	AX011428
62.2	28	6	BD253026	BD253026 Regulatio	C 330	11.2	62.2	59	6	BD225719	BD225719
62.2	29	6	BD253505	BD253505 Regulatio	C 331	11.2	62.2	60	6	AR098097	AR098097
62.2	29	6	BD258156	BD258156 Regulatio	C 332	11.2	62.2	60	6	AX612398	AX612398
62.2	29	6	AX328910	AX328910 Sequence	C 333	11.2	62.2	60	6	AR174176	AR174176
62.2	29	6	AX339538	AX339538 Sequence	C 334	11.2	62.2	15	6	AR039533	AR039533
62.2	29	6	AX350086	AX350086 Sequence	C 335	11.2	62.2	17	6	AX496095	AX496095
62.2	29	6	BD197148	BD197148 Method an	C 336	11.2	62.2	20	4	DOGP40001	DOGP40001
62.2	29	6	AR055772	AR055772 Homo sapi	C 337	11.2	62.2	20	6	E09057	E09057
62.2	30	6	E49556	E49556 Glucose deh	C 338	11.2	62.2	20	6	AX587381	AX587381
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02710 52 bp DNA linear PAT 24-NOV-2003
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02710
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thetic construct

artificial sequences.
1
AUTHORS Karlisen,F.
TITLE Method for detecting human papillomavirus mRNA
JOURNAL Patent: WO 03057914-A 220 17-JUL-2003;
NORCHIP A/S (NO)
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RESULT 2
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DEFINITION Sequence 88 from Patent WO03057927.
ACCESSION AX803056
VERSION AX803056.1 GI:38501721
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

REFERENCE 1
AUTHORS Karlisen,F.
TITLE Detection of human papillomavirus e6 mRNA
JOURNAL Patent: WO 03057927-A 88 17-JUL-2003;
NORCHIP A/S (NO)
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Best Local Similarity 88.9%; Pred. No. 1.2e+04;
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Db 47 CTCATTGGGAATCGTGCC 30

RESULT 3
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DEFINITION Sequence 11109 from patent US 6537751.
ACCESSION AR299374
VERSION AR299374.1 GI:31686658
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high densit;
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 11109 25-MAR-2003;
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1 09:38:22 2004

us-10-090-326-16.max.rge

/mol\_type="genomic DNA"

77.8%; Score 14; DB 6; Length 20;  
ilarity 100.0%; Pred. No. 3.6e+04;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTGGAAATTTG 16  
|||||  
ATTGGAAATTTG 16

39529 17 bp DNA linear PAT 29-SEP-1999  
ence 377 from patent US 5807743.  
19529  
19529.1 GI:5958892

own.  
own.  
assified.  
(bases 1 to 17)  
rlecomb,D.T. and McSwiggen,J.A.  
rleukin-2 receptor gamma-chain ribozymes  
nt: US 5807743-A 377 15-SEP-1998;  
Location/Qualifiers  
1..17  
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74.4%; Score 13.4; DB 6; Length 17;  
ilarity 93.3%; Pred. No. 7.7e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CAATTGGAATTTT 15  
|||||  
GATTTGGAAATTTT 17

3828 21 bp DNA linear PAT 17-JUL-2003  
tification of microorganism causing acute respiratory tract  
action (ARI).

3828  
3828.1 GI:33033598  
002526088-A/3.  
hetic construct  
hetic construct  
ficial sequences.  
bases 1 to 21)  
es,G. and Schmitt,H.J.  
tification of microorganism causing acute respiratory tract  
ction (ARI)  
nt: JP 2002526088-A 3 20-AUG-2002;  
GENETICS NV  
Artificial Sequence  
JP 2002526088-A/3  
20-AUG-2002  
22-SEP-1999 JP 2000574290  
24-SEP-1998 EP 98870203.1  
GEERT JANNES,HEINZ JOSEF SCHMITT  
CI2N15/09,CI2Q1/68,CI2N15/00  
Description of Artificial Sequence:oligonucleotide FH Key  
Location/Qualifiers  
source 1..21  
/organism='Artificial Sequence'.  
Location/Qualifiers  
1..21  
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/mol\_type="genomic DNA"

ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 21;  
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Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 1 CTCATTGGAAATTTT 15  
|||||  
Db 15 CTCATTGGAAATTTT 1

RESULT 6  
BD223838/c

LOCUS BD223838 21 bp DNA linear PAT  
DEFINITION Identification of microorganism causing acute respirato  
infection (ARI).

ACCESSION BD223838  
VERSION BD223838.1 GI:33033608  
KEYWORDS JP 2002526088-A/13.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Jannes,G. and Schmitt,H.J.  
TITLE Identification of microorganism causing acute respirato  
infection (ARI)  
JOURNAL Patent: JP 2002526088-A 13 20-AUG-2002;  
INNOGENETICS NV

COMMENT OS Artificial Sequence  
FN JP 2002526088-A/13  
PD 20-AUG-2002  
PF 22-SEP-1999 JP 2000574290  
PR 24-SEP-1998 EP 98870203.1  
PI GEERT JANNES,HEINZ JOSEF SCHMITT  
PC CI2N15/09,CI2Q1/68,CI2N15/00  
CC Description of Artificial Sequence:oligonucleotide  
Location/Qualifiers  
FT source 1..21  
/organism='Artificial Sequence'.  
Location/Qualifiers  
1..21

FEATURES  
source

ORIGIN

Query Match 74.4%; Score 13.4; DB 6; Length 21;  
Best Local Similarity 93.3%; Pred. No. 7.4e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 1 CTCATTGGAAATTTT 15  
|||||  
Db 15 CTCATTGGAAATTTT 1

RESULT 7  
AR088737/c

LOCUS AR088737 30 bp DNA linear PAT  
DEFINITION Sequence 33 from patent US 5990091.  
ACCESSION AR088737

VERSION AR088737.1 GI:10015500  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)  
AUTHORS Tartaglia,J., Cox,W.I., Gettig,R.Robert., Martinez,H., P  
and Pincus,S.E.  
TITLE Vectors having enhanced expression, and methods of makir  
thereof  
JOURNAL Patent: US 5990091-A 33 23-NOV-1999;  
FEATURES Location/Qualifiers

L 09:38:22 2004

us-10-090-326-16.max.rge

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/mol_type="unassigned DNA"

73.3%; Score 13.2; DB 6; Length 30;
ilarity 83.3%; Pred. No. 9e+04; 3; Indels 0; Gaps 0;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACTTTGGAATTGGCC 18
|||||
ACTTTGGAATTGGCC 12

15464
ence 18 from patent US 6004777.
30 bp DNA linear PAT 08-SEP-2000
15464
15464.1 GI:10023359
town.
lassified.
(bases 1 to 30)
:aglia,J., Jacobs,B.L., Goebel,S.J., Cox,W.I., Gettig,R.Robert.,
us,S.E. and Paoletti,E.
:ors having enhanced expression, and methods of making and uses
eof
nt: US 6004777-A 18 21-DEC-1999;
Location/Qualifiers
1..30
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/mol_type="unassigned DNA"

73.3%; Score 13.2; DB 6; Length 30;
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Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACTTTGGAATTGGCC 18
|||||
ACTTTGGAATTGGCC 12

12465
ence 33 from patent US 6130066.
30 bp DNA linear PAT 16-MAY-2001
12465
12465.1 GI:14092365
town.
lassified.
(bases 1 to 30)
:aglia,J., Cox,W.I., Gettig,R.Robert., Martinez,H., Paoletti,E.
Pincus,S.E.
:ors having enhanced expression and methods of making and uses
eof
nt: US 6130066-A 33 10-OCT-2000;
Location/Qualifiers
1..30
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/mol_type="unassigned DNA"

73.3%; Score 13.2; DB 6; Length 30;
ilarity 83.3%; Pred. No. 9e+04; 3; Indels 0; Gaps 0;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACTTTGGAATTGGCC 18
|||||
ACTTTGGAATTGGCC 12
```

```
Db 29 CTACTTTGGAATTGGCC 12

RESULT 10
BD070730/c
LOCUS
DEFINITION
30 bp DNA linear PAT
Vectors having enhanced expression, and methods of makin
thereof.
ACCESSION
BD070730
VERSION
BD070730.1 GI:22616333
KEYWORDS
JP 2001514518-A/33.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 30)
Tartaglia,J., Cox,W.I., Gettig,R.R., Martinez,H., Paolet
Pincus,S.E.
Vectors having enhanced expression, and methods of makin
thereof
JOURNAL
Patent: JP 2001514518-A 33 11-SEP-2001;
VIROGENETICS CORP
COMMENT
OS Artificial Sequence
PN JP 2001514518-A/33
PD 11-SEP-2001
PF 13-FEB-1998 JP 1998539564
PR 12-MAR-1997 US 08/816155
PI JAMES TARTAGLIA,WILLIAM I COX,RUSSELL R
GETTIG,HECTOR MARTINEZ,
PI ENZO PAOLETTI,STEVEN E PINCUS
PC C12N15/64,C12N15/67,C12N15/86,A61K48/00
CC Vectors having enhanced expression, and methods of
uses thereof
FH Key Location/Qualifiers
FT source 1..30
/organism='Artificial Sequence'.

FEATURES
source
1..30
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/mol_type="genomic DNA"
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ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 30;
Best Local Similarity 83.3%; Pred. No. 9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCAATTGGAAATTGGCC 18
|||||
29 CTACTTTGGAATTGGCC 12
Db

RESULT 11
BD070756/c
LOCUS
DEFINITION
30 bp DNA linear PAT
Vectors having enhanced expression, and methods of makin
thereof.
ACCESSION
BD070756
VERSION
BD070756.1 GI:22616359
KEYWORDS
JP 2001514519-A/17.
SOURCE
Vaccinia virus
ORGANISM
Vaccinia virus
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordc
Orthopoxvirus.
REFERENCE
1 (bases 1 to 30)
Tartaglia,J., Jacobs,B.L., Goebel,S.J., Cox,W.I., Gettig
Pincus,S.E. and Paoletti,E.
Vectors having enhanced expression, and methods of makin
thereof
JOURNAL
Patent: JP 2001514519-A 17 11-SEP-2001;
VIROGENETICS CORP,ARIZONA STATE UNIVERSITY
COMMENT
OS Vaccinia virus
PN JP 2001514519-A/17
PD 11-SEP-2001
```

25-FEB-1998 JP 1998539591  
 12-MAR-1997 US 08/815809  
 JAMES TARTAGLIA, BERTRAM L JACOBS, SCOTT J GOBBEL, WILLIAM I COX,  
 RUSSELL ROBERT GETTIG, STEVEN E PINCUS, ENZO PAOLETTI PC  
 15/63, A61K39/12, A61K39/285  
 Vectors having enhanced expression, and methods of making and  
 uses thereof  
 Key Location/Qualifiers  
 source 1..30  
 /organism="Vaccinia virus".  
 Location/Qualifiers  
 1..30  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10245"

73.3%; Score 13.2; DB 6; Length 30;  
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 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 CATTGGGAATTTGCC 18  
 ||||| |||||  
 ACTTTGGGAATATGCC 12

3439 43 bp DNA linear PAT 25-SEP-2002  
 ance 9 from patent US 6420113.  
 3439  
 3439.1 GI:23319216

own.  
 assified.  
 ases 1 to 43)  
 nler, J., Valkirs, G. and Gray, J.  
 eric polyclonal antibodies  
 nt: US 6420113-A 9 16-JUL-2002;  
 Location/Qualifiers  
 1..43  
 /organism="unknown"  
 /mol\_type="genomic DNA"

73.3%; Score 13.2; DB 6; Length 43;  
 ilarity 83.3%; Pred. No. 8.5e+04; 3; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 TATTTGGGAATTTGCC 18  
 ||||| |||||  
 TATTTCGGGTTTGGC 11

3225 43 bp mRNA linear PAT 12-JUN-2003  
 ance 28 from patent US 6555310.  
 3225  
 3225.1 GI:31699617

own.  
 assified.  
 ases 1 to 43)  
 .J., Buechler, J. and Valkirs, G.  
 clonal libraries  
 nt: US 6555310-A 28 29-APR-2003;  
 Location/Qualifiers  
 1..43  
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## ORIGIN

Query Match 73.3%; Score 13.2; DB 6; Length 43;  
 Best Local Similarity 83.3%; Pred. No. 8.5e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;  
 QY 1 CTCATTGGGAATTTGCC 18  
 ||||| |||||  
 Db 28 CTCATTTCGGGTTTGGC 11

RESULT 14  
 AR360210/c  
 LOCUS AR360210 53 bp DNA linear PAT  
 DEFINITION Sequence 101 from patent US 6596279.  
 ACCESSION AR360210  
 VERSION AR360210.1 GI:33767091  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 53)  
 AUTHORS Paoletti, E.; Tartaglia, J., Cox, W. I., Gallo, R. and Franch  
 TITLE Immunodeficiency recombinant poxvirus  
 JOURNAL Patent: US 6596279-A 101 22-JUL-2003;  
 FEATURES  
 Location/Qualifiers  
 source 1..53  
 /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

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 QY 1 CTCATTGGGAATTTGCC 18  
 ||||| |||||  
 Db 47 CTACTTTGGGAATATTTGCC 30

RESULT 15  
 AX487503/c  
 LOCUS AX487503 24 bp DNA linear PAT  
 DEFINITION Sequence 4803 from Patent WO02053728.  
 ACCESSION AX487503  
 VERSION AX487503.1 GI:22321651  
 KEYWORDS  
 SOURCE Candida albicans  
 ORGANISM Candida albicans  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharo  
 Saccharomycetales; mitosporic Saccharomycetales; Candida  
 REFERENCE 1  
 AUTHORS Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K. L.  
 TITLE Gene disruption methodologies for drug target discovery  
 JOURNAL Patent: WO 02053728-A 4803 11-JUL-2002;  
 FEATURES  
 Location/Qualifiers  
 source 1..24  
 /organism="Candida albicans"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:5476"

## ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 5 TTTTGGGAATTTGCC 17  
 ||||| |||||  
 Db 14 TTTTGGGAATTTGCC 2

## RESULT 16

15740 25 bp DNA linear PAT 11-MAY-2001  
ence 863 from Patent WO0129262.  
15740  
15740.1 GI:14032682  
thetic construct  
thetic construct  
ificial sequences.  
ult-Newburg, L. and Pohl, M.  
ccopying reagents, kits and methods of use thereof  
ent: WO 0129262-A 863 26-APR-2001;  
hid BioSciences, Inc. (US)  
Location/Qualifiers  
1. .25  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"  
72.2%; Score 13; DB 6; Length 25;  
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Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
ATTGGGAATTTT 15  
|||||  
ATTGGGAATTTT 15  
65018 50 bp DNA linear PAT 22-JUN-2001  
ence 213 from Patent WO0138586.  
65018  
65018.1 GI:14545847  
o sapiens (human)  
o sapiens  
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
nkets, R.A. and Leach, M.  
leic acids containing single nucleotide polymorphisms and  
hods of use thereof  
ent: WO 0138586-A 213 31-MAY-2001;  
agen Corporation (US)  
Location/Qualifiers  
1. .50  
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/db\_xref="taxon:9606"  
25\_-26  
/note="Nucleotide deleted between bases 25 and 26  
Accession number cg4393591"  
26  
/note="single nucleotide polymorphism"  
72.2%; Score 13; DB 6; Length 50;  
milarity 100.0%; Pred. NO. 1.1e+05; Mismatches 0; Indels 0; Gaps 0;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
ATTGGGAATTTT 15  
|||||  
ATTGGGAATTTT 14  
15741 51 bp DNA linear PAT 11-MAY-2001  
ence 864 from Patent WO0129262.

ACCESSION AX115741  
VERSION AX115741.1 GI:14032683  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Picoult-Newburg, L. and Pohl, M.  
TITLE Genotyping reagents, kits and methods of use thereof  
JOURNAL Patent: WO 0129262-A 864 26-APR-2001;  
Orchid BioSciences, Inc. (US)  
FEATURES  
source  
1. .51  
Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
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Best Local Similarity 100.0%; Pred. NO. 1.1e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0;  
QY 3 CATTGGGAATTTT 15  
|||||  
Db 3 CATTGGGAATTTT 15  
RESULT 19  
AX203928/c  
LOCUS AX203928 51 bp DNA linear PAT  
DEFINITION Sequence 34 from Patent WO0148245.  
ACCESSION AX203928  
VERSION AX203928.1 GI:15393385  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphism  
methods of use thereof  
JOURNAL Patent: WO 0148245-A 34 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES  
source  
1. .51  
Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
variation  
26  
/note="single nucleotide polymorphism"  
Accession number cg43969076"  
ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 51;  
Best Local Similarity 100.0%; Pred. NO. 1.1e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0;  
QY 1 CTCATTGGGAATT 13  
|||||  
Db 13 CTCATTGGGAATT 1  
RESULT 20  
AR142576  
LOCUS AR142576 17 bp DNA linear PAT  
DEFINITION Sequence 35 from patent US 6203801.  
ACCESSION AR142576  
VERSION AR142576.1 GI:15103862  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

FEATURES		source	
PC	A61K39/21, A61K39/215,A61K39/235,A61K39/255,A61K39/39,A61P33/3, C07K14/455,C12N15/09, PC G01N33/569,C12N15/00 CC Strandedness: Double; CC Topology: Linear; FH Key FT source FT	Location/Qualifiers 1. .17 /organism='Unidentified'. Location/Qualifiers 1. .17 /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'	
ORIGIN			
Query Match 71.1%; Score 12.8; DB 6; Length 17; Best Local Similarity 87.5%; Pred. No. 1.6e+05; Matches 14; Conservative 0; Mismatches 2; Indels 0;			
QY	2 TCATTGGGAATTTGTC 17 		
DB	2 TCAATTGGGATTTGTC 17 		
RESULT 23			
E49171	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	E49171 Coccidiosis vaccine. E49171 E49171.1 GI:18629296 JP 2000219635-A/31. unidentified unclassified.	17 bp DNA linear PAT:
REFERENCE AUTHORS TITLE JOURNAL COMMENT			
1 (bases 1 to 17) Schaep,T.C., Kaiberu,K.M. and Fuerumuren,A.N. Coccidiosis vaccine Patent: JP 2000219635-A 31 08-AUG-2000; AKZO NOBEL NV OS Unidentified PN JP 2000219635-A/31 PD 08-AUG-2000 PF 01-OCT-1999 JP 1999281680 PR 07-OCT-1998 EP 98203384.7,16-OCT-1998 EP 9820345 THEODORUS CORNELIS SCHAEF,KATARINA MARIA KAJBERU, PI A NICHOLAS FUERUMUREN PC A61K39/00,A61K39/012,A61K39/108,A61K39/112,A61K39/15,A61K A61K39/21, A61K39/215,A61K39/235,A61K39/255,A61K39/39,A61P33/02 C07K14/455,C12N15/09, PC G01N33/569,C12N15/00 CC Strandedness: Double; CC Topology: Linear; FH Key FT source FT			
Location/Qualifiers 1. .17 /organism='Unidentified'. Location/Qualifiers 1. .17 /organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'			
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source			
ORIGIN			
Query Match 71.1%; Score 12.8; DB 6; Length 17; Best Local Similarity 87.5%; Pred. No. 1.6e+05; Matches 14; Conservative 0; Mismatches 2; Indels 0;			
QY	2 TCATTGGGAATTTGTC 17 		
DB	2 TCAATTGGGATTTGTC 17 		

12683  
ence 46 from patent US 6403089.  
12683  
12683.1 GI:23309470

town.  
town.  
lassified.  
(bases 1 to 19)  
,G. and Clark,D.A.  
ods of modulating immune coagulation  
nt: US 6403089-A 46 11-JUN-2002;  
Location/Qualifiers  
1. .19  
/organism="unknown"  
/mol\_type="genomic DNA"

71.1%; Score 12.8; DB 6; Length 19;  
ilarity 87.5%; Pred. No. 1.5e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
TTTGGGAATTTTGGC 18  
|||||  
TTTAGAATTTTGGC 4

12543  
ence 53 from Patent WO03057914.  
2543  
2543.1 GI:38501241

helic construct  
helic construct  
ficial sequences.  
sen,F.  
od for detecting human papillomavirus mRNA  
nt: WO 03057914-A 53 17-JUL-2003;  
hip A/S (NO)  
Location/Qualifiers  
1. .21  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="HPV primer"

71.1%; Score 12.8; DB 6; Length 21;  
ilarity 87.5%; Pred. No. 1.5e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
CATTTGGGAATTTTG 16  
|||||  
CATTTGGGAATCGTG 1

3055  
ence 87 from Patent WO03057927.  
3055  
3055.1 GI:38501720

a papillomavirus  
a papillomavirus  
ses; dsDNA viruses, no RNA stage; Papillomaviridae;  
llomavirus.

REFERENCE  
1  
AUTHORS  
Karlsen,F.  
TITLE  
Detection of human papillomavirus e6 mRNA  
JOURNAL  
Patent: WO 03057927-A 87 17-JUL-2003;  
Norchip A/S (NO)  
FEATURES  
Location/Qualifiers  
source  
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/organism="Human papillomavirus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10566"

ORIGIN  
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Best Local Similarity 87.5%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;  
Qy 1 CTCATTGGGAATTTTG 16  
|||||  
Db 16 CTCATTGGGAATCGTG 1

RESULT 27  
AX803276/c  
LOCUS  
AX803276 DNA linear PAT  
DEFINITION  
Sequence 308 from Patent WO03057927.  
ACCESSION  
AX803276  
VERSION  
AX803276.1 GI:38501941  
KEYWORDS  
SOURCE  
Human papillomavirus  
Human papillomavirus  
ORGANISM  
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
Papillomavirus.

REFERENCE  
1  
AUTHORS  
Karlsen,F.  
TITLE  
Detection of human papillomavirus e6 mRNA  
JOURNAL  
Patent: WO 03057927-A 308 17-JUL-2003;  
Norchip A/S (NO)  
FEATURES  
Location/Qualifiers  
source  
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/db\_xref="taxon:10566"

ORIGIN  
Query Match 71.1%; Score 12.8; DB 6; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1.5e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;  
Qy 1 CTCATTGGGAATTTTG 16  
|||||  
Db 16 CTCATTGGGAATCGTG 1

RESULT 28  
AR152786  
LOCUS  
AR152786 DNA linear PAT  
DEFINITION  
Sequence 66 from patent US 6235470.  
ACCESSION  
AR152786  
VERSION  
AR152786.1 GI:15120318  
KEYWORDS  
SOURCE  
Unknown.  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 22)  
AUTHORS  
Sidransky,D.  
TITLE  
Detection of neoplasia by analysis of saliva  
JOURNAL  
Patent: US 6235470-A 66 22-MAY-2001;  
FEATURES  
Location/Qualifiers  
source  
1. .22  
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/mol\_type="unassigned DNA"



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ORIGIN
Query Match          71.1%;   Score 12.8;   DB 6;   Length 22;
Best Local Similarity 87.5%;   Pred. No. 1.5e+05;
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QY      3  CATTGGGAATTGGCC 18
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DB      6  CATCTTGAATTGGCC 21

RESULT 31
BD107065
LOCUS      Alpha 1-3 galactosyl transferase gene knockout cell and
DEFINITION constructing the same.
ACCESSION  BD107065
VERSION     BD107065.1  GI:23201883
KEYWORDS    JP 2002017360-A/4.
SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    1 (bases 1 to 29)
AUTHORS      Sawada,T., Murakami,T., Yokoyama,N., Urakawa,M., Uruno,K
              Aoyagi,T.
TITLE        Alpha 1-3 galactosyl transferase gene knockout cell and
JOURNAL      Patent: JP 2002017360-A 4 22-JAN-2002;
              NATIONAL FEDERATION OF AGRICULTURAL COOPERATIVE ASSOCIAT
COMMENT      WOMEN'S MEDICAL COLLEGE
              OS Artificial Sequence
              PN JP 2002017360-A/4
              PD 22-JAN-2002
              PF 04-JUL-2000  JP 2000202748
              PI TKIHIKO SAWADA,TORU MURAKAMI,NAOHIKO YOKOYAMA,MAMI
              EI KATSUYOSHI URUNO,TAKAHITO AOYAGI
              PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,C12N15/00,C1
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FEATURES
source
Location/Qualifiers
1..29
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Best Local Similarity 87.5%;   Pred. No. 1.5e+05;
Matches 14;   Conservative 0;   Mismatches 2;   Indels 0;

QY      3  CATTGGGAATTGGCC 18
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DB      9  CATTGGGAATTGGAC 24

RESULT 32
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LOCUS      Glucose dehydrogenase.
DEFINITION  E49553
ACCESSION  E49553
VERSION     E49553.1  GI:18622043
KEYWORDS    JP 2000350588-A/4.
SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    1 (bases 1 to 30)
AUTHORS      Hayade,K.
TITLE        Glucose dehydrogenase
JOURNAL      Patent: JP 2000350588-A 4 19-DEC-2000;

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HAYADE  
Artificial Sequence  
JP 2000350588-A/4  
19-DEC-2000  
18-JAN-2000 JP 2000009152

KOJI HAYADE  
C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/04, PC  
21/54, C12N15/09,  
C12N5/00

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ATTGGGAATTTTGGC 18  
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TTTGGGAATTTTCC 16

91284 30 bp DNA linear PAT 17-JUL-2003  
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91284  
91284.1 GI:32956731  
icobacter pylori  
icobacter pylori  
teria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
icobacteraceae; Helicobacter.

rain, P., Rain, J.C., Colland, F., de Reuse, H. and Labigne, A.  
tein-protein interactions in Helicobacter pylori  
ent: WO 02066501-A 3748 29-AUG-2002;  
rigenics (FR); INSTITUT PASTEUR (FR)

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CATATGGGAATTTTAC 21

792291 30 bp DNA linear PAT 17-JUL-2003  
quence 4755 from Patent WO02066501.  
792291  
792291.1 GI:32957738

icobacter pylori  
icobacter pylori  
teria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
icobacteraceae; Helicobacter.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1  
Legrain, P., Rain, J.C., Colland, F., de Reuse, H. and Labi  
Protein-protein interactions in Helicobacter pylori  
Patent: WO 02066501-A 4755 29-AUG-2002;  
Hybrigenics (FR); INSTITUT PASTEUR (FR)

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DB 6 TCATTTGGAGTTTTC 21

RESULT 35

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LOCUS  
DEFINITION Process for producing glucose dehydrogenase.  
ACCESSION BD000721  
VERSION SD000721.1 GI:18623834  
KEYWORDS JP 2000354495-A/4.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
1 (bases 1 to 30)

REFERENCE  
AUTHORS Hayade, K.  
TITLE Process for producing glucose dehydrogenase  
JOURNAL Patent: JP 2000354495-A 4 26-DEC-2000;  
COMMENT KOJI HAYADE

OS Artificial Sequence  
PN JP 2000354495-A/4  
PD 26-DEC-2000  
PF 12-MAY-2000 JP 2000140344  
PI KOJI HAYADE  
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Query Match 71.1%; Score 12.8; DB 6; Length 30;  
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Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGGAATTTTGGC 18  
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DB 1 CCTTTGGGAATTTTCC 16

RESULT 36

BD176724 30 bp DNA linear PAT  
LOCUS  
DEFINITION Glucose dehydrogenase.  
ACCESSION BD176724  
VERSION BD176724.1 GI:29122434  
KEYWORDS WO 02072839-A/5.  
SOURCE synthetic construct

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```

etic construct
ficial sequences.
bases 1 to 30)
,K. and Igarashi, S.
ose dehydrogenase
nt: WO 02072839-A 5 19-SEP-2002;
SODE,SATOSHI IGARASHI
Artificial Sequence
WO 02072839-A/5
19-SEP-2002
07-MAR-2002 WO 2002JP002124
13-MAR-2001 JP 01P 070413
KOJI SODE,SATOSHI IGARASHI
C12N15/53,C12N9/04,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/
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TTTGGAAATTTTCC 16

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'13.1 GI:23956600

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61257 51 bp DNA linear PAT 22-JUN-2001
uence 4585 from Patent WO0140521.
61257
61257.1 GI:14542588
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
1
REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms
JOURNAL Methods of use thereof
Patent: WO 0140521-A 4585 07-JUN-2001;
Curagen Corporation (US)
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RESULT 39
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DEFINITION Sequence 4586 from Patent WO0140521.
ACCESSION AX161258
VERSION AX161258.1 GI:14542589
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
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REFERENCE
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphism:
methods of use thereof
Patent: WO 0140521-A 4586 07-JUN-2001;
Curagen Corporation (US)
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16 CATTGGAATCTTGCC 1
Db

RESULT 40
AX199396
LOCUS AX199396 51 bp DNA linear PAT
DEFINITION Sequence 326 from Patent WO0151670.
ACCESSION AX199396
VERSION AX199396.1 GI:15389790
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
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alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 kets, R.A. and Leach, M.D.  
 eic acids containing single nucleotide polymorphisms and  
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 nt: WO 0151670-A 326 19-JUL-2001;  
 gen Corporation (US)  
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 139527 17 bp DNA linear PAT 29-SEP-1999  
 uence 375 from patent US 5807743.  
 139527  
 139527.1 GI:5958890  
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 (bases 1 to 17)  
 nchcomb, D.T. and McSwiggen, J.A.  
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 ACCESSION  
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 KEYWORDS  
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 ORGANISM  
 Mus musculus  
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 Telerman, A., Amson, R. and Tuijinder, M.  
 Sequences involved in phenomena of tumour suppression,  
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 JOURNAL  
 Patent: WO 03025176-A 463 27-MAR-2003;  
 Molecular Engines Laboratories (FR)  
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 LOCUS  
 DEFINITION  
 Sequence 1034 from Patent WO0151627.  
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 ORGANISM  
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 1  
 Haughe, B.M., Wang, M.L., Parsons, J.D. and Parnell, L.D.  
 Nucleic acid molecules and other molecules associated w  
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 Patent: WO 0151627-A 1034 19-JUL-2001;  
 MONSANTO COMPANY (US)  
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1288  
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cobacter pylori  
cobacter pylori  
eria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
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ain, P., Rain, J.C., Collard, F., de Reuse, H. and Labigne, A.  
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GenCore version 5.1.6  
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February 29, 2004, 07:46:14 ; Search time 153.584 Seconds  
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JS-10-090-326-16

18

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IDENTITY\_NUC

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3373863 seqs, 2124099041 residues

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length: 0

length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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1: geneseqn1980s.\*

2: geneseqn1990s.\*

3: geneseqn2000s.\*

4: geneseqn2001as.\*

5: geneseqn2001bs.\*

6: geneseqn2002s.\*

7: geneseqn2003as.\*

8: geneseqn2003bs.\*

9: geneseqn2003cs.\*

10: geneseqn2004s.\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
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#### SUMMARIES

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82.2	52	9	ADD22161	Add22161	HPV E6 ge
77.8	20	3	AAX52730	Aax52730	Human gen
77.8	20	3	AAX276753	Aax276753	Human bia
76.7	41	4	AH49769	Aah49769	Human gro
74.4	17	2	AAV94759	Aav94759	Human IL-
74.4	21	2	AAV65069	Aav65069	Farainflu
74.4	21	3	AAAI4173	Aaal4173	Piv-3 fus
74.4	21	3	AAAI4163	Aaal4163	Piv-3 fus
73.3	23	4	AAH27357	Aah27357	PCR prime
73.3	30	2	AAV58254	Aav58254	HIV Pol2
73.3	30	2	AAV60282	Aav60282	HIV-1 Pol
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73.3	30	9	ADC21256	Adc21256	E. coli 1
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73.3	41	6	ABV76517	Abv76517	Human cyt
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73.3	43	9	AAD61290	Aad61290	Mouse imm
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39	8	ADA73939	Ada73939	Carcinoma	c 201	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 202	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 203	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 204	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 205	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 206	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 207	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 208	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 209	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 210	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 211	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 212	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 213	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 214	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 215	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 216	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 217	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 218	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 219	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 220	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 221	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 222	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 223	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 224	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 225	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 226	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 227	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 228	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 229	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 230	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 231	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 232	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 233	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 234	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 235	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 236	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 237	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 238	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 239	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 240	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 241	11.8	65.6	50	6	ABZ06247	Abz06247
39	8	ADA73939	Ada73939	Carcinoma	c 242	11.8	65.6	50	6	ABZ06247	Abz06247

64.4	41	4	AAH47808	11.4	316	63.3	25	6	ABL50083	1
64.4	41	7	ABZ25879	11.4	317	63.3	25	8	ACK24090	1
64.4	42	2	AAX78675	11.4	318	63.3	26	3	ACC58107	1
64.4	42	2	AAX78676	11.4	319	63.3	27	3	AAAL4283	1
64.4	42	2	AAV84727	11.4	320	63.3	28	4	AAH41087	1
64.4	43	3	ABZ26816	11.4	321	63.3	27	4	ABK11935	1
64.4	43	6	AAZ68522	11.4	322	63.3	28	4	AAO09015	1
64.4	47	3	AAQ35570	11.4	323	63.3	29	4	AAO08993	1
64.4	48	6	AAQ35570	11.4	324	63.3	29	4	AAO08993	1
64.4	48	6	AAQ35570	11.4	325	63.3	29	4	AAO08993	1
64.4	50	2	AAV40154	11.4	326	63.3	30	2	AAQ31448	1
64.4	50	4	AAI77516	11.4	327	63.3	30	2	AAQ31448	1
64.4	50	6	ABZ02067	11.4	328	63.3	30	2	AAQ31448	1
64.4	50	6	ABZ04559	11.4	329	63.3	30	2	AAQ31448	1
64.4	50	6	ABZ04139	11.4	330	63.3	30	6	ABX69073	1
64.4	50	6	ABZ05325	11.4	331	63.3	30	6	ABX69073	1
64.4	51	2	ABX78694	11.4	332	63.3	30	7	ACC58544	1
64.4	51	4	AAI78112	11.4	333	63.3	31	3	AAH44274	1
64.4	51	4	AAI78111	11.4	334	63.3	31	4	AAH44274	1
64.4	51	4	AAI78110	11.4	335	63.3	31	4	AAH44274	1
64.4	51	4	AAI76267	11.4	336	63.3	32	7	ABZ77834	1
64.4	51	4	AAI78114	11.4	337	63.3	32	7	ABZ77834	1
64.4	52	2	AAI78114	11.4	338	63.3	34	2	AAV37944	1
64.4	52	2	AAI78114	11.4	339	63.3	34	2	AAV37944	1
64.4	56	3	AAI78114	11.4	340	63.3	34	2	AAV37944	1
64.4	56	3	AAI78114	11.4	341	63.3	34	2	AAV37944	1
64.4	57	3	AAI78114	11.4	342	63.3	35	6	AAV37944	1
64.4	60	6	ABN43584	11.4	343	63.3	36	2	AAV37944	1
64.4	60	6	ABN43584	11.4	344	63.3	36	2	AAV37944	1
64.4	60	6	ABN43584	11.4	345	63.3	36	2	AAV37944	1
64.4	60	6	ABN43584	11.4	346	63.3	36	2	AAV37944	1
64.4	60	6	ABN43584	11.4	347	63.3	37	2	AAV37944	1
64.4	60	6	ABN43584	11.4	348	63.3	37	2	AAV37944	1
64.4	60	6	ABN43584	11.4	349	63.3	39	9	AAV37944	1
64.4	60	6	ABN43584	11.4	350	63.3	39	9	AAV37944	1
64.4	60	6	ABN43584	11.4	351	63.3	41	2	AAV37944	1
64.4	60	6	ABN43584	11.4	352	63.3	41	2	AAV37944	1
64.4	60	6	ABN43584	11.4	353	63.3	41	2	AAV37944	1
64.4	60	6	ABN43584	11.4	354	63.3	41	6	ABZ46038	1
64.4	60	6	ABN43584	11.4	355	63.3	41	6	ABZ46038	1
64.4	60	6	ABN43584	11.4	356	63.3	41	8	ADAL4244	1
64.4	60	6	ABN43584	11.4	357	63.3	42	2	AAV37944	1
64.4	60	6	ABN43584	11.4	358	63.3	42	2	AAV37944	1
64.4	60	6	ABN43584	11.4	359	63.3	42	2	AAV37944	1
64.4	60	6	ABN43584	11.4	360	63.3	43	6	ABZ27947	1
64.4	60	6	ABN43584	11.4	361	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	362	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	363	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	364	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	365	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	366	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	367	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	368	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	369	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	370	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	371	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	372	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	373	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	374	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	375	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	376	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	377	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	378	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	379	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	380	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	381	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	382	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	383	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	384	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	385	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	386	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	387	63.3	47	3	AAZ67092	1
64.4	60	6	ABN43584	11.4	388	63.3	47	3	AAZ67092	1



62.2	17	3	Aaz94914	Eimeria t	C 462	11.2	62.2	42	2	AAT47616	Aat47616
62.2	17	3	Aaf06330	Hammerhea	C 463	11.2	62.2	42	2	AAV17709	Aav17709
62.2	18	3	Aaz93505	TRADD ant	C 464	11.2	62.2	42	2	AAV26985	Aav26985
62.2	20	2	Aat27521	Mouse and	C 465	11.2	62.2	42	2	AAV18808	Aav18808
62.2	20	2	Aaz11551	Mouse and	C 466	11.2	62.2	42	2	Aaz08491	Aaz08491
62.2	20	2	Aax03831	Regulator	C 467	11.2	62.2	42	4	AAFS5028	Aaf55028
62.2	20	2	Aax97397	Primer us	C 468	11.2	62.2	42	4	AAF75821	Aaf75821
62.2	20	3	AAZ73529	Mouse and	C 469	11.2	62.2	42	4	AAf28311	Aaf28311
62.2	20	4	AD11554	Human gly	C 470	11.2	62.2	42	6	ABK15602	Abk15602
62.2	20	5	AH80414	Oligonucle	C 471	11.2	62.2	42	6	ABI98949	Abi98949
62.2	20	6	AB145397	Human chr	C 472	11.2	62.2	42	7	ABZ25307	Abz25307
62.2	20	6	AD44754	Mouse and	C 473	11.2	62.2	42	7	ABZ25442	Abz25442
62.2	20	7	ABZ88402	Human oli	C 474	11.2	62.2	42	8	AA155878	Aal55878
62.2	20	7	ACD42114	Antisense	C 475	11.2	62.2	42	9	ADD15071	Adi15071
62.2	20	9	AD61626	PCR prime	C 476	11.2	62.2	42	9	ADD15019	Adi15019
62.2	20	9	AD81305	HIV PRT a	C 477	11.2	62.2	42	9	AAD60794	Aad60794
62.2	21	2	Aaz26664	Human pol	C 478	11.2	62.2	42	9	AD81031	Ad81031
62.2	22	2	Aax92251	Primer us	C 479	11.2	62.2	42	4	AAI71512	Aai71512
62.2	22	2	Aax27975	PCR prime	C 480	11.2	62.2	42	4	ABQ82198	Abq82198
62.2	22	3	AAA46221	Primer IP	C 481	11.2	62.2	42	5	AAT28095	Aat28095
62.2	24	3	AAL38161	Human BH3	C 482	11.2	62.2	42	5	ADD15016	Adi15016
62.2	24	7	ACC00110	Primer #1	C 483	11.2	62.2	42	7	AAZ52618	Aax52618
62.2	25	6	AD37476	Interleuk	C 484	11.2	62.2	42	7	AAZ52568	Aax52568
62.2	25	8	AC187433	Human mic	C 485	11.2	62.2	42	3	AAZ67948	Aaz67948
62.2	25	8	AC194315	Human mic	C 486	11.2	62.2	42	3	AAZ68396	Aaz68396
62.2	25	8	ACK19413	Human mic	C 487	11.2	62.2	42	3	AAZ66560	Aaz66560
62.2	25	8	AC191941	Human mic	C 488	11.2	62.2	42	3	AAZ67153	Aaz67153
62.2	27	2	AAX05255	Primer 15	C 489	11.2	62.2	42	3	AAZ65990	Aaz65990
62.2	27	6	ABK87106	S. aureus	C 490	11.2	62.2	42	6	ABQ82191	Abq82191
62.2	27	10	ADE84730	Vesicular	C 491	11.2	62.2	42	4	AAI30842	Aai30842
62.2	28	2	AAT80548	Methanol	C 492	11.2	62.2	42	5	AAI33658	Aai33658
62.2	29	2	AAA16948	Aryl hydr	C 493	11.2	62.2	42	6	ABZ07760	Abz07760
62.2	29	2	AAV92960	Human B-r	C 494	11.2	62.2	42	5	ABZ03095	Abz03095
62.2	29	2	AAV91896	Human C-r	C 495	11.2	62.2	42	5	ABZ03147	Abz03147
62.2	29	3	ABL50861	Transcrip	C 496	11.2	62.2	42	5	ABZ08035	Abz08035
62.2	29	3	AAZ46119	Oestrogen	C 497	11.2	62.2	42	5	ABZ05507	Abz05507
62.2	29	3	AAFO1307	Hammerhea	C 498	11.2	62.2	42	5	ABZ07856	Abz07856
62.2	29	3	AAF00828	Hammerhea	C 499	11.2	62.2	42	5	AAI30876	Aai30876
62.2	29	3	AAFO5958	Hammerhea	C 500	11.2	62.2	42	5	AAI27273	Aai27273
62.2	29	6	ABL91602	Chlamydia	C 501	11.2	62.2	42	5	AAI76482	Aai76482
62.2	29	6	ABK15061	B. rapus	C 502	11.2	62.2	42	5	AAI74644	Aai74644
62.2	30	2	Aaz30432	Arabidops	C 503	11.2	62.2	42	5	AAI76483	Aai76483
62.2	30	3	AAC63952	Acinetoba	C 504	11.2	62.2	42	5	AAI76646	Aai76646
62.2	30	4	AAF24606	PCR prime	C 505	11.2	62.2	42	5	AAH89544	Aah89544
62.2	31	3	AAI15263	PCR prime	C 506	11.2	62.2	42	5	AAH79758	Aah79758
62.2	31	3	AAAL5722	PCR prime	C 507	11.2	62.2	42	5	AAT21090	Aat21090
62.2	33	6	ABN86844	Human syn	C 508	11.2	62.2	42	5	Aaz96924	Aaz96924
62.2	34	2	AAT94903	Forward p	C 509	11.2	62.2	42	5	ABK14852	Abk14852
62.2	34	2	AAV18035	PMADS3 p	C 510	11.2	62.2	42	6	AAZ51953	Aaz51953
62.2	34	2	AAV91896	Porphorym	C 511	11.2	62.2	42	6	ABN32584	Abn32584
62.2	34	2	AAV91978	Porphorym	C 512	11.2	62.2	42	6	ABN37858	Abn37858
62.2	37	2	AAV56252	C. elegans	C 513	11.2	62.2	42	6	ABN49050	Abn49050
62.2	37	9	ADD15070	Primer to	C 514	11.2	62.2	42	6	ABN39896	Abn39896
62.2	38	2	AAT82048	Human c-m	C 515	11.2	62.2	42	6	ABN46717	Abn46717
62.2	38	2	AAT82137	Human c-m	C 516	11.2	62.2	42	6	ABN37281	Abn37281
62.2	38	4	ABK04090	Human NOG	C 517	11.2	62.2	42	6	ABN33266	Abn33266
62.2	38	4	ABK05254	Human NOG	C 518	11.2	62.2	42	6	ABN44510	Abn44510
62.2	38	6	ABK20623	Human ERG	C 519	11.2	62.2	42	6	ABN46983	Abn46983
62.2	38	6	ABK58021	Human CLC	C 520	11.2	62.2	42	6	ABN36945	Abn36945
62.2	38	9	ADD15018	Primer to	C 521	11.2	62.2	42	5	AB154631	Abi54631
62.2	39	9	ADD15059	PCR prime	C 522	11.2	62.2	42	5	AB118625	Abi18625
62.2	40	2	AAQ12333	HPV type	C 523	11.2	62.2	42	5	ABH80254	Abh80254
62.2	40	2	AAT71193	HPV type	C 524	11.2	62.2	42	5	AB115341	Abi15341
62.2	41	2	AAT28096	Probe 07U	C 525	11.2	62.2	42	5	AB106432	Abi06432
62.2	41	2	AAV50622	Brassica	C 526	11.2	62.2	42	5	AB152553	Abi52553
62.2	41	2	AAV50885	Maize pol	C 527	11.2	62.2	42	5	AB118624	Abi18624
62.2	41	6	ABL96051	Brassica	C 528	11.2	62.2	42	5	ABH73426	Abh73426
62.2	41	9	ADC51453	Interfero	C 529	11.2	62.2	42	5	ABF08426	Abf08426
62.2	42	2	AAQ35434	PCR prime	C 530	11.2	62.2	42	5	ABC14979	Abc14979
62.2	42	2	AAQ67825	Canarypox	C 531	11.2	62.2	42	5	ABC24018	Abc24018
62.2	42	2	AAT00918	Canarypox	C 532	11.2	62.2	42	5	ABF01914	Abf01914
62.2	42	2	AAT69996	Canarypox	C 533	11.2	62.2	42	5	ABF30368	Abf30368
62.2	42	2			C 534	11.2	62.2	42	5	ABF92184	Abf92184

61.1	13	5	ABC52427	Abc52427 Oligonuc	608	10.8	60.0	17	2	AAx73365
61.1	13	5	ABC30524	Abc30524 Oligonuc	609	10.8	60.0	17	2	AAx73366
61.1	13	5	ABF08427	Abf08427 Oligonuc	c 610	10.8	60.0	17	2	AAx71026
61.1	13	5	ABC72794	Abc72794 Oligonuc	c 611	10.8	60.0	17	2	AAa21487
61.1	13	5	ABC72795	Abc72795 Oligonuc	c 612	10.8	60.0	17	2	AAa21488
61.1	13	5	ABC14978	Abc14978 Oligonuc	c 613	10.8	60.0	17	2	AAa21489
61.1	13	5	ABC85628	Abc85628 Oligonuc	c 614	10.8	60.0	17	3	AAa36335
61.1	13	5	ABF94613	Abf94613 Oligonuc	c 615	10.8	60.0	17	3	AAa36336
61.1	13	5	ABC85629	Abc85629 Oligonuc	c 616	10.8	60.0	17	7	AAf06331
61.1	13	5	ABF94612	Abf94612 Oligonuc	c 617	10.8	60.0	17	7	AAf06332
61.1	13	5	ABF08130	Abf08130 Oligonuc	c 618	10.8	60.0	17	7	AAf06333
61.1	13	5	ABC24019	Abc24019 Oligonuc	c 619	10.8	60.0	17	9	AAf06334
61.1	13	5	ABC52426	Abc52426 Oligonuc	c 620	10.8	60.0	17	9	AAf06335
61.1	13	5	ABC30525	Abc30525 Oligonuc	c 621	10.8	60.0	18	2	AAV13362
61.1	13	5	ABF08131	Abf08131 Oligonuc	c 622	10.8	60.0	18	2	AAV13363
61.1	13	5	ABF30369	Abf30369 Oligonuc	c 623	10.8	60.0	18	4	AAV37865
61.1	13	5	ABF01915	Abf01915 Oligonuc	c 624	10.8	60.0	18	4	AAV37866
61.1	13	5	ABF92185	Abf92185 Oligonuc	c 625	10.8	60.0	18	4	AAV37867
61.1	17	2	AAV94761	AAv94761 Human IL-	c 626	10.8	60.0	18	6	AAV37868
61.1	17	6	ABQ96210	Abq96210 Tumour su	c 627	10.8	60.0	20	2	AAV37869
61.1	17	6	AAQ84974	Aaq84974 E. coli P	c 628	10.8	60.0	20	2	AAQ82291
61.1	20	6	ABT13254	Abt13254 Fancoi a	c 629	10.8	60.0	20	2	AAV85914
61.1	20	6	ABL45348	Ab145348 Human chr	c 630	10.8	60.0	20	2	AAV85915
61.1	20	6	ABL44504	Ab144504 Human chr	c 631	10.8	60.0	20	2	AAV85916
61.1	20	7	ABZ89718	Abz89718 Human oli	c 632	10.8	60.0	20	4	AAV85917
61.1	20	7	ABZ85199	Abz85199 Human oli	c 633	10.8	60.0	20	4	AAV85918
61.1	20	7	ABZ85200	Abz85200 Human oli	c 634	10.8	60.0	20	4	AAV85919
61.1	20	9	ADC42491	Adc42491 FANCD2 PC	c 635	10.8	60.0	20	5	AAH80754
61.1	21	2	AAZ18208	Aaz18208 Serine th	c 636	10.8	60.0	20	5	AAH80755
61.1	21	2	ABZ22860	Abz22860 Clonal T	c 637	10.8	60.0	20	5	AAH80756
61.1	22	7	AAV63028	AAv63028 D. immiti	c 638	10.8	60.0	20	5	AAH80757
61.1	23	2	AAV63316	AAv63316 Forward P	c 639	10.8	60.0	20	5	AAH80758
61.1	23	3	AAA58201	Aaa58201 Onchocerc	c 640	10.8	60.0	20	5	AAH80759
61.1	23	3	AAAL37887	Aal37887 Ankyrin c	c 641	10.8	60.0	20	6	AAH80760
61.1	23	6	ABT11220	Abt11220 TRC8 rela	c 642	10.8	60.0	20	6	AAH80761
61.1	23	6	ABK10442	Abk10442 Human TRC	c 643	10.8	60.0	20	7	AAH80762
61.1	24	6	AAAS14957	Aas14957 Human cyc	c 644	10.8	60.0	20	7	AAH80763
61.1	27	3	AAAS28444	Aaa28444 Synthetic	c 645	10.8	60.0	20	9	AAH80764
61.1	27	8	ABX13222	Abx13222 DNA encod	c 646	10.8	60.0	20	9	AAH80765
61.1	27	8	ADB39111	Adb39111 Human tum	c 647	10.8	60.0	20	9	AAH80766
61.1	29	6	ABSS3583	Abss3583 Aminoketo	c 648	10.8	60.0	20	9	AAH80767
61.1	29	6	AAV69389	AAv69389 Human ATG	c 649	10.8	60.0	20	9	AAH80768
61.1	30	2	AAAX34667	Aax34667 Human ATG	c 650	10.8	60.0	20	9	AAH80769
61.1	31	2	AAV67634	AAv67634 Nucleotid	c 651	10.8	60.0	20	9	AAH80770
61.1	31	2	AAV58219	AAv58219 Candida C	c 652	10.8	60.0	20	9	AAH80771
61.1	34	3	AAZ08277	Aaz08277 PCR prime	c 653	10.8	60.0	20	9	AAH80772
61.1	34	3	AAZ57187	Aaz57187 Human DET	c 654	10.8	60.0	20	9	AAH80773
61.1	40	7	ABX94276	Abx94276 PCR prime	c 655	10.8	60.0	20	9	AAH80774
61.1	40	9	ADD12872	Add12872 Fusion pr	c 656	10.8	60.0	20	9	AAH80775
61.1	41	4	AAI99689	Aai99689 Human TNF	c 657	10.8	60.0	20	9	AAH80776
61.1	41	4	AAI99690	Aai99690 Human TNF	c 658	10.8	60.0	20	9	AAH80777
61.1	41	6	ABA92437	Ab92437 Human L1	c 659	10.8	60.0	20	9	AAH80778
61.1	41	6	ABA92438	Ab92438 Human L1	c 660	10.8	60.0	20	9	AAH80779
61.1	42	3	AAZ55060	Aaz55060 Neisseria	c 661	10.8	60.0	20	9	AAH80780
61.1	42	3	AAZ55062	Aaz55062 Neisseria	c 662	10.8	60.0	20	9	AAH80781
61.1	45	8	ACF05705	Acf05705 Tyrosinas	c 663	10.8	60.0	20	9	AAH80782
61.1	47	6	ABK40779	Abk40779 Human obe	c 664	10.8	60.0	20	9	AAH80783
61.1	48	5	AAAS44152	Aaa44152 Neisseria	c 665	10.8	60.0	20	9	AAH80784
61.1	50	6	ABZ00825	Abz00825 Human leu	c 666	10.8	60.0	20	9	AAH80785
61.1	50	6	ABZ02713	Abz02713 Human leu	c 667	10.8	60.0	20	9	AAH80786
61.1	51	4	ABZ28523	Abz28523 Human SNP	c 668	10.8	60.0	20	9	AAH80787
61.1	51	4	AAI78721	Aai78721 Human sil	c 669	10.8	60.0	20	9	AAH80788
61.1	51	4	AAI77317	Aai77317 Human sil	c 670	10.8	60.0	20	9	AAH80789
61.1	51	4	AAI76201	Aai76201 Human sil	c 671	10.8	60.0	20	9	AAH80790
61.1	51	4	AAI76200	Aai76200 Human sil	c 672	10.8	60.0	20	9	AAH80791
61.1	54	2	AAV76018	AAv76018 Staphyloc	c 673	10.8	60.0	20	9	AAH80792
61.1	60	6	ABN36322	Abn36322 Human spl	c 674	10.8	60.0	20	9	AAH80793
61.1	60	6	ABN42302	Abn42302 Human spl	c 675	10.8	60.0	20	9	AAH80794
61.1	60	6	ABN45336	Abn45336 Human spl	c 676	10.8	60.0	20	9	AAH80795
61.1	60	6	ABN41847	Abn41847 Human spl	c 677	10.8	60.0	20	9	AAH80796
61.1	60	6	ABN32590	Abn32590 Human spl	c 678	10.8	60.0	20	9	AAH80797
61.1	60	6	ABN46342	Abn46342 Human spl	c 679	10.8	60.0	20	9	AAH80798
61.1	15	4	AAV98036	AAv98036 Human IGE	c 680	10.8	60.0	20	9	AAH80799

60.0	25	8	ACI03292	Acio3292 Human mic	754	10.8	60.0	37	2	AAZ20421
60.0	25	8	ACI48766	AcI48766 Human mic	755	10.8	60.0	37	7	ABX12321
60.0	25	8	ACI37164	AcI37164 Human mic	C 756	10.8	60.0	38	4	AAT81823
60.0	25	8	ACI51074	AcI51074 Human mic	C 757	10.8	60.0	38	4	AAH96661
60.0	25	8	ACI81790	AcI81790 Human mic	C 758	10.8	60.0	38	4	AAH96516
60.0	25	8	ACI59107	AcI59107 Human mic	C 759	10.8	60.0	38	4	ABK04191
60.0	25	8	ACI54715	AcI54715 Human mic	C 760	10.8	60.0	38	4	ABK04191
60.0	25	8	ACK05015	ACK05015 Human mic	761	10.8	60.0	39	2	AAQ98268
60.0	25	8	ACI93271	ACI93271 Human mic	762	10.8	60.0	39	7	ABV93840
60.0	25	8	ACI54714	ACI54714 Human mic	763	10.8	60.0	39	7	ABV93536
60.0	25	8	ACH51672	ACH51672 DNA targe	764	10.8	60.0	40	3	AAZ48355
60.0	26	2	AAV37565	AAV37565 L. welshi	C 765	10.8	60.0	41	3	AAA95683
60.0	26	2	AAQ81619	AAQ81619 PCR prime	C 766	10.8	60.0	41	3	ABV77356
60.0	27	2	AAQ74398	AAQ74398 sense deg	767	10.8	60.0	41	6	ABL58643
60.0	27	2	AAQ72555	AAQ72555 Mouse flk	C 768	10.8	60.0	41	6	ABZ49311
60.0	27	2	AAQ86063	AAQ86063 PCR prime	769	10.8	60.0	41	6	ABZ49883
60.0	27	3	AAQ73600	AAQ73600 Reverse p	770	10.8	60.0	41	6	ABZ43699
60.0	27	4	AAH19584	AAH19584 PCR prime	771	10.8	60.0	41	6	ABZ47506
60.0	27	5	AAF29341	AAF29341 PCR prime	C 772	10.8	60.0	41	6	ABZ43743
60.0	27	6	ABL91377	ABL91377 Chlamydia	C 773	10.8	60.0	41	6	ABZ44239
60.0	27	6	ABK29293	ABK29293 Candida d	C 774	10.8	60.0	41	6	ABA05969
60.0	28	4	AAH19816	AAH19816 Antisense	C 775	10.8	60.0	41	6	ABA05970
60.0	28	6	AD311897	AD311897 Borrelia	C 776	10.8	60.0	42	4	AAI13888
60.0	28	6	AD311954	AD311954 Human can	C 777	10.8	60.0	42	6	AAI13888
60.0	29	2	AAQ98233	AAQ98233 Primer us	C 778	10.8	60.0	42	6	AAI13888
60.0	29	2	AAQ98233	AAQ98233 Secreted	C 779	10.8	60.0	44	4	AAI13888
60.0	29	2	AAQ98233	AAQ98233 Oligonuc	C 780	10.8	60.0	44	7	AAI13888
60.0	29	2	AAQ98233	AAQ98233 B. subtil	781	10.8	60.0	45	2	AAQ61685
60.0	29	2	AAQ98233	AAQ98233 Leptospir	782	10.8	60.0	45	2	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Neisseria	783	10.8	60.0	46	2	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Canine IL	C 784	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	785	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	786	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	787	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	788	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	789	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	790	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	791	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	792	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	793	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 794	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	795	10.8	60.0	47	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 796	10.8	60.0	48	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 797	10.8	60.0	49	2	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 798	10.8	60.0	50	2	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 799	10.8	60.0	50	2	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	800	10.8	60.0	50	2	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 801	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 802	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	803	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	804	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 805	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	806	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 807	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	808	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	809	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	810	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	811	10.8	60.0	50	6	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 812	10.8	60.0	51	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 813	10.8	60.0	51	3	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	814	10.8	60.0	51	4	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 815	10.8	60.0	51	4	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	816	10.8	60.0	51	4	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	817	10.8	60.0	51	4	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 818	10.8	60.0	51	4	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 819	10.8	60.0	51	4	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 820	10.8	60.0	51	5	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	821	10.8	60.0	51	5	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 822	10.8	60.0	51	5	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	823	10.8	60.0	51	5	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 824	10.8	60.0	51	5	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 825	10.8	60.0	51	5	AAQ61685
60.0	30	3	AAQ98233	AAQ98233 Novel Hel	C 826	10.8	60.0	51	5	AAQ61685



58.9 32 2 AAT97443 Human cyt  
 58.9 32 3 AAZ54714 Neisseria  
 58.9 32 6 ABK66218 Human gen  
 58.9 32 6 ABK66220 Human gen  
 58.9 33 2 AAT16703 Forward p  
 58.9 33 2 AAX31827 PCR prime  
 58.9 33 5 AAF63960 Human tan  
 58.9 33 6 ABK13250 Yeast SLF  
 58.9 33 6 ABK13250 Yeast SLF  
 58.9 33 6 ABQ72946 Calman cr  
 58.9 33 6 AAL39946 Human lar  
 58.9 33 6 AAL42595 Human dyn  
 58.9 33 6 ABX14183 Zinc fing  
 58.9 33 6 ABN87605 Human cop  
 58.9 33 9 ACF79280 Phage T5/  
 58.9 34 2 AAX91970 Porphorym  
 58.9 35 3 AAZ55061 Neisseria  
 58.9 35 6 ABS67336 Chlamydia  
 58.9 36 2 AAG74604 Primer fo  
 58.9 36 2 AAG74513 Primer fo  
 58.9 36 2 AAT61298 Primer A  
 58.9 36 6 ABS76584 Human ind  
 58.9 40 6 ABX10490 Human BRC  
 58.9 41 2 AAO26585 CAEV PCR  
 58.9 41 4 AAH49770 Human gro  
 58.9 41 6 AAL39948 Human lar  
 58.9 41 6 AAL39949 Human lar  
 58.9 41 6 ABQ79276 Probe #2  
 58.9 41 9 ADE25942 GalNAC-tr

## ALIGNMENTS

standard; DNA; 18 BP.

) (first entry)

se PCR primer SEQ ID NO:16.

oma; oesophagus; malignancy; PCR primer; ss.

s.

-Al.

; 2002WO-US006504.

2001US-0273277P.

V PITTSBURGH.

Luketich JD, Raja S, Kelly LA, Finkelstein SD;

32795/79.

PCR method for detecting malignancies, e.g. adenocarcinoma of  
 the esophagus comprising conducting a PCR amplification on a DNA sample in  
 a mixture.

age 40; 141pp; English.

The invention describes a multiplex polymerase chain reaction  
 comprising conducting PCR on a DNA sample in a reaction  
 mixture comprising denaturing, annealing and elongating steps  
 in which the second amplification stage of (M1) is conducted under  
 the same temperature as the first amplification stage of (M1).

CC different reaction conditions from that of the first amplification  
 CC to modulate the relative rate of production of the first amplification  
 CC first primer set and a second amplification by a second primer set  
 CC first and second amplification stages. Also described: (1) an  
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) intr  
 CC PCR diagnostic; (3) rapid detection of a malignancy or of metast  
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use in  
 CC automated PCR system. (M1) is useful for detecting malignancies  
 CC adenocarcinoma of the oesophagus. (M1) eliminates contamination  
 CC decreases the time it takes to carry out a PCR reaction. The pr  
 CC sequence represents a glucuronidase (gus) PCR primer, which is  
 CC example from the present invention

XX Sequence 18 BP; 3 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0;

QY 1 CTCATTGGGAATTTGGC 18  
 |||||  
 Db 1 CTCATTGGGAATTTGGC 18

RESULT 2

ABQ82537

ID ABQ82537 standard; DNA; 22 BP.

XX AC ABQ82537;

DT 18-DEC-2002 (first entry)

DE Beta-glucuronidase PCR primer SEQ ID NO:3.

KW Adenocarcinoma; oesophagus; malignancy; PCR primer; ss.

OS Homo sapiens.

XX WO200270751-A1.

XX 12-SEP-2002.

PF 04-MAR-2002; 2002WO-US006504.

PR 02-MAR-2001; 2001US-0273277P.

XX (UYP1-) UNIV PITTSBURGH.

XX Godfrey TE, Luketich JD, Raja S, Kelly LA, Finkelstein SD;

XX WPI; 2002-732795/79.

XX Multiplex PCR method for detecting malignancies, e.g. adenocarc  
 PT the esophagus comprises conducting a PCR amplification on a DNA  
 PT a PCR reaction mixture.

PS Claim 4; Page 30; 141pp; English.

XX The present invention describes a multiplex polymerase chain re  
 CC (PCR) (M1) comprising conducting PCR on a DNA sample in a react  
 CC mixture conducted in first and second amplification stages, eac  
 CC or more PCR cycles comprising denaturing, annealing and elongat  
 CC where the elongating step may be conducted at the same temperat  
 CC annealing step. The second amplification stage of (M1) is condu  
 CC different reaction conditions from that of the first amplificat  
 CC to modulate the relative rate of production of the first amplif  
 CC first primer set and a second amplification by a second primer set  
 CC first and second amplification stages. Also described: (1) an  
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) intr  
 CC PCR diagnostic; (3) rapid detection of a malignancy or of metast  
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use in  
 CC automated PCR system. (M1) is useful for detecting malignancies  
 CC adenocarcinoma of the oesophagus. (M1) eliminates contamination

ie time it takes to carry out a PCR reaction. The present  
presents a beta-glucuronidase (beta-gus) PCR primer, which is  
example from the present invention

BP; 4 A; 4 C; 4 G; 10 T; 0 U; 0 Other;

100.0%; Score 18; DB 6; Length 22;

ilarity 100.0%; Pred. No. 43;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTGGGAATTTGCC 18

|||||

ATTGGGAATTTGCC 18

undard; DNA; 22 BP.

(first entry)

relating to the invention ZC40,574 SEQ ID NO:128.

umer; zcytor17; antiinflammatory; dermatological;  
ssive; antimicrobial; vaccine; inflammatory disease;  
/ bowel disease; ulcerative colitis; Crohn's disease;  
itis; eczema; psoriasis; endotoxaemia; septicemia;  
syndrome; infectious disease.

-A2.

: 2003WO-US001984.

: 2002US-0350325P.

: 2002US-0375323P.

: 2002US-0435315P.

GENETICS INC.

Kuijper JL, Dasovich MM, Grant FJ, Hammond AK;  
Bross JA, Dillon SR;

18179/58.

7 ligand polypeptides, useful for treating inflammatory  
ach as inflammatory bowel disease, ulcerative colitis, Crohn's  
pic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.

SEQ ID NO 128; 372pp; English.

on relates to a novel isolated zcytor17 ligand polypeptide. A  
of the invention has antiinflammatory, dermatological,  
assive, and antimicrobial activity, and may have a use in a  
a polypeptide is useful for treating inflammatory diseases,  
lammatory bowel disease, ulcerative colitis, Crohn's disease,  
atitis, eczema, psoriasis, endotoxaemia, septicemia, toxic  
me or infectious diseases. The present sequence is used in  
fication of the invention.

BP; 4 A; 4 C; 4 G; 10 T; 0 U; 0 Other;

100.0%; Score 18; DB 9; Length 22;

ilarity 100.0%; Pred. No. 43;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CATTGGGAATTTGCC 18

|||||

Db 1 CTCATTGGGAATTTGCC 18

RESULT 4

ADD36583/C

ID ADD36583 standard; DNA; 52 BP.

XX

AC ADD36583;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human papillomavirus E6 gene-specific preferred PCR primer/prob

XX

XX cervical carcinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervic

XX

XX cervical cell; cervix; PCR; primer; probe; ss.

XX

OS Human papillomavirus.

XX

FN WO2003057914-A2.

XX

PD 17-JUL-2003.

XX

PF 07-JAN-2003; 2003WO-GB000034.

XX

PR 07-JAN-2002; 2002GB-00000239.

PR

19-JUN-2002; 2002GB-00014124.

XX

PA (NORC-) NORCHIP AS.

PA

(ALLA/) ALLARD S J.

XX

PI Karlsen F;

XX

DR MPI; 2003-587136/55.

XX

PT An in vitro method of screening human subjects to assess their

PT

developing cervical carcinoma, comprises screening the subject

PT

expression of mRNA transcripts from the L1 gene and the E6 gene

PT

papillomavirus.

XX

PS Disclosure; Page 47; 102pp; English.

XX

CC This invention relates to a novel method for the detection of h

CC

papillomavirus mRNA for use in the screening of human female su

CC

assesses their risk of developing cervical carcinoma. The inventi

CC

comprises screening the subject for expression of mRNA transcri

CC

the L1 gene and the E6 gene of human papillomavirus, where subj

CC

positive for expression of L1 and/or E6 mRNA are scored as bein

CC

of developing cervical carcinoma. The presence of the human

CC

papillomavirus (in particular HPV16 and HPV18) has been associa

CC

cervical cancer in numerous epidemiological studies. The method

CC

invention are useful for screening human subjects to assess the

CC

developing cervical carcinoma, or for identifying human subj

CC

abnormal cell changes in the cervix. The present sequence is th

CC

preferred PCR primer (which may also be suitable as a probe) wh

CC

used to amplify the E6 gene of human papillomavirus in the meth

CC

invention.

XX

Sequence 52 BP; 19 A; 12 C; 10 G; 11 T; 0 U; 0 Other;

Query Match

82.2%; Score 14.8; DB 9; Length 52;

Best Local Similarity 88.9%; Pred. No. 1.5e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 1 CTCATTGGGAATTTGCC 18

|||||

47 CTCATTGGGAATCGTGCC 30

Db

RESULT 5

ADD22161/c

ID ADD22161 standard; DNA; 52 BP.

XX

AC ADD22161;

(first entry)

transcribed mRNA detecting NASBA primer/probe #63.

apillomavirus; HPV; NASBA; primer; probe; PCR; ss.

lomavirus type 31.

7-A2.

; 2003WO-GB000030.

; 2002GB-00000258.

CHIP AS.

ARD S J.

87141/55.

cleotide primer and probe for detecting the presence of mRNA from the E6 gene of a human papillomavirus in clinical

Page 19; 28pp; English.

on relates to a novel oligonucleotide molecule used for RNA transcribed from the E6 gene of a human papillomavirus oligonucleotide comprises any of the 133 fully defined having 17-26 bp given in the specification. The invention provides the detection of HPV mRNA in a test sample suspected of HPV, comprising performing an amplification reaction on a of a nucleic acid isolated from the test sample to amplify a the mRNA transcribed from the E6 gene of HPV, where the on reaction is performed using the primer-pair of tide cited above. The invention also provides: a reagent kit the detection of HPV by NASBA, comprising an oligonucleotide and, optionally, an enzyme mixture comprising an RNA directed ase, a ribonuclease that hydrolyzes the RNA strand of an RNA- without hydrolyzing single or double stranded RNA or DNA, and merase that recognises the promoter sequence present in at ASBA P1 primer oligonucleotide included in the reagent kit. cleotide of the invention is useful in detecting mRNA from the E6 gene of HPV in clinical samples. This ide sequence represents an oligonucleotide used for detecting ribed from the E6 gene of a human papillomavirus (HPV) of the

BP; 19 A; 12 C; 10 G; 11 T; 0 U; 0 Other;

ilarity 82.2%; Score 14.8; DB 9; Length 52;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

'CATTGGGAATTTTGGC 18

|||||

'CATTGGGATCGTGGC 30

andard; DNA; 20 BP.

(first entry)

ie biallelic marker primer 98.

KW Biallelic marker; human; high density disequilibrium map; disea  
KW identification; Alzheimer's disease; drug response; drug effica  
KW drug toxicity; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9904038-A2.

XX PD 28-JAN-1999.

XX PF 17-JUL-1998; 98WO-IB001193.

XX PR 18-JUL-1997; 97EP-00401740.

XX PR 21-APR-1998; 98US-0082614P.

XX PA (GEST ) GENSET.

XX FI Cohen D, Blumenfeld M, Tchoumakov I;

XX DR WPI; 1999-132278/11.

XX Production of biallelic markers - by obtaining a genomic DNA li  
PT determining the order and sequence of DNA fragments and identif  
PT nucleotides which vary between individuals.

XX Example 7; Page 227; 288pp; English.

XX This invention describes a novel method for obtaining a set of  
CC markers represented in AAX52533-X52632 and AAX52833-X52843 for  
CC constructing a high density equilibrium map of the human genome  
CC method involves (a) obtaining a nucleic acid library comprising  
CC DNA fragments comprising the full genome or a portion (b) deter  
CC order of genomic DNA fragments in the genome, (c) determining t  
CC sequence of selected regions of the genomic DNA fragments and (d  
CC identifying nucleotides in the genomic DNA fragments which vary  
CC individuals, thereby defining a set of biallelic markers. The m  
CC be used for identifying traits such as disease (e.g. Alzheimer  
CC disease), drug response, drug efficacy and drug toxicity. They  
CC used for selecting an individual for inclusion in a clinical tr  
CC method is used to map the position of genes in a genome (prefer  
CC human genome). The sequences described in AAX52633-X52832 and A  
CC X52868 represent primers used in the method of the invention  
XX

SQ Sequence 20 BP; 5 A; 2 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 77.8%; Score 14; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0;

Qy 3 CATTGGGAATTTTG 16

|||||

Db 3 CATTGGGAATTTTG 16

RESULT 7

AAZ76753

ID AAZ76753 standard; DNA; 20 BP.

XX AAZ76753;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID N  
XX Human genome; biallelic marker; high density disequilibrium map  
XX genomic map; haplotype; phenotype; polymorphic base; genotyping  
XX haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
XX diagnosis; ss.

OS Homo sapiens.

99WO-1B000822.  
 98US-0082614P.  
 98US-0109732P.  
 RET.  
 umenfeld M, Chumakov I;  
 3267/01.  
 ilar markers used to construct a high density disequilibrium  
 human genome.  
 je 2599; 2745pp; English.  
 AAZ69578 represent human biallelic markers from the present  
 which contain a polymorphic base at position 24 of their  
 sequences. AAZ69579 to AAZ77440 represent amplification  
 the biallelic markers. The biallelic markers of the invention  
 ity of uses: they can be used for high density mapping of the  
 , and in complex association studies and haplotyping studies  
 eful in determining the genetic basis for disease states.  
 ; and methods of the invention can also be useful for the  
 on of the targets for the development of pharmaceutical  
 diagnostic methods, as well as the characterisation of the  
 . efficacious responses to and side effects from  
 al agents acting on a disease as well as other treatment.  
 ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3237 and  
 it actually given a sequence in the Sequence Listing from the  
 ntion  
 BP; 5 A; 2 C; 5 G; 8 T; 0 U; 0 Other;  
 77.8%; Score 14; DB 3; Length 20;  
 larity 100.0%; Pred. No. 3.5e+03;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 TTGGAATTG 16  
 |||||  
 TTGGAATTG 16  
 andard; DNA; 41 BP.  
 (first entry)  
 i hormone protein family 10 coding sequence probe #1.  
 h hormone protein family 10; cancer; HIV infection;  
 immunological disease; inflammation; gene therapy; probe; ss.  
 3.  
 -A1.  
 : 2000WO-CN000654.  
 : 99CN-00127207.  
 / FUDAN.  
 NGHAI BIO DOOR GENE TECHNOLOGY LTD.

PI Mao Y, Xie Y;  
 XX WPI; 2001-432886/46.  
 XX  
 PT Growth hormone protein family 10 and encoded polynucleotide, us  
 PT diagnosis and treatment of malignant tumor, hemopathy, human  
 PT immunodeficiency virus infection, immunological diseases and  
 PT inflammation.  
 XX  
 PS Example 7; Page 21; 35pp; Chinese.  
 XX  
 CC The present invention provides the protein and coding sequences  
 CC growth hormone protein family 10. The sequences are useful in th  
 CC treatment of cancer, HIV infection, haemopathy, immunological di  
 CC and inflammation. The present sequence is a probe for the coding  
 CC of the invention  
 XX  
 SQ Sequence 41 BP; 14 A; 6 C; 9 G; 12 T; 0 U; 0 Other;  
 Query Match 76.7%; Score 13.8; DB 4; Length 41;  
 Best Local Similarity 88.2%; Pred. No. 4.5e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0;  
 QY 2 TCATTGGAAATTTGCC 18  
 DB 8 TGATTGAAATTTGCC 24  
 RESULT 9  
 AAV94759  
 ID AAV94759 standard; RNA; 17 BP.  
 XX  
 AC AAV94759;  
 XX  
 DT 24-FEB-1999 (first entry)  
 XX  
 DE Human IL-2 receptor g-chain substrate position 1238.  
 XX  
 KW Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain  
 KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; c  
 KW autoimmune disease; psoriasis; allergy; inflammatory disease;  
 KW graft rejection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9824913-A2.  
 XX  
 PD 11-JUN-1998.  
 XX  
 PF 02-DEC-1997; 97WO-US021748.  
 XX  
 PR 03-DEC-1996; 96US-00758306.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Stinchcomb DT, Mcswiggen JA;  
 PI WPI; 1998-333332/29.  
 XX  
 DR Ribozymes targetted to interleukin 2 - useful for treating e.g.  
 PT autoimmune disease and allergies.  
 PT  
 XX Claim 4; Page 36; 6lpp; English.  
 PS  
 XX The present sequence describes ribozymes targeted to n  
 CC the synthesis and/or expression of interleukin (IL)-2R gamma enc  
 CC AAV93889 to AAV94574 represent specifically claimed ribozymes, a  
 CC AAV94575 to AAV95260 represent specifically claimed substrate se  
 CC from the present invention. The ribozymes can be used for the t  
 CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis,  
 CC and other inflammatory conditions. The ribozymes are also used t  
 CC tolerance in a recipient to alloantigen from a donor  
 XX



BP; 3 A; 1 C; 5 G; 0 T; 8 U; 0 Other;

74.4%; Score 13.4; DB 2; Length 17;  
ilarity 40.0%; Pred. No. 6.7e+03;  
Conservative 8; Mismatches 1; Indels 0; Gaps 0;

CATTGGAAATTT 15  
:|||||:  
GAUUGGAAUUU 17

andard; DNA; 21 BP.

(first entry)

zavirus Type 3 detecting biotinylated probe PIV3C.

microorganism; infectious disease pathogen; screening;  
polymerase chain reaction; digoxigenin-labelling; diagnostic;  
tract; antibiotic; detection; ss.

za virus.

Al.

;

; 97DE-01016456.

; 97DE-01016456.

MITT H.

84377/50.

ion of microorganisms, especially respiratory tract pathogens  
lex polymerase chain reaction on sample which been partly  
o reverse transcription and then digoxigenin-labelling the  
h probes corresponding to primers used in PCR.

ge 5; 7pp; German.

5070 are probes used in a process for the identification of  
sms, especially infectious disease pathogens. The method  
forming a simultaneous amplification of several target  
multiplex polymerase chain reaction) in which a patient sample  
d with a solution containing several primers and where a part  
le has been subjected to a previous reverse transcription for  
A-possessing pathogen. The PCR product is subjected to  
labelling with selected probes corresponding to the primers  
sence of a microorganism (relating to the primer) is detected  
sample-evaluation and/or photometrically measurable colour  
tion of the sample. The method allows the rapid screening of  
fectious diseases especially of the respiratory tract and can  
a diagnostic aid indicating whether antibiotics are required

BP; 10 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

74.4%; Score 13.4; DB 2; Length 21;  
ilarity 93.3%; Pred. No. 6.8e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CATTGGAAATTT 15  
:|||||:  
CTTTGGAAATTT 1

RESULT 11  
AAA14173/c  
ID AAA14173 standard; DNA; 21 BP.  
XX  
AC AAA14173;  
XX  
DT 15-SEP-2003 (revised)  
DT 21-JUL-2000 (first entry)  
XX  
DE PIV-3 fusion protein gene 5' non-coding region probe piv31, SEQ  
XX  
KW Acute respiratory tract infection; multiplex reverse transcript  
KW paediatric; detection; identification; human respiratory syncyt  
KW parainfluenza virus type 1; parainfluenza virus type 3;  
KW Mycoplasma pneumoniae; Chlamydia pneumoniae; human enterovirus;  
KW influenza virus type A; influenza virus type B; adenovirus;  
KW Bordetella pertussis; Bordetella parapertussis; hybridisation f  
XX  
OS Human parainfluenza virus 3.  
XX  
PN WO200017391-Al.  
XX  
PD 30-MAR-2000.  
XX  
PF 22-SEP-1999; 99WO-EP007065.  
XX  
PR 24-SEP-1998; 98EP-00870203.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI James G, Schmitt H;  
XX  
DR WPI; 2000-283612/24.  
XX  
PT Identifying organisms causing acute respiratory tract infection  
PT reverse transcription-polymerase chain reactions.  
XX  
PS Claim 7; Page 23; 45pp; English.  
XX  
CC The invention relates to a novel method for the detection of ac  
CC respiratory tract infection via multiplex reverse transcriptase  
CC PCR. The method comprises the simultaneous amplification of se  
CC target nucleotide sequences of different species origin present  
CC biological sample, and uses primer sets designed to amplify ger  
CC of a variety of organisms implicated in causing acute respirat  
CC infection. The amplified DNA is then detected via the use of a  
CC and gene-specific probe. The gene regions that are amplified ar  
CC in the method of the invention are the human respiratory syncyt  
CC (RSV) fusion glycoprotein F1 subunit gene; the parainfluenza vi  
CC (PIV-1) haemagglutinin neuraminidase gene; the parainfluenza vi  
CC (PIV-3) fusion protein gene 5' non-coding region; the 16S rRNA  
CC from Mycoplasma pneumoniae and Chlamydia pneumoniae; the human  
CC enterovirus 5' non-coding region; the non-structural protein ge  
CC adeno virus type A (InfA) and type B (InfB); and the hexon  
CC adenoviruses. The spacer region between the 16S and 23S rRNA se  
CC M. pneumoniae, C. pneumoniae, Bordetella pertussis and Bordetel  
CC parapertussis may also be amplified and detected. The method of  
CC invention makes it possible to detect the presence of a range c  
CC microorganisms which infect the respiratory tract, particularly  
CC children, using one amplification step. The different microorga  
CC be detected simultaneously within one day. The precise identifi  
CC the causative organism(s) of acute respiratory tract infection  
CC patient should result in more tailored antibiotic therapies, an  
CC usage of antibiotics. This would in turn help to delay the emer  
CC antibiotic resistant bacteria, and would reduce side-effects an  
CC healthcare costs. Sequences AAA14161-A14176, AAA14184-A14194 ar  
CC - AAA14217 represent gene-specific hybridisation probes used in  
CC practice and exemplifications of the invention. (Updated on 15-  
CC to standardise OS field)  
XX  
SQ Sequence 21 BP; 10 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

74.4%; Score 13.4; DB 3; Length 21;  
 Clarity 93.3%; Pred. No. 6.8e+03;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TATTTGGGAATTTT 15  
 |||||  
 TTTTGGGAATTTT 1

standard; DNA; 21 BP.

(revised)  
 (first entry)

1 protein gene 5' non-coding region probe, SEQ ID NO:3.

ratory tract infection; multiplex reverse transcriptase-PCR;  
 detection; identification; human respiratory syncytial virus;  
 za virus type 1; parainfluenza virus type 3;  
 pneumoniae; Chlamydia pneumoniae; human enterovirus;  
 irus type A; influenza virus type B; adenovirus;  
 pertussis; Bordetella parapertussis; hybridisation probe; ss.  
 nfluenza virus 3.

-Al.

; 99WO-EP007065.

; 98EP-00870203.

XGENETICS NV.

Schmitt H;

33612/24.

organisms causing acute respiratory tract infections via a  
 ascription-polymerase chain reactions.

Page 15; 45pp; English.

on relates to a novel method for the detection of acute  
 tract infection via multiplex reverse transcriptase-PCR (RT-  
 athod comprises the simultaneous amplification of several  
 actide sequences of different species origin present in a  
 sample, and uses primer sets designed to amplify gene regions  
 of organisms implicated in causing acute respiratory tract  
 the amplified DNA is then detected via the use of a species-  
 acific probe. The gene regions that are amplified and detected  
 of the invention are the human respiratory syncytial virus  
 1 glycoprotein F1 subunit gene; the parainfluenza virus type 1  
 agglutinin neuraminidase gene; the parainfluenza virus type 3  
 ion protein gene 5' non-coding region; the 16S rRNA sequences  
 asma pneumoniae and Chlamydia pneumoniae; the human  
 5' non-coding region; the non-structural protein genes from  
 irus type A (InfA) and type B (InfB); and the hexon gene from  
 s. The spacer region between the 16S and 23S rRNA sequences of  
 ae, C. pneumoniae, Bordetella pertussis and Bordetella  
 is may also be amplified and detected. The method of the  
 asks it possible to detect the presence of a range of  
 sms which infect the respiratory tract, particularly in  
 sing one amplification step. The different microorganisms can  
 simultaneously within one day. The precise identification of  
 ve organism(s) of acute respiratory tract infection in a  
 uid result in more tailored antibiotic therapies, and reduced

CC usage of antibiotics. This would in turn help to delay the emer  
 CC antibiotic resistant bacteria, and would reduce side-effects an  
 CC healthcare costs. Sequences AAA14161-A14176, AAA14184-A14194 an  
 CC - AAA14217 represent gene-specific hybridisation probes used in  
 CC practice and exemplifications of the invention. (Updated on 15-  
 CC to standardise OS field)

XX SQ Sequence 21 BP; 10 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 74.4%; Score 13.4; DB 3; Length 21;  
 Best Local Similarity 93.3%; Pred. No. 6.8e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 1 CTCATTGGGAATTTT 15  
 |||||  
 Db 15 CTCATTGGGAATTTT 1

RESULT 13

AAH27357  
 ID AAH27357 standard; DNA; 23 BP.

XX AC AAH27357;

XX DT 08-AUG-2001 (first entry)

XX DE PCR primer #26.

XX KW Tumour suppressor gene 16; TSG16; immune response modulator;  
 KW inflammatory response modulator; signal transduction activator;  
 KW cytokine inhibitor; gene therapy; anticancer; anti-inflammatory  
 KW autoimmune disorder; infection; chromosome 16q24.3; human;  
 KW cellular proliferation suppressor; PCR primer; ss.

XX OS Homo sapiens.

XX DN WO200132861-A1.

XX PD 10-MAY-2001.

XX PF 30-OCT-2000; 2000WO-AU001329.

XX PR 29-OCT-1999; 99AU-00003771.

XX PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.

XX PI Callen DF, Whitmore SA, Kremmidiotis G, Kochetkova M, Crawf

XX DR WPI; 2001-316439/33.

XX PT New nucleic acid representing the human tumour suppressor gene 1  
 PT useful e.g. for diagnosis and treatment of tumors, inflammatory  
 PT immunological disorders.

XX PS Disclosure; Page 192; 215pp; English.

XX CC The present invention relates to human tumour suppressor gene 1  
 CC see AAH23688). TSG16 was isolated from chromosome 16q24.3. TSG1  
 CC suppresses cellular proliferation. TSG16 is useful for treating  
 CC associated with decreased expression or activity of TSG16, e.g.  
 CC (auto)immune disorders, inflammation, complications of wound he  
 CC infections (by viruses, bacteria, fungi, parasites, protozoa or  
 CC helminths). The present sequence is a PCR primer, which was use  
 CC present invention

XX SQ Sequence 23 BP; 3 A; 5 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 4; Length 23;  
 Best Local Similarity 83.3%; Pred. No. 8.5e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTGCC 18  
 |||||

CTTTTGAATTTTGTC 20

standard; DNA; 30 BP.

(first entry)

agment PCR primer MPSYN787.

e therapy; vaccine; ALVAC; translation factor; K3L; E3L; HIV; ; ss.

odeficiency virus 1.

1.

; 98WO-US003710.

; 97US-00815809.

OGENETICS CORP.  
V ARIZONA STATE.

, Jacobs BL, Goebel SJ, Cox WI, Gettig RR, Pincus SE;

20819/44.

xpression of nucleic acids in cells - by using modified  
ch comprise the nucleic acid and also nucleic acid encoding a  
factor.

Page 50; 90pp; English.

YN787 and MPSYN788 (see AAV58255) were used in the PCR  
on of a 210 bp fragment (C) containing HIV Pol2, using PHXBD2,  
ins the entire proviral DNA sequence of HIV IIB, as template.  
, a 270 bp fragment (D) containing Nef1 was obtained using  
YN789 and MPSYN790 (see AAV58256-57), and a 170 bp fragment  
ing Poll was prepared using primers MPSYN791 and MPSYN92 (see  
). Fragments C and D were combined using MPSYN787/MPSYN790,  
, and E using MPSYN789/MPSYN792, and fragments C+D and D+E  
rs MPSYN787/MPSYN792 to produce a Pol2/Nef central  
) fragment. This was utilised in the 'string of beads'  
pMPC5H6PN and hence in recombinants vCP1433 (see AAV58243)  
(see AAV58244). The invention relates to novel vectors that  
ed expression of nucleic acids in cells through the actions of  
rus K3L and E3L sequences (see AAW71644 and AAW30564) that  
nslation. Immunological, vaccine and therapeutic compositions  
such vectors are claimed

; BP; 10 A; 8 C; 5 G; 7 T; 0 U; 0 Other;

ilarity 73.3%; Score 13.2; DB 2; Length 30;

Conservative 83.3%; Pred. No. 8.6e+03; Mismatches 0; Gaps 0;

CTTTTGAATTTTGCC 18

TACTTTGGAATATTGCC 12

standard; DNA; 30 BP.

AC AAV60282;  
XX 15-FEB-1999 (first entry)  
DT  
XX  
DE HIV-1 Pol2 fragment PCR primer MPSYN787.  
XX  
KW Vector; gene therapy; vaccine; ALVAC; translation factor; K3L;  
XX HIV-1; PCR; primer; ss.  
XX  
XX Synthetic.  
OS Human immunodeficiency virus 1.  
XX  
FN W09840501-A1.  
XX  
PD 17-SEP-1998.  
XX  
PF 13-FEB-1998; 98WO-US002669.  
XX  
PR 12-MAR-1997; 97US-00816155.  
XX  
PA (VIRO-) VIROGENETICS CORP.  
XX  
XX Tartaglia J, Cox WI, Gettig RR, Martinez H, Paoletti E;  
PI Pincus SE;  
PI  
XX MPI; 1998-520820/44.  
DR  
XX  
XX Enhancing expression of nucleic acids in cells - by using modif  
PT vectors which comprise nucleic acid and also nucleic acid encod  
PT transcription factor and optionally translation factor.  
XX  
PS Example 2; Page 60; 102pp; English.  
XX  
XX Primers MPSYN787 and MPSYN788 (see AAV60283) were used in the P  
CC amplification of a 210 bp fragment (C) containing HIV Pol2, usi  
CC which contains the entire proviral DNA sequence of HIV IIB, as  
CC In addition, a 270 bp fragment (D) containing Nef1 was obtained  
CC primers MPSYN789 and MPSYN790 (see AAV60284-85), and a 170 bp f  
CC (E) containing Poll was prepared using primers MPSYN791 and MPS  
CC AAV60286-87). Fragments C and D were combined using MPSYN787/M  
CC fragments D and E using MPSYN789/MPSYN792, and fragments C+D an  
CC (Nef1/Poll) fragment. This was utilised in the 'string of bead  
CC cassette of pMPC5H6PN and hence in recombinants vCP1433 (see A  
CC and vCP1452 (see AAV60250). The invention relates to novel vect  
CC show enhanced expression of nucleic acids in cells through the  
CC vaccinia virus K3L and E3L sequences (see AAW71365 and AAW30571  
CC enhance translation. Immunological, vaccine and therapeutic com  
CC comprising such vectors are claimed  
XX  
SQ Sequence 30 BP; 10 A; 8 C; 5 G; 7 T; 0 U; 0 Other;  
Query Match 73.3%; Score 13.2; DB 2; Length 30;  
Best Local Similarity 83.3%; Pred. No. 8.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;  
QY 1 CTCATTTGGAATTTTGCC 18  
||| ||||| |||||  
DB 29 CTACTTTGGAATATTGCC 12  
RESULT 16  
ABT44474/c  
ID ABT44474 standard; DNA; 30 BP.  
XX  
XX  
AC ABT44474;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
XX PCR primer Seq ID31 related to nucleic acid delivery and expres  
DE Nucleic acid delivery; nucleic acid expression; bacterium;  
KW bacteriophage P1; bacteriophage mediated transformation;  
KW

. promoter; Pac; Bof; Doc; Coi; host cell transformation;  
psid; prokaryotic cell; eukaryotic cell; PCR; primer; ss.

-A2.

2002WO-US035891.

2001US-0347839P.

2002US-0410398P.

: FOUND RES DEV.

Schofield DA, Westwater C, Dolan JW, Hoel BD;  
Norris JS;

18513/56.

1 nucleic acid comprising a C1-regulated promoter sequence  
linked to a nucleic acid sequence, and a promoter sequence  
linked to a second nucleic acid sequence, useful for  
host cells.

Page 44; 126pp; English.

on relates to a novel methods and materials involved in  
delivery and expression. In particular, the invention  
methods and materials involved in bacteriophage mediated  
on of bacteria. The isolated nucleic acid of the invention  
bacteriophage P1 C1-regulated promoter sequence operably  
nucleic acid sequence, and a promoter sequence operably  
second nucleic acid sequence, wherein the C1-regulated  
quence, the nucleic acid sequence, and second nucleic acid  
e heterologous. Bacteriophage P1 proteins Pac, Bof, Doc and  
g the nucleic acid sequences used for the exemplification of  
n. The nucleic acids of the invention may be useful for  
a wide range of host cells. Nucleic acid vectors such as  
capsids may be used to deliver the nucleic acids of the  
r the transformation of prokaryotic and eukaryotic cells. The  
ence is that of a PCR primer which was used in the  
ion of the invention

BP; 8 A; 6 C; 8 G; 8 T; 0 U; 0 Other;

larity 73.3%; Score 13.2; DB 8; Length 30;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TATTGGAATTTTGGC 18

|||||

TATTAGGATTCGGC 3

undard; DNA; 30 BP.

(first entry)

PCR primer #2.

non-lytic; bacteriophage; pathogenic; antimicrobial; PCR;

coli.

-A2.

PD 18-SEP-2003.  
XX  
PF 06-MAR-2003; 2003WO-US006941.  
XX  
PR 06-MAR-2002; 2002US-0362409P.  
PR 15-APR-2002; 2002US-0372892P.  
PR 13-DEC-2002; 2002US-0433178P.  
XX  
PA (MUSC-) MUSC FOUND RES DEV.  
XX  
PI Kasman IM, Kasman A, Westwater C, Dolan JW, Schmidt MG;  
PI Norris JS, Schofield DA,  
XX  
DR WPI; 2003-748394/70.  
XX  
PT New non-lytic bacteriophage comprising a nucleic acid encoding a  
PT agent, useful for treating an infection by a pathogenic organism  
PT delivering nucleic acids encoding antigens or antimicrobial agen  
PT bacteria.

Example 1; Page 22; 94pp; English.

XX The invention relates to a novel non-lytic bacteriophage compris  
XX nucleic acid encoding a lethal agent for treating an infection  
XX pathogenic organism. A bacteriophage of the invention has antim  
XX activity. The non-lytic bacteriophage is useful for treating an  
XX by a pathogenic organism, or for delivering nucleic acids encod  
XX more polypeptides (e.g. antigens or antimicrobial agents) to bac  
XX The present sequence represents a PCR primer used in the exampl  
XX of the invention.

SQ Sequence 30 BP; 8 A; 6 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 9; Length 30;  
Best Local Similarity 83.3%; Pred. No. 8.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTTGGC 18

Db 20 CTCATTGGGAATTTTGGC 3

RESULT 18

ABV76515/c

ID ABV76515 standard; DNA; 33 BP.

XX AC ABV76515;

XX DT 20-FEB-2003 (first entry)

XX DE Human cytochrome constitutive protein 9.02 PCR primer, SEQ ID N  
XX KW Human; cytochrome constitutive protein 9.02; recombinant product  
KW gene therapy; malignant tumour; cancer; blood disease; HIV infect  
KW human immunodeficiency virus; immune disorder; inflammatory con  
XX cytostatic; antiinflammatory; immunomodulator; PCR; primer; ss.  
XX OS Homo sapiens.

XX PN CN1358756-A.

XX PD 17-JUL-2002.

XX PF 13-DEC-2000; 2000CN-00127871.

XX PR 13-DEC-2000; 2000CN-00127871.

XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX PI Mao Y, Xie Y;

XX DR WPI; 2002-733545/80.

XX

epitide-human cytochrome constitutive protein 9.02 and ide for encoding the polypeptide.

Page 18 (Disclosure); 32pp; Chinese.

on relates to human cytochrome constitutive protein 9.02 and nucleic acids encoding it (ABV76512). The protein has a eight of 9.02 kb. The invention also relates to a method for nant production of the protein, an antagonist of the protein, of the protein, gene and antagonist in therapeutic s. Cytochrome constitutive protein 9.02 can be used in the f a variety of diseases such as malignant tumours, blood IV (human immunodeficiency virus) infection, immune disorders atory conditions. Sequences ABV76515-ABV76516 represent PCR d in an exemplification of the invention to amplify human constitutive protein 9.02 cDNA for cloning

BP; 11 A; 8 C; 7 G; 7 T; 0 U; 0 Other;

ilarity 73.3%; Score 13.2; DB 6; Length 33;  
Conservative 83.3%; Pred. No. 8.7e+03;  
Mismatches 3; Indels 0; Gaps 0;

CATTGGGAATTTGTC 18  
| | | | | | | | | |  
CCTTTGGGAATTTGTC 16

andard; DNA; 41 BP.

(first entry)

hrome constitutive protein 9.02 probe, SEQ ID NO:8.

chrome constitutive protein 9.02; recombinant production;  
Y; malignant tumour; cancer; blood disease; HIV infection;  
odeficiency virus; immune disorder; inflammatory condition;  
antiinflammatory; immunomodulator; probe; ss.

s.

; 2000CN-00127871.

; 2000CN-00127871.

NGHAI BIOWINDOW GENE DEV INC.

Y;

33545/80.

epitide-human cytochrome constitutive protein 9.02 and ide for encoding the polypeptide.

Page 20 (Disclosure); 32pp; Chinese.

on relates to human cytochrome constitutive protein 9.02 and nucleic acids encoding it (ABV76512). The protein has a eight of 9.02 kb. The invention also relates to a method for nant production of the protein, an antagonist of the protein, of the protein, gene and antagonist in therapeutic s. Cytochrome constitutive protein 9.02 can be used in the f a variety of diseases such as malignant tumours, blood IV (human immunodeficiency virus) infection, immune disorders atory conditions. Sequences ABV76517-ABV76518 represent human

CC cytochrome constitutive protein 9.02 probes used in an exemplif  
CC the invention

XX Sequence 41 BP; 11 A; 13 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 73.3%; Score 13.2; DB 6; Length 41;  
Best Local Similarity 83.3%; Pred. No. 8.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTGTC 18  
| | | | | | | | | |  
Db 23 CACCTTTGGGAATTTGTC 6

RESULT 20

ABS70690/c  
ID ABS70690 standard; DNA; 43 BP.

XX AC ABS70690;

XX DT 26-NOV-2002 (first entry)

XX DE Mouse immunoglobulin heavy chain PCR primer #50.

XX KW Chimeric antibody library; display screening method; mouse;  
XX KW immunoglobulin heavy chain; PCR; primer; ss.

XX OS Mus sp.

XX PN US6420113-B1.

XX PD 16-JUL-2002.

XX PF 02-OCT-1999; 99US-00410903.

XX PR 04-APR-1997; 97US-00832985.

XX PR 04-APR-1997; 97US-00835159.

XX PR 03-APR-1998; 98WO-US006704.

XX PA (BIOS-) BIOSITE DIAGNOSTICS INC.

XX PI Buechler J, Valkirs G, Gray J;

XX DR WPI; 2002-626079/67.

XX PT Producing polyclonal libraries of chimeric antibodies for use,  
XX PS diagnostic or therapeutic reagents, using display screening met

XX Example 3; Fig 1; 54pp; English.

XX The present invention relates to a new method of producing a ch  
XX antibody library having affinity for a target, using display sc  
XX methods. The method enriches conventional display libraries for  
XX displaying more than one copy of the polypeptide. The method al  
XX subclones nucleic acids from a display vector to an expression  
XX where the nucleic acids encode the displayed polypeptides. The  
XX the invention can be used to produce polyclonal libraries of ch  
XX antibodies for use, e.g., as diagnostic or therapeutic reagents  
XX method is based in part on two related but self-sufficient impr  
XX in conventional display methods. The first improvement provides  
XX of enriching conventional display libraries for members display  
XX than one copy of a polypeptide prior to affinity screening of s  
XX libraries with a target of interest. These methods can achieve  
XX populations in which the vast majority of members retaining ful  
XX coding sequences encode polypeptides having specific affinity f  
XX target. Additionally, the invention provides methods of sub-clo  
XX nucleic acids encoding displayed polypeptides of enriched libra  
XX a display vector to an expression vector without the need for c  
XX isolation of individual members. The present nucleic acid sequ  
XX represents a PCR primer that was used in the methods of the inv  
XX amplify the mouse immunoglobulin heavy chain

XX Sequence 43 BP; 12 A; 9 C; 13 G; 9 T; 0 U; 0 Other;

73.3%; Score 13.2; DB 6; Length 43;  
 ilarity 83.3%; Pred. No. 8.8e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 TATTGGGAATTTGCC 18  
 |||||  
 TATTGGGCTTTGCC 11  
 andard; DNA; 43 BP.

(first entry)  
 yglobulin heavy (H) chain gene amplifying primer# 50.  
 library; diagnostic kit; antibody library; immunoglobulin;  
 / chain; H chain; PCR; primer; ss.

1.  
 ; 97US-00835159.  
 ; 97US-00835159.  
 SITE DIAGNOSTICS INC.  
 achler J, Valkirs G;  
 36289/74.  
 polypeptide library having affinity for a target for use in  
 and therapeutic purposes, comprises producing modified forms  
 sion vector before expression and screening of polypeptides.  
 Fig 1; 50pp; English.  
 on relates to a method for producing a polypeptide library  
 nity for a target. The method involves subcloning DNA encoding  
 : polypeptides of a library of viral particles into multiple  
 i expression vector to produce modified forms of the  
 vector, introducing the modified forms into a host and  
 a library of 10 different polypeptides. The method is used for  
 polypeptide library or an antibody library having affinity  
 :. It is also used to prepare a diagnostic kit or reagent or a  
 composition containing the library of polypeptides. The  
 nence is a PCR primer used for amplifying mouse immunoglobulin  
 ain gene. This sequence is used to illustrate the method of  
 on

BP; 12 A; 9 C; 13 G; 9 T; 0 U; 0 Other;  
 73.3%; Score 13.2; DB 9; Length 43;  
 ilarity 83.3%; Pred. No. 8.8e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 TATTGGGAATTTGCC 18  
 |||||  
 TATTGGGCTTTGCC 11  
 andard; DNA; 51 BP.

AC AAL27046;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 XX Human SNP oligonucleotide #254.  
 DE  
 XX  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytosta  
 neuroprotective; antimicrobial; gene therapy; vaccine; amylase;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadhe  
 cyclin; polymerase; oncogene; histone; kinase; colony stimulat  
 KW complement related protein; cytochrome; kinesin; cytokine; inte  
 KW interleukin; G-protein coupled receptor; thioesterase; inflamma  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US035498.  
 XX  
 PR 28-DEC-1999; 99US-0173419P.  
 PR 27-DEC-2000; 2000US-00173419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 XX Shimkets RA, Leach M;  
 XX WPI; 2001-465210/50.  
 DR  
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, poly  
 PT oncogenes and histones, useful for diagnosing and treating, e.g  
 PT autoimmune diseases and infections.  
 XX  
 XX Claim 1; Page 1467; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides encoding poly  
 variants of proteins related to amylases, amyloid proteins, ang  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncoq  
 CC histones, kinases, colony stimulating factors, complement relat  
 CC proteins, cytochromes, kinesins, cytokines, interferons, interl  
 CC protein coupled receptors and thioesterases. The present sequen  
 CC such oligonucleotide. The oligonucleotides and the peptides enc  
 CC them may be used in the prevention, diagnosis and treatment of  
 CC associated with inappropriate expression of the proteins listed  
 CC Disorders that may be prevented, diagnosed and/or treated inclu  
 CC multifactorial diseases with a genetic component, such as autoi  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabet  
 CC systemic lupus erythematosus and Grave's disease), inflammatio  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of  
 CC organisms  
 XX  
 SQ Sequence 51 BP; 18 A; 15 C; 10 G; 8 T; 0 U; 0 Other;  
 Query Match 73.3%; Score 13.2; DB 4; Length 51;  
 Best Local Similarity 83.3%; Pred. No. 8.9e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0;  
 QY 1 CTCATTGGGAATTTGCC 18  
 | | | | | | | | | | | | | | | |  
 Db 35 CCATTGGGAAGTTGAC 18  
 RESULT 23  
 AAT04743/C  
 ID AAT04743 standard; DNA; 53 BP.  
 XX  
 AC AAT04743;  
 XX  
 DT 10-JUN-1996 (first entry)

P2A, used in the construction of pCSPOL75A.

CPV; ALVAC; attenuated; therapy; prevention; rabies; vector;  
ribbody; CTL1; CTL2; PCR; primer; HIV; ss.

1.

; 95WO-US003989.

; 94US-00223842.

; 95US-00417210.

OGENETICS CORP.

Tartaglia J, Cox WI;

66231/47.

attenuated virus encoding an immunodeficiency virus epitope -  
penhagen strain of vaccinia virus, used in the prevention and  
of diseases, e.g. vaccination against HIV.

Page 127; 208pp; English.

4752 are PCR primers used in the construction of pCSPOL75A, a  
tg. attenuated virus ALVAC recombinant expressing 3 CTL pol  
IVI gag (pro), gp120 and transmembrane region. ALVAC-based  
viruses expressing extrinsic immunogens are efficacious as  
tators. Attenuated recombinant viruses such as ALVAC or NVAC  
needed to comprise exogenous DNA in a non-essential region of  
e, the exogenous DNA encodes at least one immunodeficiency  
pe. Such attenuated viruses (as above) and derived antigens  
ies are used in the prevention, therapy and diagnosis of  
NA from the recombinant viruses can be used as probes or for  
primers or for immunisation. Attenuated recombinant viruses  
ed safety making them safer for use in vaccines

BP; 21 A; 8 C; 8 G; 16 T; 0 U; 0 Other;

ilarity 73.3%; Score 13.2; DB 2; Length 53;

Conservative 83.3%; Pred. No. 8.9e+03;  
3; Mismatches 3; Indels 0; Gaps 0;

'CATTGGGAATTTGGCC 18

|||||

'ACTTTGGGAATTTGGCC 30

andard; DNA; 60 BP.

; (first entry)

red transcript detection oligonucleotide SEQ ID NO:22707.

ie; rat; splice transcript; detection; RNA transcript;  
.ant; transcriptome; oligonucleotide library; ss.

19.

1-A2.

2.

1; 2001WO-IB001903.

XX

PR 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX

PA (COMP-) COMPUGEN INC.

XX

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR

XX MPI; 2002-257383/30.

XX

PT New oligonucleotide libraries comprising oligonucleotides which  
selectively hybridize to mRNAs transcribed from a transcription  
genome, useful for detecting tissue-, pathology-, and developme  
specific genes.

PT

XX

FS Example 1; SEQ ID NO 22707; 47pp; English.

XX

CC The present invention describes oligonucleotide libraries for d  
messenger RNAs that populate a (sub-)transcriptome, where the ( )  
transcriptome comprises messenger RNAs transcribed from multip  
transcription units that populate a genome. The library compris  
oligonucleotides, each capable of hybridising selectively to a  
messenger RNAs transcribed from a given transcription unit of t  
which encodes one or more messenger RNA splice variants. The  
oligonucleotide libraries are useful for detecting mRNAs from a  
biological sample, in expression profiling studies, in qualitat  
quantitatively characterising the corresponding transcriptome,  
detecting RNA transcripts and splice variants of human or anima  
transcriptomes. The libraries may also be used as specialised m  
libraries to detect transcripts of a sub-transcriptome under a  
biological or pathological state, and so allowing the detection  
- and pathology-specific genes such as those genes only express  
specific tissue under a specific pathological condition; to det  
developmental specific genes; and to detect RNA transcripts and  
variants of a transcriptome of a patient suffering from a parti  
disorder. ABN27253 to ABN59589 represent oligonucleotide sequen  
rats, humans and mice, which are used in the exemplification of  
present invention. N.B. The sequence data for this patent did n  
part of the printed specification, but was obtained in electron  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 60 BP; 12 A; 24 C; 11 G; 13 T; 0 U; 0 Other;

Query March

73.3%; Score 13.2; DB 6; Length 60;

Best Local Similarity 83.3%; Pred. No. 9e+03; 3; Indels 0;

Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTGGCC 18

|||||

Db 38 CTCATTGGGAATTTGGCC 55

RESULT 25

ABF80741/c

ID ABF80741 standard; DNA; 13 BP.

XX

AC ABF80741;

XX

DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 180738 for detecting SNP TSC0044732.

XX

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; car  
peptide nucleic acid; cytosine methylation; cardiovascular; pri  
central nervous system; gastrointestinal; respiratory; immune;

XX

OS Homo sapiens.

XX

PN WO200177384-A2.

XX

PD 18-OCT-2001.

XX

PF 06-APR-2001; 2001WO-IB000713.

09:38:22 2004

us-10-090-326-16.max.rng

2000DE-01019173.

GENOMICS AG.

penbrock C, Berlin K;

37177/75.

nucleotides, useful for diagnosis and cell typing, is detect single-nucleotide polymorphisms and cytosine status.

ID NO 180738; 29pp + Sequence Listing; German.

on describes novel oligonucleotide primers or peptide nucleic oligomers for detecting single nucleotide polymorphisms (SNP) methylation status in chemically pretreated genomic DNA. The oligomers are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-BF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH182073 are oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 7 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 ATTGGAAATTTG 16

|||||

1 ATTGGAAATTTG 1

undard; DNA; 13 BP.

(first entry)

side SEQ ID NO 180737 for detecting SNP TSC0044732.

nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; nucleic acid; cytosine methylation; cardiovascular; primer; ss; nervous system; gastrointestinal; respiratory; immune; metabolic.

1.

A2.

2001WO-1B000713.

2000DE-01019173.

GENOMICS AG.

penbrock C, Berlin K;

37177/75.

nucleotides, useful for diagnosis and cell typing, is detect single-nucleotide polymorphisms and cytosine status.

Claim 1; SEQ ID NO 180737; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms and cytosine methylation status in chemically pretreated genomic DNA. The oligomers are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH182073 are oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 13 BP; 3 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+04; 0; Indels 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0;

4 ATTGGAAATTTG 16

|||||

1 ATTGGAAATTTG 13

RESULT 27

ABZ30652/c

ID ABZ30652 standard; DNA; 24 BP.

AC ABZ30652;

30-JAN-2003 (first entry)

Candida albicans GRACE strain PCR primer SEQ ID NO 4803. Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal; PCR; pr;

Candida albicans.

WO200253728-A2.

11-JUL-2002.

26-DEC-2001; 2001WO-US049486.

29-DEC-2000; 2000US-0259128P.

20-FEB-2001; 2001US-00792024.

22-AUG-2001; 2001US-0314050P.

(ELIT-) ELITRA PHARM INC.

Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

WPI; 2002-566694/60.

Constructing strains for identifying gene products as effective for therapeutic intervention, by inactivating in the strain one a gene and placing other allele of the gene under conditional expression.

Claim 36; SEQ ID NO 4803; 167pp + Sequence Listing; English.

The invention relates to constructing (M1) a strain of diploid cells in which both alleles of a gene are modified, comprising one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a hetero promoter, so that expression of the second allele is regulated by a promoter. (M1) is useful for constructing a strain of diploid cells in which both alleles of a gene are modified. The diploid cells having both alleles modified are useful for identifying a



1 to the survival or growth of a fungus, a gene that to the virulence and/or pathogenicity of a fungus, a gene butes to the resistance of a diploid fungus to an antifungal ntifungal agent that inhibits the growth of a diploid fungus ntifying a therapeutic agent for treatment of a mammalian 1) is useful for identifying a compound which modulates the a gene product, preferably enzymatic activity, carbon tabolism, biosynthetic, transporter, transcriptional, al, signal transduction, DNA replication and cell division he method is useful for identifying a compound having the inhibit growth or proliferation of C. albicans cells and for fection by C. albicans. The present sequence is that of a PCR in the method of the invention. Note: The sequence data for is not represented in the printed specification but is based information supplied to Derwent by the European Patent Office

BP; 11 A; 8 C; 1 G; 4 T; 0 U; 0 Other;

72.2%; Score 13; DB 6; Length 24;  
ilarity 100.0%; Pred. No. 1.1e+04;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TGGAATTTC 17  
|||||  
TGGAATTTC 2

andard; DNA; 25 BP.

(first entry)

c SNPE primer SEQ ID 863.

eoride polymorphism; SNP; single nucleotide primer extension;  
yping; agammaglobulinaemia; diabetes insipidus; cancer;  
' syndrome; muscular dystrophy; familial hypercholesterolaemia;  
kidney disease; osteogenesis imperfecta; autoimmune disease;  
mittent porphyria; rheumatoid arthritis; multiple sclerosis;  
n; forensic investigation; paternity analysis; primer; ss.

is.

-A2.

; 200WO-US028436.

; 99US-0160096P.

HID BIOSCIENCES INC.

burg L, Pohl M;

90930/30.

ing oligonucleotide, useful for detecting the presence,  
identity of single polynucleotide polymorphism in a nucleic

ge 54; 83pp; English.

AH37205 - AAH40944 represent PCR primers, single nucleotide  
ngle (SNPE) primers, and the sequences of regions flanking  
single nucleotide polymorphisms SNPs. The present invention  
ts for determining the presence or absence of a SNP, using the  
ides of the invention. The PCR primers are used to amplify a  
ig sequence, the SNPE primer is used as a genotyping primer.  
cleotides are useful for genotyping a nucleic acid sample by

performing a single-nucleotide primer extension reaction. The  
oligonucleotides are useful for determining the presence, abser  
identity of a SNP and for genotyping nucleic acid samples, for  
asses by association analysis the genotype of an individual or  
CC individuals, having a pathological phenotypic trait suspected c  
CC caused by one or more SNPs. Phenotypic traits include diseases  
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome,  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney d  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenoc  
CC traits also include symptoms of or susceptibility to multifact  
CC disease of which a component is or may be genetic such as autoi  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by  
CC microorganism. The method is also useful in forensic investigat  
CC paternity analysis. The present sequence represents a single nu  
CC primer extension (SNPE) primer specific for a human SNP contain  
CC sequence

Sequence 25 BP; 7 A; 4 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 72.2%; Score 13; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0;

Qy 3 CATTGGAAATTT 15  
|||||  
Db 3 CATTGGAAATTT 15

RESULT 29

ABX03639/c

ID ABX03639 standard; DNA; 30 BP.

AC ABX03639;

DT 07-JAN-2003 (first entry)

Human aurora 2 protein phosphorylating enzyme related primer #2

Aurora 2 protein phosphorylating enzyme; Aurora 2 protein phosf

primer; ss.

OS Synthetic.

XX JP2002236125-A.

XX 23-AUG-2002.

XX 06-FEB-2001; 2001JP-00029774.

XX 06-FEB-2001; 2001JP-00029774.

(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.

XX WPI; 2002-744730/81.

Determination of protein phosphorylation enzyme activity with a  
PT which specifically recognizes a phosphorylated substrate with h  
PT Aurora2 protein phosphorylating enzyme.

XX Example 5; Page 16; 29pp; Japanese.

The invention describes a method of determination of human Auro  
protein phosphorylating enzyme activity comprising (a) contact  
CC Aurora 2 protein phosphorylating enzyme and a substrate to be  
CC phosphorylated to give phosphorylated substrate, (b) antibody b  
CC step composed of binding of an antibody that solely recognises  
CC phosphorylated substrate and the phosphorylated substrate; and k  
CC determination of the bound product. The method, antibody and k  
CC useful for the determination of phosphorylating activity of hum  
CC 2 protein phosphorylase. This sequence represents a human auro  
CC protein phosphorylating enzyme associated primer

09:38:22 2004

us-10-090-326-16.max.rng

BP; 10 A; 6 C; 7 G; 7 T; 0 U; 0 Other;  
72.2%; Score 13; DB 6; Length 30;  
Identity 100.0%; Pred. No. 1.1e+04;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
ATTGGAATT 13  
|||||  
ATTGGAATT 5  
undard; DNA; 50 BP.  
(first entry)  
: noncoding SNP oligonucleotide SEQ ID NO:213.  
le nucleotide polymorphism; SNP; polymorphism; cytostatic;  
ssive; antiinflammatory; neuroprotective; antimicrobial;  
disease; inflammation; cancer; nervous system disease;  
polymorphic protein; ds.  
s.  
-A2.  
: 2000WO-US032311.  
99US-0167383P.  
GEN CORP.  
Leach M;  
5949/37.  
an nucleic acids comprising one or more single nucleotide  
as, useful for treating a subject suffering from a pathology,  
une diseases, ascribed to the presence of a sequence  
n.  
je 311; 674pp; English.  
ABL01104 represent human nucleic acid oligonucleotides  
one or more single nucleotide polymorphisms (SNPs). ABB56531  
represent human peptides encoded by some of the SNP  
ides. The sequences from the present invention can have  
ssive, cytostatic, antiinflammatory, neuroprotective and  
al activities. Nucleic acids, polypeptides, oligonucleotides  
ies from the present invention can be used for treating a  
-ering from, at risk for, or suspected of, suffering from a  
cribed to the presence of a sequence polymorphism. The  
y be autoimmune diseases, inflammation, cancer, diseases of  
system, and infection by pathogenic microorganisms. The SNPs  
aful for determining which forms of a characterised  
n are present in individuals. The antibodies may be used in  
on, quantitation and/or cellular or tissue localisation of a  
protein (e.g., for use in measuring levels of the polymorphic  
ain appropriate physiological samples)  
BP; 11 A; 9 C; 6 G; 24 T; 0 U; 0 Other;  
72.2%; Score 13; DB 5; Length 50;  
Identity 100.0%; Pred. No. 1.1e+04;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
TTTGGAAATTT 15

Db  
|||||  
2 CATTGGAATTT 14  
RESULT 31  
AAH38068  
ID AAH38068 standard; DNA; 51 BP.  
XX  
AC AAH38068;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE Human SNP flanking oligonucleotide SEQ ID 864.  
XX  
KW Single nucleotide polymorphism; SNP; single nucleotide primer es  
SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cance  
Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholest  
polycystic kidney disease; osteogenesis imperfecta; autoimmune  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sc  
KW inflammation; forensic investigation; paternity analysis; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200129262-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028436.  
XX  
PR 15-OCT-1999; 99US-0160096P.  
XX  
PA (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
PI Picoult-Newburg L, Pohl M;  
XX  
DR WPI; 2001-290930/30.  
XX  
PT New genotyping oligonucleotide, useful for detecting the presen  
PT absence or identity of single polynucleotide polymorphism in a  
PT acid sample.  
XX  
PS Claim 1; Page 54; 83pp; English.  
XX  
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nuc  
primer extension (SNPE) primers, and the sequences of regions f  
sites of single nucleotide polymorphisms SNPs. The present inve  
CC includes kits for determining the presence or absence of a SNP,  
CC oligonucleotides of the invention. The PCR primers are used to  
CC SNP flanking sequence, the SNPE primer is used as a genotyping  
CC The oligonucleotides are useful for genotyping a nucleic acid s  
performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absen  
identity of a SNP and for genotyping nucleic acid samples, for  
CC assess by association analysis the genotype of an individual or  
CC individuals, having a pathological phenotypic trait suspected o  
caused by one or more SNPs. Phenotypic traits include diseases  
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome,  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney di  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenol  
CC traits also include symptoms of or susceptibility to multifacto  
CC disease of which a component is or may be genetic such as autoi  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by  
CC microorganism. The method is also useful in forensic investigat  
CC paternity analysis. The present sequence represents a fragment  
CC DNA flanking the site of a single nucleotide polymorphism  
XX  
SQ Sequence 51 BP; 14 A; 12 C; 7 G; 18 T; 0 U; 0 Other;  
Query Match 72.2%; Score 13; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0;

TTTGGAAATTTT 15  
|||||  
TTTGGAAATTTT 15

andard; DNA; 51 BP.

(first entry)

ontaining single nucleotide polymorphism SEQ ID NO. 34.

le nucleotide polymorphism; SNP; angiotensinogen; tyrosine; dehydrogenase; protein therapy; riphosphate-dependent RNA helicase; compatibility complex Class I histocompatibility antigen; MHC; erate kinase; immunosuppressive; immunostimulatory; ic; antileukemic; antidiabetic; antiinflammatory; cytostatic; c; neuroprotective; antimicrobial; gene therapy; vaccine; ds.

S.

-A2.

; 2000WO-US035346.

; 99US-00472688.

AGEN CORP.

Leach M;

18297/44.

nucleic acids encoding e.g. angiotensin, dehydrogenase, riphosphate-dependent RNA helicase and/or phosphoglycerate ful for diagnosing and treating, e.g. cancer, autoimmune d infections.

ge 68; 484pp; English.

on relates to nucleic acids (AAH79386-AAH80036) encoding variants of proteins (AAG98010-AAG98238) related to n, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate dent RNA helicase, major histocompatibility complex (MHC) tocompatibility antigen and/or phosphoglycerate kinase. These d single nucleotide polymorphisms (SNPs) and the encoded ve potential immunosuppressive, immunostimulatory, ic, antileukemic, antidiabetic, antiinflammatory, cytostatic, c, neuroprotective and antimicrobial activity and may be ene/protein therapy, vaccines, modulation of the expression y of proteins related to angiotensin, 4-hydroxybutyrate, se, adenosine triphosphate (ATP)-dependent RNA helicase, major ibility complex (MHC) Class I histocompatibility antigen, phoglycerate kinase. Disorders that may be prevented, nd/or treated by the above methods include multifactorial th a genetic component, such as autoimmune diseases (e.g. arthritis, multiple sclerosis, diabetes, systemic lupus osus and Grave's disease), inflammation, cancer (e.g. cancers ilder, brain, breast, colon and kidney, leukemia), diseases of ; system, an infection of pathogenic organisms. They may also alter phenotypic traits such as longevity, appearance, ped and endurance

BP; 14 A; 14 C; 6 G; 17 T; 0 U; 0 Other;

ilarity 72.2%; Score 13; DB 4; Length 51; 100.0%; Pred. No. 1.1e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0;

Qy 1 CTCATTGGGAATT 13  
|||||  
Db 13 CTCATTGGGAATT 1

RESULT 33

AAZ94932  
ID AAZ94932 standard; DNA; 17 BP.

XX AAZ94932;

XX 01-AUG-2000 (first entry)

XX Eimeria tenella hydrophilic polypeptide DNA probe.  
XX Coccidiosis; vaccine; poultry; superoxide dismutase; hybridisat  
KW probe; ss.

XX Eimeria tenella.

XX EP995799-A2.

XX 26-APR-2000.

XX 01-OCT-1999; 99EP-00203214.

XX 07-OCT-1998; 98EP-00203384.

XX 16-OCT-1998; 98EP-00203457.

XX (ALKU) AKZO NOBEL NV.

XX Schaap TC, Kuijper CM, Vermeulen AN;

XX WPI; 2000-305655/27.

XX Novel hydrophilic Eimeria polypeptides comprise sequences with 70% homology with sequences of 13-223 amino acids, useful as va against Coccidiosis in poultry.  
XX Disclosure; Page 26; 30pp; English.

XX This oligonucleotide is 1 of 32 probes (see AAZ94902-33) design cover all possible nucleic acid sequences encoding a peptide (s CC AAY79503) derived from a newly identified 25 kDa superoxide dis CC like protein of Eimeria tenella strain Weybridge (see also AAY7 CC mixed probe set can be used to detect the gene encoding the 25 CC protein, and in the identification of genes encoding related pr CC Eimeria spp. The invention provides 6 hydrophilic polypeptides CC AAY79494-99) of Eimeria. These polypeptides, their homologues, CC immunogenic fragments of them, can be used in vaccines to prote CC against the pathogenic effects of Eimeria, the causative agent CC intestinal coccidiosis. The polypeptides are also useful for de CC antibodies against Eimeria infection in poultry. DNA encoding t CC polypeptides can be used to detect Eimeria parasites and as a v CC optionally in a live recombinant carrier  
XX SQ Sequence 17 BP; 3 A; 2 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 3; Length 17;

Best Local Similarity 87.5%; Pred. No. 1.3e+04; Mismatches 2; Indels 0;

Qy 2 TCATTGGGAATTTC 17  
|||||  
Db 2 TCATTGGGAATTTC 17

RESULT 34

AAZ94930  
ID AAZ94930 standard; DNA; 17 BP.

XX

(first entry)

illa hydrophilic polypeptide DNA probe.

vaccine; poultry; superoxide dismutase; hybridisation;

illa.

99EP-00203214.

98EP-00203384.

98EP-00203457.

NOBEL NV.

Kuijper CM, Vermeulen AN;

95655/27.

hilic Eimeria polypeptides comprise sequences with at least  
with sequences of 13-223 amino acids, useful as vaccines  
;idosis in poultry.

Page 25; 30pp; English.

cleotide is 1 of 32 probes (see AAZ94902-33) designed to  
assemble nucleic acid sequences encoding a peptide (see  
derived from a newly identified 25 kDa superoxide dismutase  
of Eimeria tenella strain Weybridge (see also AA79494). The  
set can be used to detect the gene encoding the 25 kDa  
in the identification of genes encoding related proteins in  
The invention provides 6 hydrophilic polypeptides (see  
of Eimeria. These polypeptides, their homologues, or  
fragments of them, can be used in vaccines to protect poultry  
pathogenic effects of Eimeria, the causative agent of  
occidiosis. The polypeptides are also useful for detecting  
against Eimeria infection in poultry. DNA encoding the  
can be used to detect Eimeria parasites and as a vaccine,  
in a live recombinant carrier

BP; 3 A; 2 C; 5 G; 7 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 3; Length 17;

larity 87.5%; Pred. No. 1.3e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ATTGGGAATTTTC 17

|||||

ATTGGGAATTTTC 17

undard; DNA; 21 BP.

(first entry)

omavirus E6 gene-specific PCR primer 199.

cinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervical cancer;  
.; cervix; PCR; primer; ss.

omavirus.

PN WO2003057914-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 07-JAN-2003; 2003WO-GB0000034.  
XX  
PR 07-JAN-2002; 2002GB-00000239.  
PR 19-JUN-2002; 2002GB-00014124.  
XX  
PA (NORC-) NORCHIP AS.  
PA (ALLA/) ALLARD S J.  
XX  
PI Karlsen F;  
XX  
XX WPI; 2003-587136/55.  
XX  
XX An in vitro method of screening human subjects to assess their  
PT developing cervical carcinoma, comprises screening the subject  
PT expression of mRNA transcripts from the L1 gene and the E6 gene  
PT papillomavirus.

Disclosure; Page 54; 102pp; English.

This invention relates to a novel method for the detection of hu  
papillomavirus mRNA for use in the screening of human female su  
assess their risk of developing cervical carcinoma. The inventio  
comprises screening the subject for expression of mRNA transcrip  
the L1 gene and the E6 gene of human papillomavirus, where subj  
positive for expression of L1 and/or E6 mRNA are scored as being  
of developing cervical carcinoma. The presence of the human  
papillomavirus (in particular HPV16 and HPV18) has been associa  
cervical cancer in numerous epidemiological studies. The method  
invention are useful for screening human subjects to assess the  
developing cervical carcinoma, or for identifying human subject  
abnormal cell changes in the cervix. The present sequence is the  
preferred PCR primer which may be used to amplify the E6 gene of  
papillomavirus in the method of the invention.

XX Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match

71.1%; Score 12.8; DB 9; Length 21;

Best Local Similarity 87.5%; Pred. No. 1.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 CTCATTGGGAATTTTC 16

|||||

Db 16 CTCATTGGGAATCGTG 1

RESULT 36

ADD36940/C

ID ADD36940 standard; DNA; 21 BP.

XX

AC ADD36940;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human papillomavirus E6 gene-specific PCR primer/probe Seq ID53.

XX

XX cervical carcinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervix  
XX cervical cell; cervix; PCR; primer; probe; ss.

XX

OS Human papillomavirus.

XX

PN WO2003057914-A2.

XX

PD 17-JUL-2003.

XX

PF 07-JAN-2003; 2003WO-GB0000034.

XX

PR 07-JAN-2002; 2002GB-00000239.

PR

19-JUN-2002; 2002GB-00014124.

XX

CHIP AS.  
ARD S J.

87136/55.

method of screening human subjects to assess their risk of cervical carcinoma, comprises screening the subject for mRNA transcripts from the L1 gene and the E6 gene of human virus.

SEQ ID NO 53; 102pp; English.

ion relates to a novel method for the detection of human virus mRNA for use in the screening of human female subjects to risk of developing cervical carcinoma. The invention screening the subject for expression of mRNA transcripts from and the E6 gene of human papillomavirus, where subjects expression of L1 and/or E6 mRNA are scored as being at risk cervical carcinoma. The presence of the human virus (in particular HPV16 and HPV18) has been associated with cancer in numerous epidemiological studies. The methods of the re useful for screening human subjects to assess their risk of cervical carcinoma, or for identifying human subjects having L1 changes in the cervix. The present sequence is that of a (which may also be suitable as a probe) which may be used to E6 gene of human papillomavirus in the method of the

BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 9; Length 21;  
ilarity 87.5%; Pred. No. 1.3e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CATTGGGATTTTG 16  
|||||||  
CATTGGGATCGTG 1

andard; DNA; 21 BP.

(first entry)

transcribed mRNA detecting RT-PCR primer #26.  
apillomavirus; HPV; NASBA; primer; RT-PCR; ss.  
lomavirus type 31.

7-A2.

; 2003WO-GB0000030.  
; 2002GB-00000258.

CHIP AS.  
ARD S J.

.87141/55.

cleotide primer and probe for detecting the presence of mRNA  
; from the E6 gene of a human papillomavirus in clinical

XX Disclosure; Page 24; 28pp; English.

XX The invention relates to a novel oligonucleotide molecule used  
CC detecting mRNA transcribed from the E6 gene of a human papillom  
CC (HPV). The oligonucleotide comprises any of the 133 fully defin  
CC sequences having 17-26 bp given in the specification. The inven  
CC further provides the detection of HPV mRNA in a test sample sus  
CC containing HPV, comprising performing an amplification reaction  
CC preparation of a nucleic acid isolated from the test sample to  
CC portion of the mRNA transcribed from the E6 gene of HPV, where  
CC amplification reaction is performed using the primer-pair of  
CC oligonucleotide cited above. The invention also provides: a rea  
CC for use in the detection of HPV by NASBA, comprising an oligonu  
CC primer-pair and, optionally, an enzyme mixture comprising an RN  
CC DNA polymerase, a ribonuclease that hydrolyzes the RNA strand o  
CC DNA hybrid without hydrolyzing single or double stranded RNA or  
CC an RNA polymerase that recognises the promoter sequence present  
CC least one NASBA P1 primer oligonucleotide included in the reage  
CC The oligonucleotide of the invention is useful in detecting mRN  
CC transcripts from the E6 gene of HPV in clinical samples. This  
CC polynucleotide sequence represents an oligonucleotide used for  
CC mRNA transcribed from the E6 gene of a human papillomavirus (HP  
CC invention.

XX Sequence 21 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 71.1%; Score 12.8; DB 9; Length 21;  
Best Local Similarity 87.5%; Pred. No. 1.3e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 1 CTCATTTGGGATTTTG 16  
Db 16 CTCATTTGGGATCGTG 1

RESULT 38

ADD21998/c  
ID ADD21998 standard; DNA; 21 BP.

XX AC ADD21998;

XX 15-JAN-2004 (first entry)

XX HPV E6 gene transcribed mRNA detecting oligonucleotide, SEQ ID  
XX E6; human papillomavirus; HPV; NASBA; primer; PCR; ss.

XX Human papillomavirus type 31.

XX WO2003057927-A2.

XX 17-JUL-2003.

XX 07-JAN-2003; 2003WO-GB0000030.

XX 07-JAN-2002; 2002GB-00000258.

XX (NORC-) NORCHIP AS.

XX (ALLA/) ALLARD S J.

XX Karlsen F;

XX WPI; 2003-587141/55.

XX New oligonucleotide primer and probe for detecting the presence  
XX transcripts from the E6 gene of a human papillomavirus in clini  
XX samples.

XX Claim 1; SEQ ID NO 37; 28pp; English.

XX The invention relates to a novel oligonucleotide molecule used  
CC detecting mRNA transcribed from the E6 gene of a human papillom

**us-10-090-326-16.max.rng**

an exemplary oligonucleotide primer, for use in the detection of unrelated gene mutations of the D3S1286 region. There are over 100 unrelated genes and suppressor genes to date, which control development, and cell differentiation. Regulation of these genes under certain circumstances, be altered and normal cells can assume growth characteristics. The invention provides a method for

09:38:22 2004

us-10-090-326-16.max.rng

to construct a probe which is in turn used to isolate mouse spanning exon 7 of PS-1

BP; 4 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 5; Length 22;

ilarity 87.5%; Pred. NO. 1.3e+04;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTATTGGAATTTG 16

|||||

GATCTGGAATTTG 22

andard; DNA; 22 BP.

(first entry)

exon 7 specific probe generating primer PSI-1.

disease; presenilin-1; PS-1 gene; FAD Swedish mutation; de; transgenic; neurotropic; neuroprotective; mouse; PCR primer;

-A2.

; 2001WO-US022693.

; 2000US-00621897.

HALON INC.

Reaume AG, Dorfman K;

27049/28.

ed, non-human mammal for human familial Alzheimer's disease compounds that decrease levels of A-beta peptide, has senilin-1, FAD Swedish mutation, and humanized A-beta

Page 22; 71pp; English.

on relates to a gene-targeted, non-human mammal (I) s or homozygous for a human familial Alzheimer's disease (AD) mprising a gene encoding a mutant protein product, of a senilin-1 (PS-1 gene), a human FAD Swedish mutation, and a beta mutation; or of PS-1 gene and a human Swedish APP695 I) or a generational offspring of (I), where mutant PS-1 gene d is useful for screening chemical compounds having ability to vivo levels of Abeta peptide, or for identifying a compound g AD. The method comprises administering the chemical compound measuring the amount of Abeta peptide in a tissue sample from where a decrease in the amount of the peptide in the tissue ndicative of a chemical compound that has the ability to vivo levels of the peptide, where tissue sample is from brain n tissue or body fluids. The chemical compounds identified are treating an individual suspected of having AD. The present presents a primer used for generating a probe specific for the gene exon 7

; BP; 4 A; 5 C; 5 G; 8 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 6; Length 22;

ilarity 87.5%; Pred. NO. 1.3e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 1 CTATTGGAATTTG 16

|||||

Db 7 CTGATCTGGAATTTG 22

RESULT 42

ACC72192/c

ID ACC72192 standard; DNA; 27 BP.

XX

AC ACC72192;

XX

DT 07-JUL-2003 (first entry)

XX

DE Ag4300 probe.

XX

KW Human; NOV; artidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; neurotropic; neuroprotective; antiparkinsonian; antilipemic; gene therapy; metabolic disorder diabetes; obesity; infection; cachexia; cancer; probe; neurodegenerative disorder; Alzheimer's disease; Parkinson's di immune disorder; haematopoietic disorder; dyslipidaemia; ss.

XX

OS Homo sapiens.

XX

PN WO2003029423-A2.

XX

PD 10-APR-2003.

XX

PF 02-OCT-2002; 2002WO-US031358.

XX

PR 02-OCT-2001; 2001US-0326483P.

PR 05-OCT-2001; 2001US-0327342P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.

PR 12-OCT-2001; 2001US-0328849P.

PR 15-OCT-2001; 2001US-0329414P.

PR 17-OCT-2001; 2001US-0330142P.

PR 22-OCT-2001; 2001US-0341058P.

PR 24-OCT-2001; 2001US-0339286P.

PR 24-OCT-2001; 2001US-0343629P.

PR 29-OCT-2001; 2001US-0349575P.

PR 01-NOV-2001; 2001US-0346357P.

PR 12-APR-2002; 2002US-0371972P.

PR 12-APR-2002; 2002US-0371980P.

PR 17-APR-2002; 2002US-0373261P.

PR 19-APR-2002; 2002US-0373805P.

PR 23-APR-2002; 2002US-0374738P.

PR 16-MAY-2002; 2002US-0381101P.

PR 17-MAY-2002; 2002US-0381635P.

PR 29-MAY-2002; 2002US-0383830P.

PR 01-OCT-2002; 2002US-00262839.

XX (CURA-) CURAGEN CORP.

XX

XX

PI Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton

PI Edinger SR, Ellerman K, Gerlach VL, Gorman L, Guo X, Ji W;

PI Ketuda R, Leach MD, Li L, Miller CE, Patturajan M, Rieger

PI Rothenberg MB, Shmukets RA, Smithson G, Spytek KA, Taupier

PI Vernet CAN, Voss EZ, Zerhusen BD, Zhong M;

XX WPI; 2003-381625/36.

XX

XX

PT NOVX polypeptides and nucleic acids useful for diagnosing, prev

PT treating NOVX-associated disorders, e.g. diabetes, obesity, can

PT dyslipidemia, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX

XX

PS Example C; Page 303; 487pp; English.

XX

invention relates to novel human NOV proteins and their uses (ACC72075-ACC72181 and ABR58363-ABR58469). The NOV is useful in manufacturing a medicament for treating a syndrome with a human disease. The NOV proteins and coding sequences to diagnose, treat or prevent metabolic disorders such as obesity, infectious, cachexia, cancer, neurodegenerative diseases such as Alzheimer's disease or Parkinson's disease, immune haematopoietic disorders and various dyslipidaemias. The invention is a probe, used in an example from the invention

BP; 11 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 7; Length 27;

ilarity 87.5%; Pred. No. 1.3e+04;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTTGGGAATTTGTC 17

|||||

TTTGGGAATTTGTC 12

indard; DNA; 29 BP.

(first entry)

actor construction related PCR primer SEQ ID NO:4.

alpha 1-3 galactosyltransferase; immunosuppressive;

; host disease; PCR primer; ss.

1-A.

2000JP-00202748.

2000JP-00202748.

OKU NOGYO KYODO KUMIAI RENGOKAI.

TOKYO JOSHI IKA.

3242/31.

actosyltransferase gene knocked down somatic cells.

pe 4; 9pp; Japanese.

invention describes mammal somatic cells with alpha 1-3 mannosidase (alpha 1-3 GT) gene knocked down gene other than mouse, particularly bovine, especially fibroblast cells. The cells are prepared by homologous recombination of a DNA domain containing part of an exon domain in genomic alpha 1-3 GT gene of mammals human and mouse, a selection marker and a promoter at the 5' end and restricting the expression of the selective marker, screening the cells with aimed recombination. The cells have selective activity. The cells can be used in the preparation of cells useful for inhibition of graft versus host disease. The invention represents a PCR primer used in the construction of a vector, which is used in an example from the present invention

BP; 5 A; 7 C; 8 G; 9 T; 0 U; 0 Other;

71.1%; Score 12.8; DB 6; Length 29;

ilarity 87.5%; Pred. No. 1.3e+04;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TTTGGGAATTTGTC 18

Db 9 CATTGGGAATTTTGAC 24

RESULT 44

AAC63949

ID AAC63949 standard; DNA; 30 BP.

XX AAC63949;

XX 09-FEB-2001 (first entry)

XX Acinetobacter calcoaceticus PQQGDH S231K mutagenic oligo, SEQ II

XX Pyroloquinoline quinone glucose dehydrogenase; PQQGDH;

XX PQQ glucose dehydrogenase; thermal stability; glucose assay;

XX diagnostic reagent; blood glucose monitoring; diabetes; mutant;

XX mutagenic oligonucleotide; ss.

XX Acinetobacter calcoaceticus.

OS Synthetic.

XX WO200061730-A1.

XX 19-OCT-2000.

XX 10-APR-2000; 2000WO-JP002322.

XX 08-APR-1999; 99JP-00101143.

PR 18-JAN-2000; 2000JP-00009152.

XX (SODE/) SODE K.

XX Sode K;

XX WPI; 2000-665126/64.

XX Modified pyroloquinolinequinone glucose dehydrogenase with imp;

PT stability for use in assay kits and sensors.

XX Example 2; Page 13; 43pp; Japanese.

XX The invention relates to novel modified forms of the water-soluble

XX pyroloquinoline quinone glucose dehydrogenase (PQGDH) of Acinetobacter

XX calcoaceticus having an amino acid substitution which confers improved

XX thermal stability. The invention also relates to a gene sequence of the

XX modified enzyme, expression vectors and host cells comprising the

XX mutant gene, and glucose assay kits and sensors containing the

XX modified enzyme. The modified enzyme may be used in glucose assay

XX and sensors for research and diagnostic purposes, such as monitoring

XX blood glucose levels (e.g., in a diabetic patient). The present

XX represents a mutagenic oligonucleotide used to generate DNA encoding

XX mutant Acinetobacter calcoaceticus pyroloquinoline quinone (PQ

XX dehydrogenase in an exemplification of the invention

XX Sequence 30 BP; 8 A; 6 C; 4 G; 12 T; 0 U; 0 Other;

XX Query Match 71.1%; Score 12.8; DB 3; Length 30;

XX Best Local Similarity 87.5%; Pred. No. 1.3e+04;

XX Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGGAATTTTGCC 18

Db 1 CCTTTGGGAATTTTGCC 16

RESULT 45

ABV73543

ID ABV73543 standard; DNA; 30 BP.

XX ABV73543;

XX 07-JAN-2003 (first entry)



er calcoaceticus PQGDH mutagenic PCR primer SEQ ID NO 8.  
er calcoaceticus; pyroquinoline-quinone glucose dehydrogenase;  
ucose sensor; diabetes; PCR; primer; ss.  
er calcoaceticus.

I-Al.

;

.; 2002WO-JP002124.

.; 2001JP-00070413.

DE K.

arashi S;

23360/78.

er calcoaceticus-originated water-soluble pyroquinoline-  
cose dehydrogenase with two subunits combined through  
ond, applicable in glucose sensors for determining serum

Page 10; 36pp; Japanese.

on relates to water-soluble pyroquinoline-quinone glucose  
se (PQGDH) (I) comprising two subunits combined with each  
disulfide bond. (I) is applicable in glucose sensors in  
serum glucose e.g. in diagnosis and management of diabetes.  
sequence is that of a mutagenic PCR primer used in examples  
ntion

BP; 8 A; 6 C; 4 G; 12 T; 0 U; 0 Other;

ilarity 71.1%; Score 12.8; DB 6; Length 30;

Conservative 87.5%; Pred. No. 1.3e+04;

Mismatches 0; Indels 2; Gaps 0;

TTTGGAAATTTGCC 18

|||||

TTTGGAAATTTGCC 16

: February 29, 2004, 09:03:34  
84 secs

09:38:22 2004

us-10-090-326-16.max.rni

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

eic search, using sw model

February 29, 2004, 08:44:24 ; Search time 33.8961 Seconds  
(without alignments)  
294.698 Million cell updates/sec

S-10-090-326-16

8 ctcatttggaatttgcc 18

IDENTITY NUC

apop 10.0 , Gapext 1.0

82709 seqs, 277475446 residues

its satisfying chosen parameters: 874574

length: 0  
length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents NA:\*

: /cgn2\_6/prodata/2/ina/5A COMB.seq\*  
: /cgn2\_6/prodata/2/ina/5B COMB.seq\*  
: /cgn2\_6/prodata/2/ina/6A COMB.seq\*  
: /cgn2\_6/prodata/2/ina/6B COMB.seq\*  
: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq\*  
: /cgn2\_6/prodata/2/ina/backfiles1.seq\*

s the number of results predicted by chance to have a  
er than or equal to the score of the result being printed,  
ved by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
77.8	20	4	US-09-422-978-11109	Sequence 11109, A
74.4	17	1	US-08-758-306-377	Sequence 377, App
73.3	30	2	US-08-816-155B-33	Sequence 33, Appl
73.3	30	3	US-08-815-809-18	Sequence 18, Appl
73.3	30	3	US-09-079-587-33	Sequence 33, Appl
73.3	43	3	US-08-832-985-28	Sequence 28, Appl
73.3	43	4	US-09-410-903-9	Sequence 9, Appli
73.3	43	4	US-08-835-159-28	Sequence 28, Appl
73.3	53	2	US-08-417-210A-101	Sequence 101, App
73.3	53	4	US-09-136-159A-101	Sequence 101, App
71.1	17	3	US-09-411-578-35	Sequence 35, Appl
71.1	17	3	US-09-411-578-37	Sequence 37, Appl
71.1	17	4	US-09-749-233-35	Sequence 35, Appl
71.1	17	4	US-09-749-233-37	Sequence 37, Appl
71.1	19	4	US-09-442-143A-46	Sequence 46, Appl
71.1	22	3	US-09-038-637-66	Sequence 66, Appl
71.1	22	3	US-09-041-185-6	Sequence 6, Appli
68.9	17	1	US-08-758-306-375	Sequence 375, App
68.9	27	3	US-08-192-271-5	Sequence 5, Appli
68.9	27	5	PCT-US94-01572-5	Sequence 5, Appli
67.8	20	3	US-09-021-701-379	Sequence 379, App
67.8	20	3	US-09-021-701-380	Sequence 380, App
67.8	20	3	US-09-021-701-381	Sequence 381, App
67.8	20	3	US-09-021-701-382	Sequence 382, App
67.8	22	4	US-09-446-301A-28	Sequence 28, Appl
67.8	22	4	US-09-099-932-26	Sequence 26, Appl
67.8	34	1	US-07-753-738B-3	Sequence 3, Appli

28	12.2	67.8	34	2	US-08-924-695A-17	Sequence
29	12.2	67.8	36	1	US-08-479-852-16	Sequence
c 30	12.2	67.8	36	1	US-08-479-852-96	Sequence
c 31	12.2	67.8	36	1	US-08-479-852-133	Sequence
c 32	12.2	67.8	36	1	US-08-479-852-137	Sequence
c 33	12.2	67.8	36	2	US-08-462-646-16	Sequence
c 34	12.2	67.8	36	2	US-08-462-646-96	Sequence
c 35	12.2	67.8	36	2	US-08-462-646-133	Sequence
c 36	12.2	67.8	36	2	US-08-462-646-137	Sequence
c 37	12.2	67.8	36	3	US-08-792-832A-11	Sequence
c 38	12.2	67.8	36	3	US-09-013-406-16	Sequence
c 39	12.2	67.8	36	3	US-09-013-406-96	Sequence
c 40	12.2	67.8	36	3	US-09-013-406-133	Sequence
c 41	12.2	67.8	36	3	US-09-013-406-137	Sequence
c 42	12.2	67.8	36	4	US-09-766-095-16	Sequence
c 43	12.2	67.8	36	4	US-09-766-095-96	Sequence
c 44	12.2	67.8	36	4	US-09-766-095-133	Sequence
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c 46	12.2	67.8	40	4	US-08-705-477B-80	Sequence
c 47	12.2	67.8	50	1	US-07-630-288A-19	Sequence
c 48	12.2	67.8	50	1	US-08-468-049-19	Sequence
c 49	12.2	67.8	59	4	US-09-331-793-63	Sequence
c 50	12.2	67.8	60	4	US-09-331-793-64	Sequence
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c 52	12	66.7	22	4	US-09-380-836-92	Sequence
c 53	12	66.7	53	4	US-08-956-171B-2738	Sequence
c 54	11.8	65.6	20	3	US-09-104-068-6	Sequence
c 55	11.8	65.6	27	4	US-08-980-241-1	Sequence
c 56	11.8	65.6	38	4	US-09-371-772B-10088	Sequence
c 57	11.8	65.6	55	1	US-08-243-870-15	Sequence
c 58	11.8	65.6	55	1	US-08-409-439A-15	Sequence
c 59	11.6	64.4	27	3	US-09-052-778-5	Sequence
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c 61	11.6	64.4	36	1	US-08-391-000-40	Sequence
c 62	11.6	64.4	36	2	US-08-741-931-40	Sequence
c 63	11.6	64.4	48	1	US-08-105-483-91	Sequence
c 64	11.6	64.4	48	1	US-08-709-209-91	Sequence
c 65	11.6	64.4	48	1	US-08-458-101-91	Sequence
c 66	11.6	64.4	50	3	US-08-660-645A-30	Sequence
c 67	11.6	64.4	50	3	US-09-298-718-30	Sequence
c 68	11.6	64.4	50	3	US-09-546-969-30	Sequence
c 69	11.6	64.4	50	3	US-08-980-832-9	Sequence
c 70	11.6	64.4	50	4	US-09-547-267-30	Sequence
c 71	11.6	64.4	50	4	US-09-920-923B-9	Sequence
c 72	11.6	64.4	52	2	US-08-417-210A-105	Sequence
c 73	11.6	64.4	52	4	US-09-136-159A-105	Sequence
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c 75	11.4	63.3	20	3	US-09-021-701-383	Sequence
c 76	11.4	63.3	20	3	US-09-021-701-384	Sequence
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c 79	11.4	63.3	20	4	US-09-861-159-16	Sequence
c 80	11.4	63.3	20	4	US-09-198-452A-4356	Sequence
c 81	11.4	63.3	21	2	US-08-776-944-14	Sequence
c 82	11.4	63.3	21	4	US-09-422-978-9774	Sequence
c 83	11.4	63.3	23	1	US-08-465-590-98	Sequence
c 84	11.4	63.3	23	1	US-08-711-417C-98	Sequence
c 85	11.4	63.3	23	4	US-09-723-909-98	Sequence
c 86	11.4	63.3	23	5	PCT-US93-08743-98	Sequence
c 87	11.4	63.3	25	4	US-09-580-497B-23	Sequence
c 88	11.4	63.3	30	3	US-08-952-089A-24	Sequence
c 89	11.4	63.3	35	2	US-08-867-941-53	Sequence
c 90	11.4	63.3	35	3	US-09-074-658-53	Sequence
c 91	11.4	63.3	36	3	US-08-951-130-7	Sequence
c 92	11.4	63.3	36	4	US-09-591-694-48	Sequence
c 93	11.4	63.3	38	3	US-08-444-818-237	Sequence
c 94	11.4	63.3	41	2	US-08-369-829A-6	Sequence
c 95	11.4	63.3	41	2	US-08-586-676E-10	Sequence
c 96	11.4	63.3	42	3	US-09-150-213-5	Sequence
c 97	11.4	63.3	47	4	US-09-422-978-1439	Sequence
c 98	11.4	63.3	47	4	US-09-422-978-2214	Sequence
c 99	11.2	62.2	17	3	US-09-411-578-19	Sequence
c 100	11.2	62.2	17	3	US-09-411-578-21	Sequence

62.2	17	3	US-09-411-578-31	Sequence 31, Appl	C 174	11	61.1	20	2	US-08-967-104-11	Sequence
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62.2	17	3	US-09-411-578-36	Sequence 36, Appl	176	11	61.1	23	1	US-08-847-429A-42	Sequence
62.2	17	3	US-09-411-578-38	Sequence 38, Appl	177	11	61.1	23	3	US-09-065-474-42	Sequence
62.2	17	4	US-08-584-040-3777	Sequence 3777, Ap	C 178	11	61.1	23	3	US-09-268-140-25	Sequence
62.2	17	4	US-09-371-772B-1544	Sequence 1544, Ap	179	11	61.1	23	4	US-09-557-034-42	Sequence
62.2	17	4	US-09-371-772B-6170	Sequence 6170, Ap	180	11	61.1	27	4	US-09-263-892A-12	Sequence
62.2	17	4	US-09-749-233-19	Sequence 19, Appl	C 181	11	61.1	40	4	US-08-463-090B-22	Sequence
62.2	17	4	US-09-749-233-21	Sequence 21, Appl	C 182	11	61.1	40	4	US-09-241-888-4	Sequence
62.2	17	4	US-09-749-233-31	Sequence 31, Appl	C 183	11	61.1	47	4	US-09-422-978-454	Sequence
62.2	17	4	US-09-749-233-33	Sequence 33, Appl	C 184	11	61.1	47	4	US-09-422-978-1724	Sequence
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62.2	18	3	US-09-143-212-75	Sequence 75, Appl	187	10.8	60.0	17	4	US-08-584-040-6115	Sequence
62.2	20	3	US-08-756-806A-41	Sequence 41, Appl	C 188	10.8	60.0	17	4	US-08-584-040-6116	Sequence
62.2	20	3	US-09-143-214-41	Sequence 41, Appl	C 189	10.8	60.0	17	4	US-09-371-772B-1543	Sequence
62.2	20	3	US-08-867-230A-5	Sequence 5, Appl	190	10.8	60.0	17	4	US-09-371-772B-2952	Sequence
62.2	20	3	US-09-021-701-378	Sequence 378, App	191	10.8	60.0	17	4	US-09-371-772B-2953	Sequence
62.2	20	4	US-09-489-765A-66	Sequence 66, Appl	C 192	10.8	60.0	18	1	US-08-290-448A-36	Sequence
62.2	20	4	US-09-506-073-43	Sequence 43, Appl	C 193	10.8	60.0	18	1	US-08-290-448A-36	Sequence
62.2	20	4	US-09-446-301A-25	Sequence 25, Appl	C 194	10.8	60.0	18	1	US-08-175-069A-36	Sequence
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62.2	20	4	US-09-099-932-23	Sequence 23, Appl	C 196	10.8	60.0	18	4	US-08-464-000-36	Sequence
62.2	20	5	PCT-US95-0711A-41	Sequence 41, Appl	197	10.8	60.0	20	2	US-08-117-952-291	Sequence
62.2	24	4	US-09-657-346A-4	Sequence 4, Appl	C 198	10.8	60.0	20	3	US-09-249-730-165	Sequence
62.2	28	1	US-08-220-606B-37	Sequence 37, Appl	199	10.8	60.0	20	3	US-09-021-701-718	Sequence
62.2	31	3	US-09-235-246-18	Sequence 18, Appl	200	10.8	60.0	20	3	US-09-021-701-719	Sequence
62.2	31	3	US-09-446-504-20	Sequence 20, Appl	201	10.8	60.0	20	3	US-09-021-701-720	Sequence
62.2	31	4	US-09-712-266-20	Sequence 20, Appl	202	10.8	60.0	20	3	US-09-021-701-721	Sequence
62.2	34	2	US-08-846-762-40	Sequence 40, Appl	203	10.8	60.0	20	3	US-09-021-701-722	Sequence
62.2	37	4	US-09-530-157B-8	Sequence 8, Appl	204	10.8	60.0	20	3	US-09-021-701-723	Sequence
62.2	38	1	US-08-373-124A-833	Sequence 833, App	205	10.8	60.0	20	4	US-09-689-255C-29	Sequence
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62.2	40	1	US-08-207-226A-5	Sequence 5, Appl	C 211	10.8	60.0	20	4	US-09-249-247-165	Sequence
62.2	41	1	US-08-332-420-53	Sequence 53, Appl	212	10.8	60.0	21	1	US-08-753-147-45	Sequence
62.2	41	3	US-08-813-507-78	Sequence 78, Appl	C 213	10.8	60.0	21	4	US-09-422-978-9573	Sequence
62.2	41	4	US-08-464-453-78	Sequence 78, Appl	214	10.8	60.0	22	1	US-07-722-798A-38	Sequence
62.2	42	1	US-08-224-657-119	Sequence 119, App	C 215	10.8	60.0	24	1	US-07-722-798A-37	Sequence
62.2	42	1	US-08-303-275-201	Sequence 201, App	216	10.8	60.0	24	2	US-08-360-606B-18	Sequence
62.2	42	2	US-08-184-009-170	Sequence 170, App	217	10.8	60.0	25	1	US-08-465-590-81	Sequence
62.2	42	2	US-08-566-398-60	Sequence 60, Appl	C 218	10.8	60.0	25	3	US-09-217-101-5	Sequence
62.2	42	2	US-08-716-284-3	Sequence 3, Appl	219	10.8	60.0	25	3	US-08-711-417C-81	Sequence
62.2	42	2	US-08-458-356-170	Sequence 170, App	220	10.8	60.0	25	4	US-09-514-302-13	Sequence
62.2	42	2	US-08-658-665-159	Sequence 159, App	221	10.8	60.0	25	4	US-09-723-909-81	Sequence
62.2	42	2	US-08-675-566-73	Sequence 73, Appl	222	10.8	60.0	25	5	PCT-US93-08743-81	Sequence
62.2	42	3	US-08-796-101-135	Sequence 135, App	C 223	10.8	60.0	26	2	US-08-756-439-71	Sequence
62.2	42	3	US-08-460-736-170	Sequence 170, App	C 224	10.8	60.0	27	1	US-08-624-545-70	Sequence
62.2	42	3	US-09-085-273-159	Sequence 159, App	C 225	10.8	60.0	27	2	US-08-995-927-6	Sequence
62.2	42	3	US-09-354-138-119	Sequence 119, App	C 226	10.8	60.0	27	4	US-09-582-096-6	Sequence
62.2	42	4	US-09-583-545-3	Sequence 3, Appl	C 227	10.8	60.0	27	4	US-08-584-040-5305	Sequence
62.2	42	4	US-09-535-370-170	Sequence 170, App	C 228	10.8	60.0	27	5	PCT-US94-03744-10	Sequence
62.2	42	4	US-09-617-594A-16	Sequence 16, Appl	C 229	10.8	60.0	29	1	US-07-681-703B-40	Sequence
62.2	42	4	US-09-916-963-159	Sequence 159, App	C 230	10.8	60.0	29	3	US-09-201-075-5	Sequence
62.2	45	1	US-08-332-420-52	Sequence 52, Appl	231	10.8	60.0	29	3	US-09-275-850-172	Sequence
62.2	47	4	US-09-671-317-661	Sequence 661, App	C 232	10.8	60.0	29	4	US-09-462-843A-17	Sequence
62.2	47	4	US-09-671-317-800	Sequence 800, App	233	10.8	60.0	30	4	US-09-304-232-877	Sequence
62.2	47	4	US-09-422-978-337	Sequence 337, App	234	10.8	60.0	30	4	US-09-322-409-146	Sequence
62.2	47	4	US-09-422-978-907	Sequence 907, App	235	10.8	60.0	30	4	US-09-451-527-146	Sequence
62.2	47	4	US-09-422-978-1064	Sequence 1064, Ap	C 236	10.8	60.0	30	4	US-09-621-625A-5	Sequence
62.2	47	4	US-09-422-978-1500	Sequence 1500, Ap	237	10.8	60.0	33	3	US-09-461-697-102	Sequence
62.2	47	4	US-09-422-978-2295	Sequence 2295, Ap	238	10.8	60.0	33	4	US-08-169-715-48	Sequence
62.2	47	4	US-09-422-978-2743	Sequence 2743, Ap	239	10.8	60.0	35	1	US-08-437-815-13	Sequence
62.2	47	4	US-09-422-978-2845	Sequence 2845, Ap	240	10.8	60.0	35	1	US-08-897-040-13	Sequence
62.2	47	4	US-09-422-978-2870	Sequence 2870, Ap	C 241	10.8	60.0	36	2	US-08-897-340-16	Sequence
62.2	60	3	US-08-896-449A-3	Sequence 3, Appl	C 242	10.8	60.0	36	3	US-09-252-329-16	Sequence
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61.1	17	1	US-08-758-306-381	Sequence 381, App	C 245	10.8	60.0	38	1	US-08-373-124A-441	Sequence
61.1	20	2	US-08-596-366-111	Sequence 11, Appl	C 246	10.8	60.0	38	1	US-08-373-124A-1488	Sequence

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60.0	47	4	US-09-671-317-673	Sequence 673, App	c 334	10.6	58.9	32	4	US-09-225-928-306	Sequence
60.0	47	4	US-09-422-978-271	Sequence 271, App	c 335	10.6	58.9	32	4	US-09-225-928-308	Sequence
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60.0	47	4	US-09-422-978-1657	Sequence 1657, Ap	c 337	10.6	58.9	32	4	US-09-225-201B-308	Sequence
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60.0	51	4	US-09-443-199C-797	Sequence 797, App	c 342	10.6	58.9	33	4	US-09-573-322-11	Sequence
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58.9	60	2	US-08-023-610-43	Sequence 43, Appl	c 468	10.4	57.8	31	3	US-09-260-283-5	Sequence
58.9	60	2	US-08-288-065A-43	Sequence 43, Appl	c 469	10.4	57.8	31	3	US-08-886-886-25	Sequence
58.9	60	2	US-08-362-240A-43	Sequence 43, Appl	c 470	10.4	57.8	31	3	US-08-886-886-27	Sequence
58.9	60	5	PCT-US95-10245-43	Sequence 43, Appl	c 471	10.4	57.8	31	3	US-09-183-217-3	Sequence
57.8	15	1	US-08-440-787A-115	Sequence 115, App	c 472	10.4	57.8	31	4	US-09-651-656-47	Sequence
57.8	17	1	US-08-758-306-391	Sequence 391, App	c 473	10.4	57.8	31	4	US-09-650-855-47	Sequence
57.8	17	1	US-08-758-306-393	Sequence 393, App	c 474	10.4	57.8	31	4	US-09-510-925A-1	Sequence
57.8	17	4	US-09-509-565-17	Sequence 17, Appl	c 475	10.4	57.8	31	4	US-09-848-464-1	Sequence
57.8	17	4	US-09-371-772B-6169	Sequence 6169, Ap	c 476	10.4	57.8	32	2	US-08-687-916-4	Sequence
57.8	18	4	US-09-651-656-61	Sequence 61, Appl	c 477	10.4	57.8	32	3	US-09-138-614-4	Sequence
57.8	18	4	US-09-650-855-61	Sequence 61, Appl	c 478	10.4	57.8	32	4	US-09-549-831-18	Sequence
57.8	20	1	US-07-910-288-6	Sequence 6, Appli	c 479	10.4	57.8	34	3	US-09-133-914-1	Sequence
57.8	20	2	US-08-928-419-17	Sequence 17, Appl	c 480	10.4	57.8	34	3	US-08-886-886-23	Sequence
57.8	20	3	US-09-106-216-29	Sequence 29, Appl	c 481	10.4	57.8	34	3	US-09-469-197-1	Sequence
57.8	20	3	US-09-034-205-65	Sequence 65, Appl	c 482	10.4	57.8	34	4	US-09-949-109-1	Sequence
57.8	20	3	US-09-021-701-387	Sequence 387, App	c 483	10.4	57.8	35	1	US-08-418-032-12	Sequence
57.8	20	3	US-09-291-283-17	Sequence 17, Appl	c 484	10.4	57.8	36	4	US-09-625-225-16	Sequence
57.8	20	4	US-09-484-617-154	Sequence 154, App	c 485	10.4	57.8	36	4	US-09-625-225-17	Sequence
57.8	20	4	US-09-677-218B-65	Sequence 65, Appl	c 486	10.4	57.8	36	4	US-09-625-225-18	Sequence
57.8	20	4	US-09-677-192-65	Sequence 65, Appl	c 487	10.4	57.8	36	4	US-09-625-225-19	Sequence
57.8	20	4	US-09-844-521-46	Sequence 46, Appl	c 488	10.4	57.8	36	4	US-09-403-422-7	Sequence
57.8	20	4	US-09-422-978-6395	Sequence 6395, Ap	c 489	10.4	57.8	37	6	5185431-27	Patent No
57.8	20	4	US-09-522-761-1	Sequence 1, Appli	c 490	10.4	57.8	38	2	US-08-316-439A-25	Sequence
57.8	21	1	US-07-952-442-1	Sequence 1, Appli	c 491	10.4	57.8	38	2	US-08-809-267-25	Sequence
57.8	21	1	US-08-269-766-1	Sequence 1, Appli	c 492	10.4	57.8	38	3	US-08-444-818-238	Sequence
57.8	21	1	US-08-319-545A-1	Sequence 1, Appli	c 493	10.4	57.8	38	3	US-09-110-517-15	Sequence
57.8	21	2	US-08-928-419-12	Sequence 12, Appl	c 494	10.4	57.8	38	3	US-09-284-832-41	Sequence
57.8	21	2	US-09-092-988-1	Sequence 1, Appli	c 495	10.4	57.8	38	4	US-09-371-772B-9731	Sequence
57.8	21	3	US-09-106-216-1	Sequence 1, Appli	c 496	10.4	57.8	38	4	US-09-371-772B-13684	Sequence
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57.8	21	3	US-09-291-283-12	Sequence 12, Appl	c 498	10.4	57.8	40	4	US-09-332-902-7	Sequence
57.8	21	4	US-09-422-978-5641	Sequence 5641, Ap	c 499	10.4	57.8	42	3	US-08-155-005A-14	Sequence
57.8	22	2	US-08-611-880-6	Sequence 6, Appli	c 500	10.4	57.8	42	3	US-09-363-783-14	Sequence
57.8	23	1	US-07-722-798A-55	Sequence 55, Appl	c 501	10.4	57.8	42	4	US-09-661-758A-14	Sequence
57.8	23	1	US-08-222-616-2	Sequence 2, Appli	c 502	10.4	57.8	46	1	US-08-766-014-15	Sequence
57.8	23	3	US-08-433-522A-52	Sequence 52, Appl	c 503	10.4	57.8	47	4	US-09-422-978-221	Sequence
57.8	23	3	US-09-135-166-52	Sequence 52, Appl	c 504	10.4	57.8	47	4	US-09-422-978-559	Sequence
57.8	23	3	US-08-943-046-52	Sequence 52, Appl	c 505	10.4	57.8	47	4	US-09-422-978-732	Sequence
57.8	23	4	US-08-446-648-2	Sequence 2, Appli	c 506	10.4	57.8	47	4	US-09-422-978-842	Sequence
57.8	23	4	US-09-982-610-2	Sequence 2, Appli	c 507	10.4	57.8	47	4	US-09-422-978-3080	Sequence
57.8	23	5	PCT-US95-04228-2	Sequence 2, Appli	c 508	10.4	57.8	47	4	US-09-422-978-3364	Sequence
57.8	24	1	US-08-374-770-4	Sequence 4, Appli	c 509	10.4	57.8	47	4	US-09-422-978-3399	Sequence
57.8	24	1	US-08-461-593B-4	Sequence 4, Appli	c 510	10.4	57.8	47	4	US-09-422-978-3528	Sequence
57.8	24	1	US-08-651-323A-4	Sequence 4, Appli	c 511	10.4	57.8	47	4	US-09-422-978-3571	Sequence
57.8	24	2	US-08-553-304-2	Sequence 2, Appli	c 512	10.4	57.8	48	4	US-09-583-447A-44	Sequence
57.8	24	3	US-08-444-818-239	Sequence 239, App	c 513	10.4	57.8	48	4	US-09-583-447A-45	Sequence
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57.8	24	4	US-09-722-348-1	Sequence 1, Appli	c 515	10.4	57.8	50	4	US-09-371-489-4	Sequence
57.8	24	4	US-09-600-031-12	Sequence 12, Appl	c 516	10.4	57.8	50	4	US-09-621-976-12165	Sequence
57.8	25	1	US-08-445-640-16	Sequence 16, Appl	c 517	10.4	57.8	50	4	US-09-621-976-13498	Sequence
57.8	25	3	US-08-170-558-16	Sequence 16, Appl	c 518	10.4	57.8	53	1	US-08-766-014-13	Sequence
57.8	25	3	US-08-447-314-16	Sequence 16, Appl	c 519	10.4	57.8	53	3	US-09-275-850-282	Sequence
57.8	25	3	US-08-445-461-16	Sequence 16, Appl	c 520	10.4	57.8	56	4	US-08-956-171E-3389	Sequence
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57.8	27	4	US-08-584-040-4897	Sequence 4897, Ap	c 523	10.4	57.8	57	4	US-09-371-489-6	Sequence
57.8	27	4	US-09-454-204A-29	Sequence 29, Appl	c 524	10.2	56.7	15	2	US-08-292-620A-224	Sequence
57.8	27	5	PCT-US95-13662A-16	Sequence 16, Appl	c 525	10.2	56.7	15	2	US-08-292-620A-225	Sequence
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57.8	28	5	PCT-US96-10545A-58	Sequence 58, Appl	c 527	10.2	56.7	15	3	US-09-071-845-225	Sequence
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57.8	29	1	US-07-910-288-16	Sequence 16, Appl	c 529	10.2	56.7	17	1	US-09-371-772B-6171	Sequence
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57.8	29	4	US-09-304-232-876	Sequence 876, App	c 531	10.2	56.7	18	1	US-08-132-168A-18	Sequence
57.8	29	4	US-08-766-014-14	Sequence 14, Appl	c 532	10.2	56.7	18	3	US-09-630-706-81	Sequence
57.8	30	1	US-08-629-001A-92	Sequence 92, Appl	c 533	10.2	56.7	20	1	US-08-185-301-1	Sequence
57.8	30	2	US-08-867-941-51	Sequence 51, Appl	c 534	10.2	56.7	20	1	US-08-588-821-49	Sequence
57.8	30	3	US-09-074-658-51	Sequence 51, Appl	c 535	10.2	56.7	20	1	US-08-915-214-49	Sequence
57.8	30	3	US-08-642-274D-171	Sequence 171, App	c 536	10.2	56.7	20	2	US-09-005-532-49	Sequence
57.8	30	4	US-09-059-584-44	Sequence 44, Appl	c 537	10.2	56.7	20	2	US-08-888-982A-16	Sequence
57.8	30	4			c 538	10.2	56.7	20	3	US-09-344-519-46	Sequence

56.7	20	3	US-09-021-701-377	Sequence 377, Appl	612	10.2	56.7	36	1	US-08-273-362-6	Sequence
56.7	20	3	US-09-488-744A-64	Sequence 64, Appl	c 613	10.2	56.7	36	1	US-08-311-486C-387	Sequence
56.7	20	4	US-09-462-261-16	Sequence 16, Appl	c 614	10.2	56.7	36	2	US-08-292-620A-1114	Sequence
56.7	20	4	US-09-506-073-105	Sequence 105, Appl	c 615	10.2	56.7	36	2	US-08-292-620A-1494	Sequence
56.7	20	4	US-09-657-346A-55	Sequence 55, Appl	c 616	10.2	56.7	36	2	US-08-585-684B-585	Sequence
56.7	20	4	US-09-422-978-8723	Sequence 8723, Ap	c 617	10.2	56.7	36	2	US-08-585-684B-1450	Sequence
56.7	20	4	US-09-188-452A-2664	Sequence 2664, Ap	c 618	10.2	56.7	36	2	US-08-585-684B-1885	Sequence
56.7	20	4	US-09-198-452A-2671	Sequence 2671, Ap	c 619	10.2	56.7	36	2	US-08-585-684B-1886	Sequence
56.7	20	4	US-09-198-452A-4621	Sequence 4621, Ap	c 620	10.2	56.7	36	2	US-08-350-260A-127	Sequence
56.7	20	4	US-09-198-452A-4730	Sequence 4730, Ap	c 621	10.2	56.7	36	3	US-09-071-845-1114	Sequence
56.7	21	4	US-09-081-149-14	Sequence 14, Appl	c 622	10.2	56.7	36	3	US-09-071-845-1494	Sequence
56.7	21	4	US-09-422-978-4378	Sequence 4378, Ap	c 623	10.2	56.7	36	3	US-09-038-073-585	Sequence
56.7	21	4	US-09-422-978-6173	Sequence 6173, Ap	c 624	10.2	56.7	36	3	US-09-038-073-1450	Sequence
56.7	22	4	US-09-422-978-6574	Sequence 6574, Ap	c 625	10.2	56.7	36	3	US-09-038-073-1885	Sequence
56.7	22	2	US-08-807-200-9	Sequence 9, Appli	c 626	10.2	56.7	36	3	US-09-038-073-1886	Sequence
56.7	22	2	US-08-836-134-11	Sequence 11, Appl	c 627	10.2	56.7	36	3	US-09-367-953B-16	Sequence
56.7	22	3	US-09-001-777-9	Sequence 9, Appli	c 628	10.2	56.7	36	4	US-09-104-337A-127	Sequence
56.7	22	4	US-09-493-784-11	Sequence 11, Appl	c 629	10.2	56.7	37	1	US-08-468-700-5	Sequence
56.7	23	1	US-08-321-356-26	Sequence 26, Appl	c 630	10.2	56.7	37	1	US-08-468-700-7	Sequence
56.7	23	3	US-09-487-445-4	Sequence 4, Appli	c 631	10.2	56.7	37	1	US-08-468-700-11	Sequence
56.7	24	1	US-08-229-781-25	Sequence 25, Appl	c 632	10.2	56.7	37	1	US-08-468-700-12	Sequence
56.7	24	1	US-08-630-918-25	Sequence 25, Appl	c 633	10.2	56.7	37	2	US-08-450-905B-13	Sequence
56.7	24	1	US-08-465-590-27	Sequence 27, Appl	c 634	10.2	56.7	37	2	US-08-704-706A-5	Sequence
56.7	24	2	US-08-702-105A-36	Sequence 36, Appl	c 635	10.2	56.7	37	2	US-08-704-706A-7	Sequence
56.7	24	3	US-08-702-110A-36	Sequence 36, Appl	c 636	10.2	56.7	37	2	US-08-704-706A-11	Sequence
56.7	24	3	US-08-711-417C-27	Sequence 27, Appl	c 637	10.2	56.7	37	2	US-08-704-706A-12	Sequence
56.7	24	3	US-09-325-571-36	Sequence 36, Appl	c 638	10.2	56.7	37	3	US-07-982-759B-13	Sequence
56.7	24	3	US-09-344-700-19	Sequence 19, Appl	c 639	10.2	56.7	37	3	US-08-985-659-5	Sequence
56.7	24	4	US-09-004-422-25	Sequence 25, Appl	c 640	10.2	56.7	37	3	US-08-985-659-7	Sequence
56.7	24	4	US-09-514-907A-3	Sequence 3, Appli	c 641	10.2	56.7	37	3	US-08-985-659-12	Sequence
56.7	24	4	US-09-723-909-27	Sequence 27, Appl	c 642	10.2	56.7	38	1	US-08-373-124A-1043	Sequence
56.7	24	4	US-09-848-585-36	Sequence 36, Appl	c 643	10.2	56.7	38	1	US-08-373-124A-1876	Sequence
56.7	24	4	US-09-896-994-3	Sequence 3, Appli	c 644	10.2	56.7	38	1	US-08-373-124A-1954	Sequence
56.7	24	4	US-09-563-897A-19	Sequence 19, Appl	c 645	10.2	56.7	38	1	US-08-435-628-1043	Sequence
56.7	24	5	PCT-US93-08743-27	Sequence 27, Appl	c 646	10.2	56.7	38	1	US-08-435-628-1876	Sequence
56.7	25	3	US-08-971-782-5	Sequence 5, Appli	c 647	10.2	56.7	38	1	US-08-435-628-1876	Sequence
56.7	25	3	US-09-309-026-5	Sequence 5, Appli	c 648	10.2	56.7	38	4	US-09-371-772B-8260	Sequence
56.7	26	3	US-09-049-569-5	Sequence 5, Appli	c 649	10.2	56.7	38	4	US-09-371-772B-10397	Sequence
56.7	26	3	US-09-402-515A-13	Sequence 13, Appl	c 650	10.2	56.7	38	4	US-09-371-772B-11991	Sequence
56.7	27	4	US-08-985-162-1637	Sequence 1637, Ap	c 651	10.2	56.7	38	4	US-09-371-772B-11991	Sequence
56.7	27	4	US-09-525-392-12	Sequence 12, Appl	c 652	10.2	56.7	38	4	US-09-371-772B-13962	Sequence
56.7	27	4	US-09-401-063-1637	Sequence 1637, Ap	c 653	10.2	56.7	39	3	US-09-461-697-132	Sequence
56.7	28	1	US-08-716-374-3	Sequence 3, Appli	c 654	10.2	56.7	39	4	US-09-270-957-34	Sequence
56.7	28	4	US-09-545-814-34	Sequence 34, Appl	c 655	10.2	56.7	40	1	US-07-811-052A-2	Sequence
56.7	28	4	US-09-386-862C-36	Sequence 36, Appl	c 656	10.2	56.7	40	1	US-07-741-940-17	Sequence
56.7	29	4	US-09-661-596A-1	Sequence 1, Appli	c 657	10.2	56.7	40	1	US-08-178-014A-2	Sequence
56.7	29	4	US-09-661-596A-3	Sequence 3, Appli	c 658	10.2	56.7	40	1	US-08-308-196A-4	Sequence
56.7	30	1	US-08-602-010A-45	Sequence 45, Appl	c 659	10.2	56.7	40	1	US-08-289-548A-17	Sequence
56.7	30	1	US-08-680-726A-45	Sequence 45, Appl	c 660	10.2	56.7	40	1	US-08-452-654-17	Sequence
56.7	31	4	US-09-082-409-45	Sequence 45, Appl	c 661	10.2	56.7	40	1	US-08-271-880A-1	Sequence
56.7	31	4	US-09-085-720-11	Sequence 11, Appl	c 662	10.2	56.7	40	1	US-08-399-696-49	Sequence
56.7	33	1	US-08-138-608-14	Sequence 14, Appl	c 663	10.2	56.7	40	1	US-08-452-655B-17	Sequence
56.7	33	1	US-08-583-318-9	Sequence 9, Appli	c 664	10.2	56.7	40	1	US-08-385-590A-22	Sequence
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56.7	33	2	US-08-377-309-11	Sequence 11, Appl	c 666	10.2	56.7	40	2	US-08-510-408-1	Sequence
56.7	33	2	US-09-186-723-11	Sequence 11, Appl	c 667	10.2	56.7	40	3	US-07-982-759F-12	Sequence
56.7	33	4	US-08-505-012-16	Sequence 16, Appl	c 668	10.2	56.7	40	3	US-09-021-520-22	Sequence
56.7	33	4	US-09-186-949A-12	Sequence 12, Appl	c 669	10.2	56.7	40	3	US-08-450-582-17	Sequence
56.7	33	4	US-08-758-757-11	Sequence 11, Appl	c 670	10.2	56.7	40	3	US-09-249-215-1	Sequence
56.7	33	4	US-10-115-701A-11	Sequence 11, Appl	c 671	10.2	56.7	40	3	US-09-113-750A-52	Sequence
56.7	33	4	US-09-940-308A-11	Sequence 11, Appl	c 672	10.2	56.7	40	4	US-09-052-521C-17	Sequence
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56.7	34	3	US-09-249-200-8	Sequence 18, Appl	c 678	10.2	56.7	42	4	US-09-097-319A-18	Sequence
56.7	34	4	US-09-537-168-17	Sequence 17, Appl	c 679	10.2	56.7	42	4	US-09-204-858-1	Sequence
56.7	34	4	US-09-672-459-18	Sequence 18, Appl	c 680	10.2	56.7	42	5	PCT-US94-01780-11	Sequence
56.7	34	4	US-10-186-042-18	Sequence 18, Appl	c 681	10.2	56.7	43	3	US-08-832-985-47	Sequence
56.7	35	3	US-08-491-954-91	Sequence 91, Appl	c 682	10.2	56.7	43	4	US-09-410-903-28	Sequence
56.7	36	1	US-08-273-362-3	Sequence 3, Appli	c 683	10.2	56.7	43	4	US-08-835-159-47	Sequence
56.7	36	1			c 684	10.2	56.7	44	2	US-08-350-260A-562	Sequence

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56.7	45	3	US-08-792-295-3	Sequence 3, Appli	759	10	55.6	22	4	US-09-246-963A-20	Sequence
56.7	45	3	US-09-076-432-3	Sequence 3, Appli	760	10	55.6	22	4	US-09-618-166-88	Sequence
56.7	45	4	US-09-254-352B-58	Sequence 58, Appli	761	10	55.6	23	1	US-08-390-850-367	Sequence
56.7	45	4	US-09-254-352B-61	Sequence 61, Appli	762	10	55.6	23	1	US-08-435-634-367	Sequence
56.7	45	4	US-09-254-352B-63	Sequence 63, Appli	763	10	55.6	23	4	US-09-457-708-3	Sequence
56.7	46	1	US-07-598-873-3	Sequence 3, Appli	764	10	55.6	23	4	US-09-950-046A-3	Sequence
56.7	46	1	US-08-073-425-3	Sequence 3, Appli	765	10	55.6	24	4	US-10-072-094-104	Sequence
56.7	46	1	US-08-396-531-3	Sequence 3, Appli	766	10	55.6	25	1	US-08-468-557-19	Sequence
56.7	47	4	US-09-641-638-819	Sequence 819, App	767	10	55.6	27	1	US-08-238-163-10	Sequence
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us-10-090-326-16.max.rni

APPLICANT: McSwiggen, James A.  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: TREATMENT OF DISEASES  
 TITLE OF INVENTION: ASSOCIATED WITH  
 TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
 TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
 NUMBER OF SEQUENCES: 1379  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/758,306  
 FILING DATE: December 3, 1996  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:

PRIOR APPLICATION NO. \_\_\_\_\_  
APPLICATION NO. \_\_\_\_\_

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/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 212/132
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 377:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-738-306-377

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RESULT 3  
US-08-816-155B-33/c  
; Sequence 33, Application US/08816155B  
; Patent No. 5990091

GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
APPLICANT: GETTIG, RUSSELL R.

/ APPLICANT: MARTINEZ, HECTOR  
 /  
 / APPLICANT: PAOLETTI, ENZO  
 /  
 / APPLICANT: PINCUS, STEVEN E.  
 /  
 / TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
 / TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF  
 /  
 / NUMBER OF SEQUENCES: 48  
 / CORRESPONDENCE ADDRESS:

;  
 ; ADDRESS: FROMMER LAWRENCE & HAUG LLP  
 ;  
 ; STREET: 745 FIFTH AVENUE  
 ;  
 ; CITY: NEW YORK  
 ; STATE: NEW YORK  
 ; COUNTRY: USA  
 ;

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51 ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
LICATON DATA:
CN NUMBER: US/08/816,155B
TE: 12-MAR-1997
ATION: 514
ENT INFORMATION:
WALSKE, THOMAS J.
ION NUMBER: 32,147
/DOCKET NUMBER: 454310-2990
CATION INFORMATION:
: 212-588-0800
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ARACTERISTICS:
30 base pairs
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73.3%; Score 13.2; DB 2; Length 30;
ilarity 83.3%; Pred. No. 1.1e+03;
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TATTGGGAATTGGC 18
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ACTTTGGAATATTGCC 12

/c
pplication US/08815809
1777
ATION:
TAGLIA, James
BEL, Scott J.
William I.
TIG, Russell R.
CUS, Steven E.
LETTI, Enzo
OBS, Bertram L.
TION: VECTORS HAVING ENHANCED EXPRESSION, AND METHODS OF
TION: MAKING AND USES THEREOF
3: 454310-3010
CATION NUMBER: US/08/815,809
3 DATE: 1997-03-12
ID NOS: 23
antIn Ver. 2.0

scinia virus

73.3%; Score 13.2; DB 3; Length 30;
ilarity 83.3%; Pred. No. 1.1e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TATTGGGAATTGGC 18
|||||
ACTTTGGAATATTGCC 12

/c
pplication US/09079587
1066

GENERAL INFORMATION:
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIG, RUSSELL R.
APPLICANT: MARTINEZ, HECTOR
APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND
METHODS OF MAKING AND USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,587
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/816,155
FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-079-587-33

Query Match 73.3%; Score 13.2; DB 3; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTGGC 18
|||
Db 29 CTACTTTGGAATATTGCC 12

RESULT 6
US-08-832-985-28/c
Sequence 28, Application US/08832985
Patent No. 6057098
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
TITLE OF INVENTION: POLYVALENT DISPLAY LIBRARIES
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

```

```

IBM Compatible
SYSTEM: DOS
FASTSEQ for Windows Version 2.0
PLICATION DATA:
ION NUMBER: US/08/832,985
ATE: 04-APR-1997
ATION: 435
ICATION DATA:
ION NUMBER:
ENT INFORMATION:
lebeschuetz, Joseph O.
ION NUMBER: 37,505
/DOCKET NUMBER: 014907-001000US
ICATION INFORMATION:
3: 415-576-0200
415-576-0300

```

```

OR SEQ ID NO: 28:

```

```

ARACTERISTICS:
43 base pairs
cleic acid
ESS: single
linear
PE: CDNA

```

```

73.3%; Score 13.2; DB 3; Length 43;
ilarity 83.3%; Pred. No. 1.2e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

CATTTGGAATTTGCC 18
|||||
CATTCGGCTTTGCC 11

```

```

C
plication US/09410903
0113

```

```

ATION:
uechler, Joe
alkirs, Gunars
ray, Jeff
osite Diagnostics Inc.
NTION: Chimeric Polyclonal Antibodies
E: 014907-002700US
CATION NUMBER: US/09/410,903
G DATE: 1999-10-02
TION NUMBER: US 08/832,985
DATE: 1997-04-04
TION NUMBER: US 08/835,159
DATE: 1997-04-04
TION NUMBER: WO PCT/US98/06704
DATE: 1998-04-03
ID NOS: 100
stSEQ for Windows Version 3.0

```

```

tificial sequence

```

```

ATION: oligo 50

```

```

73.3%; Score 13.2; DB 4; Length 43;
ilarity 83.3%; Pred. No. 1.2e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

CATTTGGAATTTGCC 18
|||||
CATTCGGCTTTGCC 11

```

# RESULT 8

```

US-08-835-159-28/c
; Sequence 28, Application US/08835159
; Patent No. 6555310
; GENERAL INFORMATION:
; APPLICANT: Gray, Jeff
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; TITLE OF INVENTION: POLYCLONAL LIBRARIES
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,159
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 014907-001100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-835-159-28

```

```

Query Match 73.3%; Score 13.2; DB 4; Length 43;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

```

```

Qy 1 CTCATTTGGAATTTGCC 18
Db 28 CTCATTTGCGCTTTGCC 11

```

# RESULT 9

```

US-08-417-210A-101/c
; Sequence 101, Application US/08417210A
; Patent No. 5863542
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

SYSTEM: PC-DOS/MS-DOS  
 PatentIn Release #1.0, Version #1.30  
 LICATION DATA:  
 ON NUMBER: US/08/417,210A  
 TE: 05-APR-1995  
 ATION: 435  
 ENT INFORMATION:  
 WALSKI, THOMAS J.  
 ION NUMBER: 32,147  
 /DOCKET NUMBER: 454310-2690  
 CATION INFORMATION:  
 : 212-840-3333  
 OR SEQ ID NO: 101:  
 ARACTERISTICS:  
 53 base pairs  
 cleic acid  
 ESS: single  
 linear  
 PE: DNA (genomic)  
 01

73.3%; Score 13.2; DB 2; Length 53;  
 ilarity 83.3%; Pred. No. 1.2e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGGAATTTGCG 18  
 |||||  
 ACTTTGGGAATATTGCG 30

11/c  
 Application US/09136159A  
 3279  
 ATION:  
 Genetics Corporation  
 oietti, Enzo  
 rtaglia, James  
 x, William I  
 ATION: Immunodeficiency recombinant poxvirus  
 : 454310-2690.1  
 ATION NUMBER: US/09/136,159A  
 ; DATE: 1998-08-14  
 ION NUMBER: US 08/417,210  
 DATE: 1995-04-05  
 ION NUMBER: US 08/223,842  
 DATE: 1994-04-06  
 ION NUMBER: US 07/897,382  
 DATE: 1992-06-11  
 ION NUMBER: US 07/715,921  
 DATE: 1991-06-14  
 ION NUMBER: US 08/105,483  
 DATE: 1993-08-12  
 ION NUMBER: US 07/847,951  
 DATE: 1992-03-06  
 ION NUMBER: US 07/713,967  
 DATE: 1991-06-11  
 ION NUMBER: US 07/666,056  
 DATE: 1991-03-07  
 ID NOS: 149  
 ntin version 3.1

## Official Sequence

ATION: Oligonucleotide primer referred to as P2A  
 1

73.3%; Score 13.2; DB 4; Length 53;  
 ilarity 83.3%; Pred. No. 1.2e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTCATTGGGAATTTGCG 18  
 |||||  
 Db 47 CTACTTTGGGATATTGCG 30  
 RESULT 11  
 US-09-411-578-35  
 ; Sequence 35, Application US/09411578  
 ; Patent No. 6203801  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schaap, Theodorus C  
 ; APPLICANT: Kuiper, Catharina M  
 ; APPLICANT: Vermeulen, Arnoldus N  
 ; TITLE OF INVENTION: Coccidiosis Vaccines  
 ; FILE REFERENCE: schaap  
 ; CURRENT APPLICATION NUMBER: US/09/411,578  
 ; CURRENT FILING DATE: 1999-10-04  
 ; EARLIER APPLICATION NUMBER: 98203384.7  
 ; EARLIER FILING DATE: 1998-10-07  
 ; EARLIER APPLICATION NUMBER: 98203457.1  
 ; EARLIER FILING DATE: 1998-10-16  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 35  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Eimeria tenella  
 US-09-411-578-35

Query Match 71.1%; Score 12.8; DB 3; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 2 TCATTGGGAATTTGCG 17  
 |||||  
 Db 2 TCAATTGGGATTTGCG 17

RESULT 12  
 US-09-411-578-37  
 ; Sequence 37, Application US/09411578  
 ; Patent No. 6203801  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schaap, Theodorus C  
 ; APPLICANT: Kuiper, Catharina M  
 ; APPLICANT: Vermeulen, Arnoldus N  
 ; TITLE OF INVENTION: Coccidiosis Vaccines  
 ; FILE REFERENCE: schaap  
 ; CURRENT APPLICATION NUMBER: US/09/411,578  
 ; CURRENT FILING DATE: 1999-10-04  
 ; EARLIER APPLICATION NUMBER: 98203384.7  
 ; EARLIER FILING DATE: 1998-10-07  
 ; EARLIER APPLICATION NUMBER: 98203457.1  
 ; EARLIER FILING DATE: 1998-10-16  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 37  
 ; LENGTH: 17  
 ; TYPE: DNA  
 ; ORGANISM: Eimeria tenella  
 US-09-411-578-37

Query Match 71.1%; Score 12.8; DB 3; Length 17;  
 Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 2 TCATTGGGAATTTGCG 17  
 |||||  
 Db 2 TCAATTGGGATTTGCG 17

RESULT 13  
 US-09-749-233-35

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us-10-090-326-16.max.rni

application US/09749233  
10061  
ATION:  
haap, Theodorus C  
uiper, Catharina M  
ermeulen, Arnoldus N  
NTION: Coccidiosis Vaccines  
E: schaa  
:CATION NUMBER: US/09749,233  
G DATE: 2000-12-27  
TION NUMBER: 09/411,578  
DATE: 1999-10-04  
TION NUMBER: 98203457.1  
DATE: 1998-10-16  
ID NOS: 41  
entIn Ver. 2.1

meria tenella

71.1%; Score 12.8; DB 4; Length 17;  
ilarity 87.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AATTGGGAATTTGC 17  
|||||  
AATTGGGAATTTGC 17

application US/09749233  
10061  
ATION:  
haap, Theodorus C  
uiper, Catharina M  
ermeulen, Arnoldus N  
NTION: Coccidiosis Vaccines  
E: schaa  
:CATION NUMBER: US/09749,233  
G DATE: 2000-12-27  
TION NUMBER: 09/411,578  
DATE: 1999-10-04  
TION NUMBER: 98203457.1  
DATE: 1998-10-16  
ID NOS: 41  
entIn Ver. 2.1

meria tenella

71.1%; Score 12.8; DB 4; Length 17;  
ilarity 87.5%; Pred. No. 1.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AATTGGGAATTTGC 17  
|||||  
AATTGGGAATTTGC 17

6/c  
pplcation US/09442143A  
3089  
ATION:  
Vy, Gary  
ark, David A.  
NTION: Methods of Modulating Immune Coagulation  
E: 9579-14

CURRENT APPLICATION NUMBER: US/09/442,143A  
CURRENT FILING DATE: 1999-11-15  
PRIOR APPLICATION NUMBER: US 60/046,537  
PRIOR FILING DATE: 1997-05-17  
PRIOR APPLICATION NUMBER: US 60/061,684  
PRIOR FILING DATE: 1997-10-10  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 46  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-442-143A-46

Query Match 71.1%; Score 12.8; DB 4; Length 19;  
Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGGAATTTGCC 18  
|||||  
Db 19 CATTAGATTTTGCC 4

RESULT 16  
US-09-038-637-66  
Sequence 66, Application US/09038637  
Patent No. 6235470  
GENERAL INFORMATION:  
APPLICANT: Sidransky, David  
TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALI  
NUMBER OF SEQUENCES: 195  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,637  
FILING DATE: 10-MAR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/579,233  
FILING DATE: 28-DEC-1995  
APPLICATION NUMBER: 08/152,313  
FILING DATE: 12-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/146001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-09-038-637-66

Query Match 71.1%; Score 12.8; DB 3; Length 22;  
Best Local Similarity 87.5%; Pred. No. 1.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

2004

SEQUENCES: 1379

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION.

1 09:38:22 2004

us-10-090-326-16.max.rni

GREGOR,, MARTIN L.  
ION NUMBER: 29,329  
3/DOCKET NUMBER: 02638-0106  
ICATION INFORMATION:  
3: (713)229-1874  
FOR SEQ ID NO: 5:  
HARACTERISTICS:  
27 base pairs  
cleic acid  
NESS: single  
linear  
PE: DNA (genomic)

68.9%; Score 12.4; DB 3; Length 27;  
ilarity 92.9%; Pred. No. 2.7e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGGGAATTTGCC 18  
|||||  
GGGAATTTGCC 11

3/c  
Application PC/TUS9401572  
INATION:  
OVERTURF,, MERRILL L.  
LOOSE-MITCHELL,, DAVID S.  
VENTION: CHOLESTEROL 7-ALPHA HYDROXYLASE  
VENTION: EXPRESSION REGULATION  
SEQUENCES: 8  
NCE ADDRESS:  
3: MARTIN L. GREGOR  
910 LOUISIANA STREET  
USTON  
X. USA  
02  
ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.25  
ICATION DATA:  
ION NUMBER: PCT/US94/01572  
ATE:  
ATION:  
ENT INFORMATION:  
GREGOR,, MARTIN L.  
ION NUMBER: 29,329  
DOCKET NUMBER: 02638-0106  
ICATION INFORMATION:  
3: (713)229-1874  
OR SEQ ID NO: 5:  
ARACTERISTICS:  
27 base pairs  
cleic acid  
NESS: single  
linear  
PE: DNA (genomic)

68.9%; Score 12.4; DB 5; Length 27;  
ilarity 92.9%; Pred. No. 2.7e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGGGAATTTGCC 18  
|||||  
GGGAATTTGCC 11

RESULT 21  
US-09-021-701-379  
Sequence 379, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
TITLE OF INVENTION: probe sequences  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Records Manager, Legal Department, Hewlett-Packar  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-236-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 379:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-021-701-379

Query Match 67.8%; Score 12.2; DB 3; Length 20;  
Best Local Similarity 82.4%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTGTC 17  
Db 4 CTACTTGGGAATATGTC 20

RESULT 22  
US-09-021-701-380  
Sequence 380, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
TITLE OF INVENTION: probe sequences  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Records Manager, Legal Department, Hewlett-Packar  
STREET: 3000 Hanover Street

lo Alto

A  
USA

04

ADABLE FORM:

PE: Floppy disk

IBM PC Compatible

SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.30

LICATION DATA:

ON NUMBER: US/09/021,701

TE: 10-FEB-1998

ATION:

ENT INFORMATION:

oi, Wendy A.

ION NUMBER: 36,697

/DOCKET NUMBER: 10971464-1

CATION INFORMATION:

: 650-236-2386

650-852-8063

DR SEQ ID NO: 380:

ARACTERISTICS:

20 base pairs

cleic acid

ESS: single

linear

PE: CDNA

G: NO

NO

0

67.8%; Score 12.2; DB 3; Length 20;

ilarity 82.4%; Pred. No. 3.3e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACTTTGGAATTTGC 17

ACTTTGGAATTTGC 19

Application US/09021701

588

ATION:

Shannon, Karen W.

Wolber, Paul K.

Delenstarr, Glenda C.

Webb, Peter G.

Kincaid, Robert H.

ENTION: Methods for evaluating oligonucleotide

ENTION: Probe sequences

QUENCES: 1165

ICE ADDRESS:

Records Manager, Legal Department, Hewlett-Packard Company M/S 20

000 Hanover Street

o Alto

USA

4

ADABLE FORM:

PE: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.30

LICATION DATA:

ON NUMBER: US/09/021,701

TE: 10-FEB-1998

ATION:

NT INFORMATION:

oi, Wendy A.

ON NUMBER: 36,697

DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 381:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-021-701-381

Query Match

Best Local Similarity 67.8%; Score 12.2; DB 3; Length 20;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

Cy

1 CTCAATTGGAATTTGC 17

Db

2 CTCAATTGGAATTTGC 18

RESULT 24

US-09-021-701-382

Sequence 382, Application US/09021701

Patent No. 6251588

GENERAL INFORMATION:

APPLICANT: Shannon, Karen W.

APPLICANT: Wolber, Paul K.

APPLICANT: Delenstarr, Glenda C.

APPLICANT: Webb, Peter G.

APPLICANT: Kincaid, Robert H.

TITLE OF INVENTION: Methods for evaluating oligonucleotide

NUMBER OF SEQUENCES: 1165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard

STREET: 3000 Hanover Street

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/021,701

FILING DATE: 10-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Choi, Wendy A.

REGISTRATION NUMBER: 36,697

REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 382:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-021-701-382

Query Match

Best Local Similarity 67.8%; Score 12.2; DB 3; Length 20;

Matches 14; Conservative 0; Mismatches 3; Indels 0;



TCATTGGAATTTGTC 17  
 ||||| |||||  
 TACTTGGAAATATGTC 17

28 Application US/09446301A  
 36893

ATION:

J. SOLH, NEVINE

ALIGNET, JEANINE

ENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE

ENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED

ENTION: COMPOUNDS

TE: 03715-0059

ICATION NUMBER: US/09/446,301A

NG DATE: 1999-12-20

ID NOS: 51

entin Ver. 2.1

tificial Sequence

ATION: Description of Artificial Sequence: Primer

18

ilarity 67.8%; Score 12.2; DB 4; Length 22;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TATTGGAAATTTGCC 18

||||| |||||

GTGTGTAATCTGCC 18

Application US/09099932

0001

ATION:

Solh, Nevine

lignet, Jeanine

ENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE

ENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED

ENTION: COMPOUNDS

TE: 03495-0173-00000

CATION NUMBER: US/09/099,932

G DATE: 1998-06-19

CATION NUMBER: 60/050,380

G DATE: 1997-06-20

ID NOS: 50

entin Ver. 2.0

tificial Sequence

ATION: Description of Artificial Sequence: primer

ilarity 67.8%; Score 12.2; DB 4; Length 22;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ATTGGAATTTGCC 18

||||| |||||

GTTTGAATCTGCC 18

US-07-753-738B-3/c  
 ; Sequence 3, Application US/07753738B  
 ; Patent No. 5304730  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lawson, Edgar C.  
 ; APPLICANT: Weiss, James D.  
 ; APPLICANT: Hemenway, Cynthia L.  
 ; APPLICANT: Turner, Nilgun E.  
 ; TITLE OF INVENTION: Virus Resistant Plants and Method  
 ; TITLE OF INVENTION: Therefore  
 ; NUMBER OF SEQUENCES: 11  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BBAF  
 ; STREET: 700 Chesterfield Village Parkway  
 ; CITY: St. Louis  
 ; STATE: Missouri  
 ; COUNTRY: USA  
 ; ZIP: 63198  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/753,738B  
 ; FILING DATE: 19910903  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Hoerner Jr., Dennis R.  
 ; REGISTRATION NUMBER: 30,914  
 ; REFERENCE/DOCKET NUMBER: 38-21(10536)A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (314)537-6099  
 ; TELEFAX: (314)537-6047  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; LENGTH: 34 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (synthetic)  
 ; US-07-753-738B-3

Query Match 67.8%; Score 12.2; DB 1; Length 34;  
 Best Local Similarity 82.4%; Pred. No. 3.4e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

OY 1 CTCATTGGAAATTTGTC 17

||||| |||||

DB 17 CTTATTTGGGGTTTTC 1

RESULT 28

US-08-924-695A-17

; Sequence 17, Application US/08924695A

; Patent No. 5998583

; GENERAL INFORMATION:

; APPLICANT: KORSMEYER, STANLEY J.

; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST

; NUMBER OF SEQUENCES: 88

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOWELL & HAFERKAMP, L.C.

; STREET: 7733 FORSYTH BLVD., SUITE 1400

; CITY: ST. LOUIS

; STATE: MISSOURI

; COUNTRY: USA

; ZIP: 63105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

DN NUMBER: US/08/924,695A  
 RE: 09-SEP-1997  
 ACTION: 514  
 ENT INFORMATION:  
 LAND, DONALD R.  
 ION NUMBER: 35,197  
 /DOCKET NUMBER: 971798  
 ACTION INFORMATION:  
 : (314) 727-5188  
 DR SEQ ID NO: 17:  
 RACTERISTICS:  
 14 base pairs  
 leic acid  
 SSS: single  
 linear  
 PE: CDNA  
 7

67.8%; Score 12.2; DB 2; Length 34;  
 ilarity 82.4%; Pred. No. 3.4e+03;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 ATTTGGAATTTTGC 18  
 . | | | | | | | | | |  
 TCCGGAATATGTC 28

plication US/08479852

385  
 ACTION:  
 Sherrol H. McDonough, Thomas B. Ryder,  
 Yeasing Yang  
 'ENTION: NUCLEIC ACID AMPLIFICATION  
 'ENTION: OLIGONUCLEOTIDES AND PROBES  
 'ENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
 QUENCES: 139  
 ICE ADDRESS:  
 Lyon & Lyon  
 11 West Sixth Street  
 Angeles  
 lifornia  
 USA  
 7  
 ADABLE FORM:  
 E: 3.5" Diskette, 1.44 Mb storage  
 IBM PS/2 Model 50Z or 55SX  
 SYSTEM: IBM P.C. DOS (Version 3.30)  
 WordPerfect (Version 5.0)  
 ICACTION DATA:  
 N NUMBER: US/08/479,852  
 E:  
 ACTION: 435  
 ACTION DATA:  
 N NUMBER: US/08/040,745  
 E:  
 N NUMBER: U.S. Serial No. 5712385 07/550,837  
 E: 7/10/90  
 N NUMBER: U.S. Serial No. 5712385 07/379,501  
 E: 7/11/89  
 NT INFORMATION:  
 burg, Richard J.  
 ON NUMBER: 32,327  
 DOCKET NUMBER: 196/189  
 ACTION INFORMATION:  
 (213) 489-1600  
 -3510  
 R SEQ ID NO: 16:  
 RACTERISTICS:  
 6

; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-479-852-16  
 Query Match 67.8%; Score 12.2; DB 1; Length 36;  
 Best Local Similarity 82.4%; Pred. No. 3.4e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;  
 QY 1 CTCATTGGAAATTTGTC 17  
 ||| | | | | | | | | |  
 Db 1 CTACTTTGGAAATATGTC 17

RESULT 30  
 US-08-479-852-96/c  
 ; Sequence 96; Application US/08479852  
 ; Patent No. 5712385  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,  
 ; APPLICANT: Yeasing Yang  
 ; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES  
 ; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
 ; NUMBER OF SEQUENCES: 139  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 611 West Sixth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 90017  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX  
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
 ; SOFTWARE: WordPerfect (Version 5.0)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/479,852  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/040,745  
 ; FILING DATE:  
 ; APPLICATION NUMBER: U.S. Serial No. 5712385 07/550,837  
 ; FILING DATE: 7/10/90  
 ; APPLICATION NUMBER: U.S. Serial No. 5712385 07/379,501  
 ; FILING DATE: 7/11/89  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 196/189  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 96:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 36  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-479-852-96

Query Match 67.8%; Score 12.2; DB 1; Length 36;  
 Best Local Similarity 82.4%; Pred. No. 3.4e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;  
 QY 1 CTCATTGGAAATTTGTC 17  
 ||| | | | | | | | | |  
 Db 36 CTACTTTGGAAATATGTC 20

1 09:38:22 2004

us-10-090-326-16.max.rni

```
33 Application US/08479852
12385
3MATION:
  Sherrol H. McDonough, Thomas B. Ryder,
  Yeasing Yang
VENTION: NUCLEIC ACID AMPLIFICATION
VENTION: OLIGONUCLEOTIDES AND PROBES
VENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
SEQUENCES: 139
ENCE ADDRESS:
3: Lyon & Lyon
611 West Sixth Street
28 Angeles
California
USA
317
ADABLE FORM:
(P: 3.5" Diskette, 1.44 Mb storage
; IBM PS/2 Model 50Z or 55SX
; SYSTEM: IBM P.C. DOS (Version 3.30)
; WordPerfect (Version 5.0)
PLICATION DATA:
ON NUMBER: US/08/479,852
TE:
ATION: 435
ATION DATA:
TE:
ON NUMBER: US/08/040,745
TE:
ON NUMBER: U.S. Serial No. 5712385 07/550,837
TE: 7/10/90
ON NUMBER: U.S. Serial No. 5712385 07/379,501
TE: 7/11/89
ENT INFORMATION:
urburg, Richard J.
ON NUMBER: 32,327
/DOCKET NUMBER: 196/189
ATION INFORMATION:
: (213) 489-1600
: (213) 955-0440
7-3510
OR SEQ ID NO: 133:
ARACTERISTICS:
36
cleic acid
ESS: single
linear
3
67.8%; Score 12.2; DB 1; Length 36;
ilarity 41.2%; Pred. No. 3.4e+03;
Conservative 7; Mismatches 3; Indels 0; Gaps 0;
CATTTGGAATTTTGC 17
:::||||:
ACUUGGAUAUUGC 17
7/c
Application US/08479852
2385
MATION:
  Sherrol H. McDonough, Thomas B. Ryder,
  Yeasing Yang
VENTION: NUCLEIC ACID AMPLIFICATION
VENTION: OLIGONUCLEOTIDES AND PROBES
VENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
SEQUENCES: 139
NCE ADDRESS:
: Lyon & Lyon
611 West Sixth Street
```

```

/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90017
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
/ COMPUTER: IBM PS/2 Model 50Z or 55SX
/ OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
/ SOFTWARE: WordPerfect (Version 5.0)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/479,852
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/040,745
/ FILING DATE:
/ APPLICATION NUMBER: U.S. Serial No. 5712385 07/550,837
/ FILING DATE: 7/10/90
/ APPLICATION NUMBER: U.S. Serial No. 5712385 07/379,501
/ FILING DATE: 7/11/89
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 196/189
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 137:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-479-852-137
Query Match 67.8%; Score 12.2; DB 1; Length 36;
Best Local Similarity 82.4%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0;
QY 1 CTCATTGGAAATTTGC 17
DB 36 CTACTTTGGAATATTC 20
RESULT 33
US-08-462-646-16
; Sequence 16, Application US/08462646
; Patent No. 5856088
; GENERAL INFORMATION:
; APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
; APPLICANT: Yeasing Yang
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,646
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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us-10-090-326-16.max.rni

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; INFORMATION FOR SEQ ID NO: 96:
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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 36
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; US-08-462-646-96

```

Query Match 67.8%; Score 12.2; DB 2; Length 36;  
Best Local Similarity 82.4%; Pred No. 3.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels

36 CTACTTTGGAAATATTGC 20

36 CTACTTTGGAATATTGC 20

GENERAL INFORMATION:  
APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,  
APPLICANT: Yeasing Yang

TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES  
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
 NUMBER OF SEQUENCES: 139  
 CORRESPONDENCE ADDRESS:

CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

ZIP: 90017  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 COMPUTER: IBM PS/2 Model 502 or 55SX  
 OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
 SOFTWARE: WordPerfect (Version 5.0)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/462,646

FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/040,745

FILING DATE: 7/10/90  
APPLICATION NUMBER: U.S. Serial No. 5856088 07/379,501  
FILING DATE: 7/11/89

REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 196/189  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

S-08-462-646-133

Query Match	67.8%	Score 12.2;	DB 2;	Length 36;
Best Local Similarity	41.2%	Pred. No. 3.4e+03;		
Matches	7;	Conservative	7;	Mismatches 3; Indels

GC 17

UACUUGGAUAUUGC 17

37/c  
Application US/08462646  
56088  
RMATION:  
Sherrol H. McDonough, Thomas B. Ryder,  
Yeasing Yang  
NVENTION: NUCLEIC ACID AMPLIFICATION  
NVENTION: OLIGONUCLEOTIDES AND PROBES  
NVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
SEQUENCES: 139  
ENCE ADDRESS:  
8: Lyon & Lyon  
611 West Sixth Street  
Los Angeles  
California  
USA  
317  
RADABLE FORM:  
VPE: 3.5" Diskette, 1.44 Mb storage  
3 SYSTEM: IBM PS/2 Model 50Z or 55SX  
: WordPerfect (Version 5.0)  
PLICATION DATA:  
ION NUMBER: US/08/462,646  
ATE: 05-JUN-1995  
ATION: 435  
ICATION DATA:  
ION NUMBER: US 08/040,745  
ATE: 26-MAR-1993  
ION NUMBER: U.S. Serial No. 5856088 07/550,837  
ATE: 7/10/90  
ION NUMBER: U.S. Serial No. 5856088 07/379,501  
ATE: 7/11/89  
SENT INFORMATION:  
urzburg, Richard J.  
ION NUMBER: 32,327  
3/DOCKET NUMBER: 196/189  
ICATION INFORMATION:  
: (213) 489-1600  
7-3510  
OR SEQ ID NO: 137:  
36  
ucleic acid  
ESS: single  
linear  
.7  
57.8%; Score 12.2; DB 2; Length 36;  
ilarity 82.4%; Pred. No. 3.4e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
'CATTTGGAATTTTGC 17  
'ACTTTGGAATTTTGC 20  
1/c  
pplication US/08792832A  
7734  
MATION:  
Summers Dr., Max D.  
Braunagel Dr., Sharon C.  
Hong Dr., Tao  
VENTION: UNIQUE NUCLEOTIDE AND AMINO ACID  
VENTION: SEQUENCE AND USES THEREOF  
EQUENCES: 56

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/792,832A  
; FILING DATE: 30-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/000,955  
; FILING DATE: 07-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/678,435  
; FILING DATE: 03-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hibler, David W.  
; REGISTRATION NUMBER: 41,071  
; REFERENCE/DOCKET NUMBER: TAMK:190  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-792-832A-11  
Query Match 67.8%; Score 12.2; DB 3; Length 36;  
Best Local Similarity 82.4%; Pred. No. 3.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;  
QY 1 CTCATTGGAAATTTTGC 17  
|||||  
Db 17 CTCATGTCGAATGTTC 1  
|||||  
RESULT 38  
US-09-013-406-16  
; Sequence 16, Application US/09013406  
; Patent No. 6252059  
; GENERAL INFORMATION:  
; APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,  
; APPLICANT: Yeasing Yang  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION  
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES  
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/013,406  
; FILING DATE:  
; CLASSIFICATION:

ATION:  
ATION DATA:  
N NUMBER: 08/479,852  
E:  
N NUMBER: U.S. Serial No. 6252059 07/550,837  
E: 7/10/90  
N NUMBER: U.S. Serial No. 6252059 07/379,501  
E: 7/11/89  
NT INFORMATION:  
burg, Richard J.  
ON NUMBER: 32,327  
DOCKET NUMBER: 196/189  
ATION INFORMATION:  
(213) 489-1600  
(213) 955-0440

Query Match	67.8%;	Score 12.2;	DB 3;	Length 36;
Best Local Similarity	41.2%;	Pred. NO. 3.4e+03;		
Matches	7; Conservative	7; Mismatches	3; Indels	0;

QY 1 CTCATTGGAAATTTTC 17

ACUUUGGAUUGC 17

Application US/09013406

2059

INVENTION: Sherrol H. McDonough, Thomas B. Ryder,

Yeasing Yang

INVENTION: NUCLEIC ACID AMPLIFICATION

INVENTION: OLIGONUCLEOTIDES AND PROBES

INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

SEQUENCES: 139

INCE ADDRESS:

Lydon & Lyon

611 West Sixth Street

Los Angeles

California

USA

17

ADABLE FORM:

PE: 3.5" Diskette, 1.44 Mb storage

IBM PS/2 Model 50Z or 55SX

SYSTEM: IBM P.C. DOS (Version 3.30)

WordPerfect (Version 5.0)

PLICATION DATA:

ON NUMBER: US/09/013,406

TE:

ATION DATA:

ON NUMBER: 08/479,852

TE:

ON NUMBER: U.S. Serial No. 6252059 07/550,837

TE: 7/10/90

ON NUMBER: U.S. Serial No. 6252059 07/379,501

TE: 7/11/89

ENT INFORMATION:

burg, Richard J.

ION NUMBER: 32,327

/DOCKET NUMBER: 196/189

CATION INFORMATION:

: (213) 489-1600

(213) 955-0440

7-3510

OR SEQ ID NO: 137:

ARACTERISTICS:

36

cleic acid

ESS: single

linear

7

67.8%; Score 12.2; DB 3; Length 36;

ilarity 82.4%; Pred.No. 3.4e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTGGAATTTGC 17

ACTTTGGAATTTGC 20

pplication US/09766095

9749

INATION:

NT: Sherrol H. McDonough, Thomas B. Ryder,

Yeasing Yang

F INVENTION: NUCLEIC ACID AMPLIFICATION

OLIGONUCLEOTIDES AND PROBES

TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,095

FILING DATE: 18-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/013,406

FILING DATE: 26-JAN-01

APPLICATION NUMBER: U.S. Serial No. 6649749 07/550,837

FILING DATE: 10-Jul-90

APPLICATION NUMBER: U.S. Serial No. 6649749 07/379,501

FILING DATE: 11-Jul-89

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 196/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-766-095-16

Query Match 67.8%; Score 12.2; DB 4; Length 36;

Best Local Similarity 82.4%; Pred.No. 3.4e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAATTTGC 17

Db 1 CTACTTTGGAATTTGC 17

RESULT 43

US-09-766-095-96/c

; Sequence 96, Application US/09766095

; Patent No. 6649749

GENERAL INFORMATION:

APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,

Yeasing Yang

TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION

OLIGONUCLEOTIDES AND PROBES

TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

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us-10-090-326-16.max.rni

APPLICATION DATA:  
PLICATION NUMBER: US/09/766,095  
LING DATE: 18-Jan-2001  
ASSIFICATION: <Unknown>  
PLICATION DATA:  
PLICATION NUMBER: 09/013,406  
LING DATE: 26-JAN-01  
PLICATION NUMBER: U.S. Serial No. 6649749 07/550,837  
LING DATE: 10-Jul-90  
PLICATION NUMBER: U.S. Serial No. 6649749 07/379,501  
LING DATE: 11-Jul-89  
Y/AGENT INFORMATION:  
ME: Warburg, Richard J.  
ISTRATION NUMBER: 32,327  
ERENCE/DOCKET NUMBER: 196/189  
UNICATION INFORMATION:  
LEPHONE: (213) 489-1600  
LEFAX: (213) 955-0440  
LEX: 67-3510  
FOR SEQ ID NO: 96:  
E CHARACTERISTICS:  
NGTH: 36  
PE: nucleic acid  
RANDEDNESS: single  
POLOGY: linear  
E DESCRIPTION: SEQ ID NO: 96:

67.8%; Score 12.2; DB 4; Length 36;  
ilarity 82.4%; Pred. No. 3.4e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTGGGAATTTCG 17  
|||||  
ACTTTGGATATTCG 20

3 Application US/09766095  
9749  
RMATION:  
NT: Sherrol H. McDonough, Thomas B. Ryder,  
Yeasing Yang  
F INVENTION: NUCLEIC ACID AMPLIFICATION  
OLIGONUCLEOTIDES AND PROBES  
TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
OF SEQUENCES: 139  
NDENCE ADDRES:  
DRESSEE: Lyon & Lyon  
REET: 611 West Sixth Street  
TY: Los Angeles  
ATE: California  
UNTRY: USA  
P: 90017  
R READABLE FORM:  
DIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
MPUTER: IBM PS/2 Model 50Z or 55SX  
ERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
FTWARE: WordPerfect (Version 5.0)  
APPLICATION DATA:  
PLICATION NUMBER: US/09/766,095  
LING DATE: 18-Jan-2001  
ASSIFICATION: <Unknown>  
PLICATION DATA:  
PLICATION NUMBER: 09/013,406  
LING DATE: 26-JAN-01  
PLICATION NUMBER: U.S. Serial No. 6649749 07/550,837  
LING DATE: 10-Jul-90  
PLICATION NUMBER: U.S. Serial No. 6649749 07/379,501  
LING DATE: 11-Jul-89  
Y/AGENT INFORMATION:  
ME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 196/189  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 133:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 133:  
US-09-766-095-133  
Query Match 67.8%; Score 12.2; DB 4; Length 36;  
Best Local Similarity 41.2%; Pred. No. 3.4e+03;  
Matches 7; Conservative 7; Mismatches 3; Indels 0;

Qy 1 CTCAITTTGAATTTCG 17  
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Db 1 CUACUUGGAUAUUGC 17

RESULT 45  
US-09-766-095-137/c  
; Sequence 137, Application US/09766095  
; Patent No. 6649749  
; GENERAL INFORMATION:  
; APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,  
; Yeasing Yang  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION  
; OLIGONUCLEOTIDES AND PROBES  
; TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM PS/2 Model 50Z or 55SX  
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
; SOFTWARE: WordPerfect (Version 5.0)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/766,095  
; FILING DATE: 18-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/013,406  
; FILING DATE: 26-JAN-01  
; APPLICATION NUMBER: U.S. Serial No. 6649749 07/550,837  
; FILING DATE: 10-Jul-90  
; APPLICATION NUMBER: U.S. Serial No. 6649749 07/379,501  
; FILING DATE: 11-Jul-89  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 196/189  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 137:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 137:



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37

67.8%; Score 12.2; DB 4; Length 36;  
ilarity 82.4%; Pred. No. 3.4e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGGAATTTGC 17  
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TACTTGGGAATATTC 20

1: February 29, 2004, 11:22:25  
61 secs



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64.4	24	12	US-10-164-749A-372	Sequence 372, App	C 164	11.4	63.3	17	14	US-10-339-782-481	Sequenc
64.4	24	14	US-10-017-081A-372	Sequence 372, App	C 165	11.4	63.3	20	10	US-09-784-674-383	Sequenc
64.4	24	14	US-10-167-749-372	Sequence 372, App	C 166	11.4	63.3	20	10	US-09-784-674-384	Sequenc
64.4	24	14	US-10-013-921A-372	Sequence 372, App	C 167	11.4	63.3	20	10	US-09-784-674-385	Sequenc
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64.4	24	14	US-10-016-177A-372	Sequence 372, App	C 169	11.4	63.3	20	15	US-10-289-762-4356	Sequenc
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64.4	24	14	US-10-002-967A-372	Sequence 372, App	C 173	11.4	63.3	25	10	US-09-771-933-130	Sequenc
64.4	24	14	US-10-017-083A-372	Sequence 372, App	C 174	11.4	63.3	25	14	US-10-098-263B-124071	Sequenc
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64.4	24	14	US-10-145-089A-372	Sequence 372, App	C 179	11.4	63.3	43	14	US-10-032-585-1894	Sequenc
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64.4	24	14	US-10-013-926A-372	Sequence 372, App	C 182	11.4	63.3	50	15	US-10-131-827-1359	Sequenc
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64.4	24	14	US-10-145-124A-372	Sequence 372, App	C 184	11.4	63.3	50	15	US-10-131-827-6179	Sequenc
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64.4	24	14	US-10-017-086A-372	Sequence 372, App	C 187	11.4	63.3	50	15	US-10-131-827-7108	Sequenc
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64.4	24	15	US-10-017-084A-372	Sequence 372, App	C 193	11.2	62.2	20	10	US-09-784-674-378	Sequenc
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64.4	24	15	US-10-143-026B-372	Sequence 372, App	C 196	11.2	62.2	20	14	US-10-253-904-25	Sequenc
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64.4	24	15	US-10-162-522A-372	Sequence 372, App	C 199	11.2	62.2	20	15	US-10-177-573-29	Sequenc
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64.4	24	15	US-10-013-925A-372	Sequence 372, App	C 201	11.2	62.2	20	15	US-10-177-573-89	Sequenc
64.4	24	15	US-10-013-927A-372	Sequence 372, App	C 202	11.2	62.2	20	15	US-10-289-762-6723	Sequenc
64.4	24	15	US-10-145-093A-372	Sequence 372, App	C 203	11.2	62.2	22	10	US-09-989-739-11	Sequenc
64.4	24	15	US-10-013-920A-372	Sequence 372, App	C 204	11.2	62.2	24	9	US-09-800-631-4	Sequenc
64.4	24	15	US-10-013-919A-372	Sequence 372, App	C 205	11.2	62.2	24	14	US-10-293-783-4	Sequenc
64.4	24	15	US-10-013-924A-372	Sequence 372, App	C 206	11.2	62.2	24	15	US-10-388-263-662	Sequenc
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64.4	26	14	US-10-209-059-33	Sequence 4391, Ap	C 211	11.2	62.2	25	15	US-10-393-905-11	Sequenc
64.4	39	9	US-09-957-641-6	Sequence 33, Appl	C 212	11.2	62.2	27	14	US-10-025-222A-23	Sequenc
64.4	39	9	US-09-957-641-14	Sequence 14, Appl	C 213	11.2	62.2	29	15	US-10-312-273-609	Sequenc
64.4	43	14	US-10-032-585-695	Sequence 695, App	C 214	11.2	62.2	31	9	US-09-971-309-20	Sequenc
64.4	48	15	US-10-131-827-862	Sequence 862, App	C 215	11.2	62.2	34	14	US-10-216-209-40	Sequenc
64.4	50	9	US-09-547-267-30	Sequence 30, Appl	C 216	11.2	62.2	38	10	US-09-780-533A-2998	Sequenc
64.4	50	15	US-10-0920-923-9	Sequence 9, Appl	C 217	11.2	62.2	38	10	US-09-780-533A-4162	Sequenc
64.4	50	15	US-10-131-827-2058	Sequence 2058, Ap	C 218	11.2	62.2	38	10	US-09-848-754A-4591	Sequenc
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64.4	50	15	US-10-131-827-4550	Sequence 4550, Ap	C 220	11.2	62.2	42	10	US-09-862-393-2	Sequenc
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64.4	60	10	US-09-908-975-16332	Sequence 16332, A	C 223	11.2	62.2	42	14	US-10-209-507-16	Sequenc
64.4	60	10	US-09-908-975-18326	Sequence 18326, A	C 224	11.2	62.2	42	14	US-10-267-384-170	Sequenc
64.4	60	10	US-09-908-975-20030	Sequence 20030, A	C 225	11.2	62.2	44	13	US-10-025-367-21	Sequenc
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64.4	60	10	US-09-908-975-22592	Sequence 22592, A	C 227	11.2	62.2	47	14	US-10-367-438-36	Sequenc
64.4	60	10	US-09-908-975-23521	Sequence 23521, A	C 228	11.2	62.2	47	14	US-10-367-438-86	Sequenc
64.4	60	10	US-09-908-975-32079	Sequence 32079, A	C 229	11.2	62.2	47	15	US-10-349-143-337	Sequenc
64.4	60	10	US-09-908-975-32079	Sequence 97, Appl	C 230	11.2	62.2	47	15	US-10-349-143-907	Sequenc
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63.3	16	14	US-10-287-919-1387	Sequence 1387, Ap	C 232	11.2	62.2	47	15	US-10-349-143-1500	Sequenc
63.3	16	14	US-10-287-919-1500	Sequence 1500, Ap	C 233	11.2	62.2	47	15	US-10-349-143-2295	Sequenc
63.3	16	14			C 234	11.2	62.2	47	15	US-10-349-143-2743	Sequenc

62.2	47	15	US-10-349-143-2845	Sequence 2845, Ap	308	10.8	60.0	25	14	US-10-098-263B-3283	Sequenc
62.2	47	15	US-10-349-143-2870	Sequence 2870, Ap	309	10.8	60.0	25	14	US-10-098-263B-37155	Sequenc
62.2	50	14	US-10-029-386-15382	Sequence 15382, A	310	10.8	60.0	25	14	US-10-098-263B-43484	Sequenc
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62.2	50	15	US-10-131-827-7751	Sequence 7751, Ap	314	10.8	60.0	25	14	US-10-098-263B-54706	Sequenc
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62.2	60	10	US-09-908-975-5332	Sequence 5332, Ap	318	10.8	60.0	25	14	US-10-098-263B-81781	Sequenc
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61.1	27	15	US-10-353-678-60	Sequence 4, Appli	336	10.8	60.0	37	14	US-10-194-550-22	Sequenc
61.1	40	14	US-10-200-013-4	Sequence 454, App	c 337	10.8	60.0	38	10	US-09-730-289B-2294	Sequenc
61.1	47	15	US-10-349-143-454	Sequence 1724, Ap	c 338	10.8	60.0	38	10	US-09-780-533A-3099	Sequenc
61.1	47	15	US-10-349-143-1724	Sequence 816, App	c 339	10.8	60.0	38	10	US-09-848-754A-5718	Sequenc
61.1	50	15	US-10-131-827-816	Sequence 2704, Ap	c 340	10.8	60.0	38	10	US-09-776-474-1730	Sequenc
61.1	50	15	US-10-131-827-2704	Sequence 1707, Ap	c 341	10.8	60.0	38	10	US-09-776-474-1875	Sequenc
61.1	54	8	US-08-781-986A-1707	Sequence 5338, Ap	c 342	10.8	60.0	38	10	US-09-792-818-921	Sequenc
61.1	60	10	US-09-908-975-5338	Sequence 5338, Ap	c 343	10.8	60.0	39	15	US-10-027-632-52430	Sequenc
61.1	60	10	US-09-908-975-9070	Sequence 9070, Ap	c 344	10.8	60.0	40	15	US-10-027-632-175486	Sequenc
61.1	60	10	US-09-908-975-14595	Sequence 14595, A	c 345	10.8	60.0	42	14	US-10-221-993-14	Sequenc
61.1	60	10	US-09-908-975-15050	Sequence 15050, A	346	10.8	60.0	44	15	US-10-373-090-3	Sequenc
61.1	60	10	US-09-908-975-18084	Sequence 18084, A	c 347	10.8	60.0	45	15	US-10-369-299-16	Sequenc
61.1	60	10	US-09-908-975-19090	Sequence 19090, A	c 348	10.8	60.0	47	9	US-09-732-914-122	Sequenc
60.0	17	10	US-09-730-289B-629	Sequence 629, App	c 349	10.8	60.0	47	14	US-10-137-473-43	Sequenc
60.0	17	10	US-09-740-332-1390	Sequence 1390, Ap	c 350	10.8	60.0	47	15	US-10-349-143-271	Sequenc
60.0	17	10	US-09-740-332-3165	Sequence 3165, Ap	351	10.8	60.0	47	15	US-10-349-143-517	Sequenc
60.0	17	10	US-09-817-879-1390	Sequence 1390, Ap	352	10.8	60.0	47	15	US-10-349-143-1657	Sequenc
60.0	17	10	US-09-817-879-3165	Sequence 3165, Ap	c 353	10.8	60.0	47	15	US-10-349-143-3212	Sequenc
60.0	18	14	US-10-287-919-764	Sequence 764, App	c 354	10.8	60.0	50	8	US-08-781-986A-2475	Sequenc
60.0	18	14	US-10-287-919-2181	Sequence 2181, Ap	c 355	10.8	60.0	50	14	US-10-322-360-45	Sequenc
60.0	18	14	US-10-128-560-5	Sequence 5, Appli	c 356	10.8	60.0	50	14	US-10-322-360-45	Sequenc
60.0	18	14	US-10-128-560-18	Sequence 18, Appli	c 357	10.8	60.0	50	15	US-10-131-827-2	Sequenc
60.0	19	14	US-10-205-309-250	Sequence 250, App	c 358	10.8	60.0	50	15	US-10-131-827-3	Sequenc
60.0	19	14	US-10-205-309-575	Sequence 575, App	359	10.8	60.0	50	15	US-10-131-827-515	Sequenc
60.0	20	10	US-09-828-344-59	Sequence 59, Appl	360	10.8	60.0	50	15	US-10-131-827-1861	Sequenc
60.0	20	10	US-09-784-674-718	Sequence 718, App	c 361	10.8	60.0	50	15	US-10-131-827-2424	Sequenc
60.0	20	10	US-09-784-674-719	Sequence 719, App	c 362	10.8	60.0	50	15	US-10-131-827-2862	Sequenc
60.0	20	10	US-09-784-674-720	Sequence 720, App	c 363	10.8	60.0	50	15	US-10-131-827-5475	Sequenc
60.0	20	10	US-09-784-674-721	Sequence 721, App	364	10.8	60.0	50	15	US-10-131-827-6481	Sequenc
60.0	20	10	US-09-784-674-722	Sequence 722, App	365	10.8	60.0	50	15	US-10-131-827-6871	Sequenc
60.0	20	10	US-09-784-674-723	Sequence 723, App	c 366	10.8	60.0	50	15	US-10-131-827-7605	Sequenc
60.0	20	10	US-09-784-674-724	Sequence 724, App	c 367	10.8	60.0	50	15	US-10-131-827-7844	Sequenc
60.0	20	14	US-10-012-456A-30	Sequence 30, Appli	c 368	10.8	60.0	57	8	US-08-781-986A-1668	Sequenc
60.0	20	14	US-10-331-907-331	Sequence 331, App	369	10.8	60.0	58	15	US-10-339-712-18	Sequenc
60.0	20	15	US-10-289-762-4004	Sequence 4004, Ap	c 370	10.8	60.0	59	9	US-09-796-071-10	Sequenc
60.0	20	15	US-10-447-136-165	Sequence 165, App	c 371	10.8	60.0	59	9	US-09-796-071-11	Sequenc
60.0	21	15	US-10-349-143-9573	Sequence 9573, Ap	372	10.8	60.0	60	10	US-09-907-111-66	Sequenc
60.0	22	14	US-10-090-011-31	Sequence 31, Appli	373	10.8	60.0	60	10	US-09-908-975-5474	Sequenc
60.0	22	14	US-10-002-623-939	Sequence 939, App	374	10.8	60.0	60	10	US-09-908-975-5513	Sequenc
60.0	23	14	US-10-085-506-487	Sequence 487, App	375	10.8	60.0	60	10	US-09-908-975-11713	Sequenc
60.0	24	13	US-10-079-818-1	Sequence 1, Appli	376	10.8	60.0	60	10	US-09-908-975-12403	Sequenc
60.0	24	13	US-10-309-775A-14	Sequence 14, Appli	377	10.8	60.0	60	10	US-09-908-975-13405	Sequenc
60.0	25	13	US-10-014-436-13	Sequence 13, Appli	378	10.8	60.0	60	10	US-09-908-975-13915	Sequenc
60.0	25	14	US-10-215-112-808	Sequence 808, App	379	10.8	60.0	60	10	US-09-908-975-16004	Sequenc
60.0	25	14			380	10.8	60.0	60	10	US-09-908-975-16629	Sequenc

60.0	60	10	US-09-908-975-16965	Sequence 16965, A	454	10.6	58.9	41	14	US-10-292-896-86	Sequenc
60.0	60	10	US-09-908-975-17447	Sequence 17447, A	C 455	10.6	58.9	43	14	US-10-193-960-10	Sequenc
60.0	60	10	US-09-908-975-17791	Sequence 17791, A	C 456	10.6	58.9	43	14	US-10-193-960-13	Sequenc
60.0	60	10	US-09-908-975-18564	Sequence 18564, A	C 457	10.6	58.9	43	14	US-10-193-960-16	Sequenc
60.0	60	10	US-09-908-975-19285	Sequence 19285, A	C 458	10.6	58.9	43	14	US-10-193-960-26	Sequenc
60.0	60	10	US-09-908-975-20722	Sequence 20722, A	C 459	10.6	58.9	45	9	US-09-915-182-3	Sequenc
60.0	60	10	US-09-908-975-22451	Sequence 22451, A	C 460	10.6	58.9	45	9	US-09-765-272-235	Sequenc
60.0	60	10	US-09-908-975-32164	Sequence 32164, A	C 461	10.6	58.9	45	10	US-09-967-301-12	Sequenc
60.0	60	14	US-10-205-009-125	Sequence 125, App	C 462	10.6	58.9	45	10	US-09-967-301-13	Sequenc
58.9	17	9	US-09-866-108-6223	Sequence 6223, App	C 463	10.6	58.9	46	10	US-09-453-234-7	Sequenc
58.9	16	10	US-09-306-333A-106	Sequence 106, App	C 464	10.6	58.9	47	14	US-10-076-802-49	Sequenc
58.9	19	15	US-10-349-143-7292	Sequence 7292, App	C 465	10.6	58.9	47	14	US-10-076-802-50	Sequenc
58.9	19	15	US-10-349-143-7338	Sequence 7338, App	C 466	10.6	58.9	47	15	US-10-367-169-49	Sequenc
58.9	20	15	US-10-349-143-6437	Sequence 6437, App	C 467	10.6	58.9	47	15	US-10-367-169-50	Sequenc
58.9	21	9	US-09-765-081-397	Sequence 397, App	C 468	10.6	58.9	47	15	US-10-349-143-201	Sequenc
58.9	21	14	US-10-084-839-3970	Sequence 3970, App	C 469	10.6	58.9	47	15	US-10-349-143-3787	Sequenc
58.9	21	15	US-10-349-143-4952	Sequence 4952, App	C 470	10.6	58.9	47	15	US-10-349-143-1579	Sequenc
58.9	22	14	US-10-084-839-3973	Sequence 3973, App	C 471	10.6	58.9	47	15	US-10-349-143-3787	Sequenc
58.9	24	14	US-09-992-665-262	Sequence 262, App	C 472	10.6	58.9	49	10	US-09-782-974C-95	Sequenc
58.9	24	14	US-10-236-745-13	Sequence 13, Appl	C 473	10.6	58.9	50	15	US-10-131-827-719	Sequenc
58.9	24	14	US-10-032-585-5531	Sequence 5531, App	C 474	10.6	58.9	50	15	US-10-131-827-719	Sequenc
58.9	24	15	US-10-309-775A-8	Sequence 8, Appli	C 475	10.6	58.9	50	15	US-10-131-827-4050	Sequenc
58.9	25	9	US-09-866-108-11115	Sequence 11115, A	C 476	10.6	58.9	50	15	US-10-131-827-5330	Sequenc
58.9	25	9	US-09-866-108-11116	Sequence 11116, A	C 477	10.6	58.9	50	15	US-10-131-827-5330	Sequenc
58.9	25	9	US-09-866-108-11117	Sequence 11117, A	C 478	10.6	58.9	50	15	US-10-131-827-5330	Sequenc
58.9	25	9	US-09-866-108-11118	Sequence 11118, A	C 479	10.6	58.9	50	15	US-10-131-827-7102	Sequenc
58.9	25	9	US-09-866-108-11119	Sequence 11119, A	C 480	10.6	58.9	50	15	US-10-131-827-7600	Sequenc
58.9	25	9	US-09-866-108-11120	Sequence 11120, A	C 481	10.6	58.9	50	15	US-10-444-925-103	Sequenc
58.9	25	9	US-09-866-108-11121	Sequence 11121, A	C 482	10.6	58.9	50	15	US-10-444-925-105	Sequenc
58.9	25	9	US-09-866-108-11122	Sequence 11122, A	C 483	10.6	58.9	52	9	US-09-547-267-28	Sequenc
58.9	25	9	US-09-866-108-11123	Sequence 11123, A	C 484	10.6	58.9	52	10	US-09-920-923-7	Sequenc
58.9	25	9	US-09-796-543-6	Sequence 6, Appli	C 485	10.6	58.9	54	8	US-08-781-986A-1965	Sequenc
58.9	25	14	US-10-215-112-6100	Sequence 6100, App	C 486	10.6	58.9	55	15	US-10-444-925-107	Sequenc
58.9	25	14	US-10-215-112-8233	Sequence 8233, App	C 487	10.6	58.9	55	15	US-10-444-925-109	Sequenc
58.9	25	14	US-10-215-112-8359	Sequence 8359, App	C 488	10.6	58.9	58	9	US-09-790-317-3	Sequenc
58.9	25	14	US-10-215-112-8864	Sequence 8864, App	C 489	10.6	58.9	58	14	US-10-262-828A-3	Sequenc
58.9	25	14	US-10-098-263B-14709	Sequence 14709, A	C 490	10.6	58.9	60	10	US-09-908-975-6435	Sequenc
58.9	25	14	US-10-098-263B-19461	Sequence 19461, A	C 491	10.6	58.9	60	10	US-09-908-975-6842	Sequenc
58.9	25	14	US-10-098-263B-19462	Sequence 19462, A	C 492	10.6	58.9	60	10	US-09-908-975-8165	Sequenc
58.9	25	14	US-10-098-263B-19477	Sequence 19477, A	C 493	10.6	58.9	60	10	US-09-908-975-9323	Sequenc
58.9	25	14	US-10-098-263B-35884	Sequence 35884, A	C 494	10.6	58.9	60	10	US-09-908-975-10647	Sequenc
58.9	25	14	US-10-098-263B-41992	Sequence 41992, A	C 495	10.6	58.9	60	10	US-09-908-975-11096	Sequenc
58.9	25	14	US-10-098-263B-51148	Sequence 51148, A	C 496	10.6	58.9	60	10	US-09-908-975-13069	Sequenc
58.9	25	14	US-10-098-263B-60280	Sequence 60280, A	C 497	10.6	58.9	60	10	US-09-908-975-13754	Sequenc
58.9	25	14	US-10-098-263B-60966	Sequence 60966, A	C 498	10.6	58.9	60	10	US-09-908-975-13922	Sequenc
58.9	25	14	US-10-098-263B-95647	Sequence 95647, A	C 499	10.6	58.9	60	10	US-09-908-975-14334	Sequenc
58.9	25	14	US-10-098-263B-115695	Sequence 115695, A	C 500	10.6	58.9	60	10	US-09-908-975-14721	Sequenc
58.9	26	14	US-10-278-455-26	Sequence 26, Appl	C 501	10.6	58.9	60	10	US-09-908-975-17682	Sequenc
58.9	26	14	US-10-278-437-26	Sequence 26, Appl	C 502	10.6	58.9	60	10	US-09-908-975-19901	Sequenc
58.9	27	15	US-10-405-806-4	Sequence 4, Appli	C 503	10.6	58.9	60	10	US-09-908-975-20473	Sequenc
58.9	27	14	US-10-084-839-3967	Sequence 3967, App	C 504	10.6	58.9	60	10	US-09-908-975-20612	Sequenc
58.9	28	14	US-10-084-839-3971	Sequence 3971, App	C 505	10.6	58.9	60	10	US-09-908-975-22542	Sequenc
58.9	30	9	US-09-564-329A-23	Sequence 23, Appl	C 506	10.6	58.9	60	10	US-09-908-975-23670	Sequenc
58.9	30	9	US-09-855-153-23	Sequence 23, Appl	C 507	10.4	57.8	17	10	US-09-780-533A-397	Sequenc
58.9	30	9	US-09-854-811-23	Sequence 23, Appl	C 508	10.4	57.8	17	10	US-09-780-533A-2234	Sequenc
58.9	30	9	US-09-934-773-23	Sequence 23, Appl	C 509	10.4	57.8	17	10	US-09-780-533A-2573	Sequenc
58.9	30	9	US-09-963-620-23	Sequence 23, Appl	C 510	10.4	57.8	17	10	US-09-780-533A-2574	Sequenc
58.9	30	10	US-09-855-632-23	Sequence 23, Appl	C 511	10.4	57.8	17	10	US-09-740-332-1391	Sequenc
58.9	30	14	US-10-085-906-148	Sequence 148, App	C 512	10.4	57.8	17	10	US-09-817-879-1391	Sequenc
58.9	30	14	US-10-225-784-23	Sequence 23, Appl	C 513	10.4	57.8	17	14	US-10-060-998-936	Sequenc
58.9	30	14	US-10-224-720-23	Sequence 23, Appl	C 514	10.4	57.8	17	14	US-10-060-998-937	Sequenc
58.9	30	14	US-10-225-779-23	Sequence 23, Appl	C 515	10.4	57.8	17	14	US-10-060-998-938	Sequenc
58.9	30	15	US-10-374-381-23	Sequence 23, Appl	C 516	10.4	57.8	17	14	US-10-060-998-939	Sequenc
58.9	30	15	US-10-446-542-23	Sequence 23, Appl	C 517	10.4	57.8	17	14	US-10-060-998-940	Sequenc
58.9	31	10	US-09-510-378-181	Sequence 181, App	C 518	10.4	57.8	17	14	US-10-114-270-329	Sequenc
58.9	32	9	US-09-824-286-8	Sequence 8, Appli	C 519	10.4	57.8	19	12	US-10-114-270-329	Sequenc
58.9	33	14	US-10-284-083-8	Sequence 8, Appli	C 520	10.4	57.8	19	14	US-10-225-023-350	Sequenc
58.9	33	14	US-10-199-937-144	Sequence 144, App	C 521	10.4	57.8	19	14	US-10-225-023-395	Sequenc
58.9	35	9	US-09-766-095-32	Sequence 32, Appl	C 522	10.4	57.8	19	14	US-10-225-023-484	Sequenc
58.9	35	9	US-09-766-095-112	Sequence 112, App	C 523	10.4	57.8	19	14	US-10-225-023-505	Sequenc
58.9	41	12	US-10-453-827-248	Sequence 248, App	C 524	10.4	57.8	19	14	US-10-225-023-536	Sequenc
58.9	41	14	US-10-080-299-43	Sequence 43, Appl	C 525	10.4	57.8	19	14	US-10-225-023-565	Sequenc
58.9	41	14			C 526	10.4	57.8	19	14	US-10-225-023-598	Sequenc

57.8	19	14	US-10-225-023-1088	Sequence 1088, Ap	C 600	10.4	57.8	34	15	US-10-283-024-7	Sequenc
57.8	19	14	US-10-225-023-1133	Sequence 1133, Ap	C 601	10.4	57.8	34	15	US-10-283-024-10	Sequenc
57.8	19	14	US-10-225-023-1222	Sequence 1222, Ap	C 602	10.4	57.8	34	15	US-10-449-710-1	Sequenc
57.8	19	14	US-10-225-023-1243	Sequence 1243, Ap	C 603	10.4	57.8	35	14	US-10-259-197-1	Sequenc
57.8	19	14	US-10-225-023-1274	Sequence 1274, Ap	C 604	10.4	57.8	35	14	US-10-259-164-1	Sequenc
57.8	19	14	US-10-225-023-1303	Sequence 1303, Ap	C 605	10.4	57.8	36	9	US-09-912-787-40	Sequenc
57.8	19	14	US-10-225-023-1336	Sequence 1336, Ap	C 606	10.4	57.8	36	9	US-09-912-787-42	Sequenc
57.8	20	10	US-09-766-450-79	Sequence 79, Appl	C 607	10.4	57.8	36	13	US-10-014-326-26	Sequenc
57.8	20	10	US-09-784-674-387	Sequence 387, Appl	C 608	10.4	57.8	36	13	US-10-014-326-28	Sequenc
57.8	20	10	US-09-882-945A-65	Sequence 65, Appl	C 609	10.4	57.8	36	14	US-10-194-985-16	Sequenc
57.8	20	14	US-10-181-107-154	Sequence 154, Appl	C 610	10.4	57.8	36	14	US-10-194-985-17	Sequenc
57.8	20	14	US-10-238-443-62	Sequence 62, Appl	C 611	10.4	57.8	36	14	US-10-194-985-18	Sequenc
57.8	20	14	US-10-309-362-62	Sequence 62, Appl	C 612	10.4	57.8	36	14	US-10-194-985-19	Sequenc
57.8	20	15	US-10-189-256-13	Sequence 13, Appl	C 613	10.4	57.8	38	14	US-10-009-823A-5	Sequenc
57.8	20	15	US-10-189-256-85	Sequence 85, Appl	C 614	10.4	57.8	47	15	US-10-349-143-221	Sequenc
57.8	20	15	US-10-349-143-6395	Sequence 6395, Ap	C 615	10.4	57.8	47	15	US-10-349-143-559	Sequenc
57.8	21	9	US-09-969-373-2678	Sequence 2678, Ap	C 616	10.4	57.8	47	15	US-10-349-143-732	Sequenc
57.8	21	10	US-09-945-943-20	Sequence 20, Appl	C 617	10.4	57.8	47	15	US-10-349-143-732	Sequenc
57.8	21	15	US-10-349-143-5641	Sequence 5641, Ap	C 618	10.4	57.8	47	15	US-10-349-143-3080	Sequenc
57.8	22	14	US-10-084-555-44	Sequence 44, Appl	C 619	10.4	57.8	47	15	US-10-349-143-3384	Sequenc
57.8	22	15	US-10-120-801-144	Sequence 144, Appl	C 620	10.4	57.8	47	15	US-10-349-143-3399	Sequenc
57.8	22	15	US-10-099-322-204	Sequence 204, Appl	C 621	10.4	57.8	47	15	US-10-349-143-3528	Sequenc
57.8	22	15	US-10-162-335-198	Sequence 198, Appl	C 622	10.4	57.8	47	15	US-10-349-143-3571	Sequenc
57.8	22	15	US-10-044-564-204	Sequence 204, Appl	C 623	10.4	57.8	48	13	US-10-007-814-44	Sequenc
57.8	23	9	US-09-982-610-2	Sequence 2, Appli	C 624	10.4	57.8	48	13	US-10-007-814-45	Sequenc
57.8	23	12	US-10-373-406B-22	Sequence 22, Appl	C 625	10.4	57.8	48	14	US-10-315-515-113	Sequenc
57.8	23	14	US-10-080-794-16	Sequence 16, Appl	C 626	10.4	57.8	50	15	US-10-131-827-258	Sequenc
57.8	23	9	US-09-223-490-16	Sequence 16, Appl	C 627	10.4	57.8	50	15	US-10-131-827-1240	Sequenc
57.8	25	11	US-09-236-939-16	Sequence 16, Appl	C 628	10.4	57.8	50	15	US-10-131-827-1424	Sequenc
57.8	25	14	US-10-215-112-5811	Sequence 5811, Ap	C 629	10.4	57.8	50	15	US-10-131-827-2308	Sequenc
57.8	25	14	US-10-098-263B-112263	Sequence 112263, Ap	C 630	10.4	57.8	50	15	US-10-131-827-2809	Sequenc
57.8	25	14	US-10-098-263B-119143	Sequence 119143, Ap	C 631	10.4	57.8	50	15	US-10-131-827-3161	Sequenc
57.8	25	14	US-10-060-998-2440	Sequence 2440, Ap	C 632	10.4	57.8	50	15	US-10-131-827-4467	Sequenc
57.8	25	14	US-10-060-998-2441	Sequence 2441, Ap	C 633	10.4	57.8	50	15	US-10-131-827-6231	Sequenc
57.8	25	14	US-10-060-998-2442	Sequence 2442, Ap	C 634	10.4	57.8	50	15	US-10-131-827-6520	Sequenc
57.8	25	14	US-10-060-998-2443	Sequence 2443, Ap	C 635	10.4	57.8	50	15	US-10-131-827-6910	Sequenc
57.8	25	14	US-10-060-998-2444	Sequence 2444, Ap	C 636	10.4	57.8	53	10	US-09-907-111-282	Sequenc
57.8	25	14	US-10-060-998-2445	Sequence 2445, Ap	C 637	10.4	57.8	53	10	US-09-882-945A-198	Sequenc
57.8	25	14	US-10-060-998-2446	Sequence 2446, Ap	C 638	10.4	57.8	55	9	US-09-998-598-122	Sequenc
57.8	25	14	US-10-060-998-2447	Sequence 2447, Ap	C 639	10.4	57.8	56	8	US-08-781-986A-3889	Sequenc
57.8	25	14	US-10-060-998-2448	Sequence 2448, Ap	C 640	10.4	57.8	57	15	US-10-027-632-51951	Sequenc
57.8	25	14	US-10-060-998-2449	Sequence 2449, Ap	C 641	10.4	57.8	57	15	US-10-027-632-51963	Sequenc
57.8	25	14	US-10-060-998-2450	Sequence 2450, Ap	C 642	10.4	57.8	59	9	US-09-860-996-15	Sequenc
57.8	25	14	US-10-060-998-2451	Sequence 2451, Ap	C 643	10.4	57.8	59	9	US-09-860-996-30	Sequenc
57.8	25	14	US-10-060-998-2452	Sequence 2452, Ap	C 644	10.4	57.8	60	10	US-09-308-975-5944	Sequenc
57.8	25	14	US-10-060-998-2453	Sequence 2453, Ap	C 645	10.4	57.8	60	10	US-09-308-975-6604	Sequenc
57.8	25	14	US-10-083-336A-12	Sequence 12, Appl	C 646	10.4	57.8	60	10	US-09-308-975-7785	Sequenc
57.8	26	14	US-10-084-555-66	Sequence 66, Appl	C 647	10.4	57.8	60	10	US-09-308-975-8433	Sequenc
57.8	27	12	US-10-416-417-7	Sequence 7, Appli	C 648	10.4	57.8	60	10	US-09-308-975-9077	Sequenc
57.8	27	14	US-10-079-167-29	Sequence 29, Appl	C 649	10.4	57.8	60	10	US-09-308-975-9766	Sequenc
57.8	27	14	US-10-032-585-5553	Sequence 5553, Ap	C 650	10.4	57.8	60	10	US-09-308-975-9971	Sequenc
57.8	28	15	US-10-449-710-6	Sequence 6, Appli	C 651	10.4	57.8	60	10	US-09-308-975-12995	Sequenc
57.8	29	9	US-09-860-996-18	Sequence 18, Appl	C 652	10.4	57.8	60	10	US-09-308-975-15145	Sequenc
57.8	29	14	US-10-336-638-478	Sequence 478, Appl	C 653	10.4	57.8	60	10	US-09-308-975-15246	Sequenc
57.8	29	14	US-10-336-638-876	Sequence 876, Appl	C 654	10.4	57.8	60	10	US-09-308-975-15920	Sequenc
57.8	30	10	US-09-989-643-7	Sequence 7, Appli	C 655	10.4	57.8	60	10	US-09-308-975-16782	Sequenc
57.8	30	10	US-09-953-348-94	Sequence 94, Appl	C 656	10.4	57.8	60	10	US-09-308-975-19470	Sequenc
57.8	31	9	US-10-267-255-94	Sequence 94, Appl	C 657	10.4	57.8	60	10	US-09-308-975-19821	Sequenc
57.8	31	9	US-09-848-464-1	Sequence 1, Appli	C 658	10.4	57.8	60	10	US-09-308-975-21054	Sequenc
57.8	31	9	US-09-976-297-8	Sequence 8, Appli	C 659	10.4	57.8	60	10	US-09-308-975-21104	Sequenc
57.8	31	15	US-10-317-444-407	Sequence 407, Appl	C 660	10.4	57.8	60	10	US-09-308-975-22148	Sequenc
57.8	31	15	US-10-317-444-408	Sequence 408, Appl	C 661	10.4	57.8	60	10	US-09-308-975-23467	Sequenc
57.8	32	13	US-10-086-127-20	Sequence 20, Appl	C 662	10.2	56.7	17	9	US-09-864-785-2146	Sequenc
57.8	32	14	US-10-191-879-18	Sequence 18, Appl	C 663	10.2	56.7	17	9	US-09-864-785-2988	Sequenc
57.8	32	14	US-10-123-481-19	Sequence 19, Appl	C 664	10.2	56.7	17	10	US-09-877-478-239	Sequenc
57.8	32	14	US-10-123-481-24	Sequence 24, Appl	C 665	10.2	56.7	17	10	US-09-877-478-930	Sequenc
57.8	32	14	US-10-123-481-28	Sequence 28, Appl	C 666	10.2	56.7	17	10	US-09-848-754A-3126	Sequenc
57.8	33	9	US-09-878-454A-10	Sequence 10, Appli	C 667	10.2	56.7	17	10	US-09-848-754A-3127	Sequenc
57.8	34	9	US-09-949-109-1	Sequence 1, Appli	C 668	10.2	56.7	17	14	US-10-339-793-42	Sequenc
57.8	34	13	US-10-024-318-31	Sequence 31, Appl	C 669	10.2	56.7	19	9	US-09-969-373-2277	Sequenc
57.8	34	14	US-10-033-300-16	Sequence 16, Appl	C 670	10.2	56.7	19	14	US-10-251-117-113	Sequenc
57.8	34	14	US-10-267-137-5	Sequence 5, Appli	C 671	10.2	56.7	19	14	US-10-251-117-362	Sequenc
57.8	34	14	US-10-088-728-1	Sequence 1, Appli	C 672	10.2	56.7	19	14	US-10-225-023-419	Sequenc

56.7	19	14	US-10-225-023-510	Sequence 510, App	746	10.2	56.7	25	14	US-10-098-263B-112005	Sequence
56.7	19	14	US-10-225-023-1157	Sequence 1157, App	747	10.2	56.7	25	14	US-10-098-263B-115806	Sequence
56.7	19	14	US-10-225-023-1248	Sequence 1248, App	c 748	10.2	56.7	25	14	US-10-098-263B-124044	Sequence
56.7	20	9	US-09-820-339A-21	Sequence 21, Appl	749	10.2	56.7	25	14	US-10-098-263B-124487	Sequence
56.7	20	9	US-09-800-631-55	Sequence 55, Appl	c 750	10.2	56.7	25	14	US-10-098-263B-125789	Sequence
56.7	20	9	US-09-895-382-23	Sequence 23, Appl	c 751	10.2	56.7	25	14	US-10-098-263B-125797	Sequence
56.7	20	10	US-09-784-674-377	Sequence 377, App	c 752	10.2	56.7	25	14	US-10-098-263B-130930	Sequence
56.7	20	14	US-10-057-550-105	Sequence 105, App	c 753	10.2	56.7	27	10	US-09-888-326-56	Sequence
56.7	20	14	US-10-173-225B-83	Sequence 83, Appl	754	10.2	56.7	27	10	US-09-888-326-493	Sequence
56.7	20	14	US-10-293-783-55	Sequence 55, Appl	755	10.2	56.7	27	10	US-09-776-479-142	Sequence
56.7	20	15	US-10-388-263-703	Sequence 703, App	c 756	10.2	56.7	27	10	US-09-776-479-143	Sequence
56.7	20	15	US-10-343-143-8723	Sequence 8723, App	c 757	10.2	56.7	27	14	US-10-112-653-135	Sequence
56.7	20	15	US-10-289-762-2664	Sequence 2664, App	c 758	10.2	56.7	27	14	US-10-112-653-136	Sequence
56.7	20	15	US-10-289-762-2671	Sequence 2671, App	759	10.2	56.7	27	14	US-10-017-995-142	Sequence
56.7	20	15	US-10-289-762-4621	Sequence 4621, App	c 760	10.2	56.7	27	14	US-10-017-995-143	Sequence
56.7	20	15	US-10-289-762-4730	Sequence 4730, App	c 761	10.2	56.7	28	13	US-10-067-989-13	Sequence
56.7	21	9	US-09-969-373-2397	Sequence 2397, App	762	10.2	56.7	29	9	US-09-839-894-11	Sequence
56.7	21	9	US-09-969-373-2398	Sequence 2398, App	c 763	10.2	56.7	29	12	US-10-188-186-227	Sequence
56.7	21	9	US-09-969-373-2400	Sequence 2400, App	c 764	10.2	56.7	29	14	US-10-288-823-1	Sequence
56.7	21	9	US-09-969-373-2402	Sequence 2402, App	c 765	10.2	56.7	29	14	US-10-288-823-3	Sequence
56.7	21	9	US-09-969-373-2475	Sequence 2475, App	c 766	10.2	56.7	30	9	US-09-993-292A-17	Sequence
56.7	21	9	US-09-995-225-62	Sequence 62, Appl	c 767	10.2	56.7	30	14	US-10-156-275-45	Sequence
56.7	21	10	US-09-995-225-62	Sequence 62, Appl	c 768	10.2	56.7	31	9	US-09-766-399-51	Sequence
56.7	21	10	US-09-866-077-6	Sequence 6, Appli	769	10.2	56.7	31	9	US-09-376-940-33	Sequence
56.7	21	14	US-10-211-296-8	Sequence 8, Appli	c 770	10.2	56.7	31	14	US-10-319-130-41	Sequence
56.7	21	14	US-10-301-840-8	Sequence 8, Appli	c 771	10.2	56.7	31	14	US-10-319-130-42	Sequence
56.7	21	15	US-10-349-143-4378	Sequence 4378, App	c 772	10.2	56.7	31	15	US-10-603-642-51	Sequence
56.7	21	15	US-10-349-143-6173	Sequence 6173, App	c 773	10.2	56.7	33	9	US-09-940-308-11	Sequence
56.7	21	15	US-10-349-143-6574	Sequence 6574, App	c 774	10.2	56.7	33	13	US-10-115-701A-11	Sequence
56.7	22	8	US-08-913-322-11	Sequence 11, Appl	775	10.2	56.7	33	15	US-10-332-065-26	Sequence
56.7	22	9	US-09-771-938B-14	Sequence 14, Appl	c 776	10.2	56.7	34	14	US-10-146-327-17	Sequence
56.7	22	13	US-10-109-885-12	Sequence 12, Appl	c 777	10.2	56.7	34	14	US-10-160-385-1	Sequence
56.7	22	14	US-10-309-280-12	Sequence 12, Appl	c 778	10.2	56.7	34	14	US-10-186-042-18	Sequence
56.7	22	15	US-10-120-801-147	Sequence 147, App	c 779	10.2	56.7	35	13	US-10-007-805-557	Sequence
56.7	23	10	US-09-766-450-13	Sequence 13, Appl	c 780	10.2	56.7	35	14	US-10-076-622-557	Sequence
56.7	23	14	US-10-181-177-4	Sequence 4, Appli	c 781	10.2	56.7	35	14	US-10-068-174-3	Sequence
56.7	23	14	US-10-005-956-822	Sequence 822, App	c 782	10.2	56.7	35	14	US-10-124-805-557	Sequence
56.7	23	14	US-10-005-956-823	Sequence 823, App	c 783	10.2	56.7	35	15	US-10-332-065-31	Sequence
56.7	24	9	US-09-918-568-25	Sequence 25, Appl	c 784	10.2	56.7	36	14	US-10-102-239-12	Sequence
56.7	24	9	US-09-969-373-2382	Sequence 2382, App	c 785	10.2	56.7	36	14	US-10-102-239-16	Sequence
56.7	24	9	US-09-848-585-36	Sequence 36, Appl	c 786	10.2	56.7	36	14	US-10-102-239-16	Sequence
56.7	24	10	US-09-896-994-3	Sequence 3, Appli	c 787	10.2	56.7	36	15	US-10-440-850-1425	Sequence
56.7	24	14	US-10-434-588-19	Sequence 19, Appl	c 788	10.2	56.7	36	15	US-10-440-850-1673	Sequence
56.7	24	14	US-10-032-585-5379	Sequence 5379, App	c 789	10.2	56.7	36	15	US-10-440-850-1870	Sequence
56.7	25	9	US-09-942-310-31	Sequence 45, Appl	c 790	10.2	56.7	37	10	US-09-877-478-6258	Sequence
56.7	25	11	US-09-730-559B-47	Sequence 47, Appl	c 791	10.2	56.7	37	10	US-09-877-478-6258	Sequence
56.7	25	14	US-10-177-987-3	Sequence 3, Appli	c 792	10.2	56.7	37	14	US-10-072-975-34	Sequence
56.7	25	14	US-10-215-112-5606	Sequence 5606, App	793	10.2	56.7	37	15	US-10-360-275-34	Sequence
56.7	25	14	US-10-215-112-10258	Sequence 10258, A	c 794	10.2	56.7	37	15	US-09-730-289B-2204	Sequence
56.7	25	14	US-10-215-112-14387	Sequence 14387, A	c 795	10.2	56.7	38	10	US-09-780-533A-3723	Sequence
56.7	25	14	US-10-098-263B-1646	Sequence 1646, App	c 796	10.2	56.7	38	10	US-09-877-478-3014	Sequence
56.7	25	14	US-10-098-263B-6258	Sequence 6258, App	c 797	10.2	56.7	38	10	US-09-877-478-3280	Sequence
56.7	25	14	US-10-098-263B-6349	Sequence 6349, App	c 798	10.2	56.7	38	10	US-09-848-754A-4133	Sequence
56.7	25	14	US-10-098-263B-6350	Sequence 6350, App	c 799	10.2	56.7	38	10	US-09-848-754A-4298	Sequence
56.7	25	14	US-10-098-263B-22324	Sequence 22324, A	c 800	10.2	56.7	38	10	US-09-848-754A-5589	Sequence
56.7	25	14	US-10-098-263B-29035	Sequence 29035, A	c 801	10.2	56.7	38	10	US-09-780-164-1358	Sequence
56.7	25	14	US-10-098-263B-29036	Sequence 29036, A	c 802	10.2	56.7	38	10	US-09-910-469-106	Sequence
56.7	25	14	US-10-098-263B-29449	Sequence 29449, A	803	10.2	56.7	38	10	US-09-910-469-116	Sequence
56.7	25	14	US-10-098-263B-30258	Sequence 30258, A	804	10.2	56.7	38	10	US-09-910-469-136	Sequence
56.7	25	14	US-10-098-263B-31487	Sequence 31487, A	c 805	10.2	56.7	38	14	US-10-156-306-670	Sequence
56.7	25	14	US-10-098-263B-44646	Sequence 44646, A	c 807	10.2	56.7	38	14	US-10-156-306-1095	Sequence
56.7	25	14	US-10-098-263B-56240	Sequence 56240, A	c 808	10.2	56.7	38	14	US-10-156-306-2235	Sequence
56.7	25	14	US-10-098-263B-61284	Sequence 61284, A	c 809	10.2	56.7	38	14	US-10-230-006-402	Sequence
56.7	25	14	US-10-098-263B-75385	Sequence 75385, A	c 810	10.2	56.7	38	15	US-10-407-079-47	Sequence
56.7	25	14	US-10-098-263B-75385	Sequence 75385, A	c 811	10.2	56.7	39	9	US-09-922-261-132	Sequence
56.7	25	14	US-10-098-263B-75617	Sequence 75617, A	c 812	10.2	56.7	39	14	US-10-102-239-14	Sequence
56.7	25	14	US-10-098-263B-81613	Sequence 81613, A	c 813	10.2	56.7	39	15	US-10-364-649-34	Sequence
56.7	25	14	US-10-098-263B-86552	Sequence 86552, A	814	10.2	56.7	40	9	US-09-998-130A-2	Sequence
56.7	25	14	US-10-098-263B-97200	Sequence 97200, A	c 815	10.2	56.7	40	14	US-10-005-956-1554	Sequence
56.7	25	14	US-10-098-263B-98069	Sequence 98069, A	c 816	10.2	56.7	40	14	US-10-187-253A-55	Sequence
56.7	25	14	US-10-098-263B-101114	Sequence 101114, A	817	10.2	56.7	40	14	US-10-199-820-143	Sequence
56.7	25	14	US-10-098-263B-106875	Sequence 106875, A	818	10.2	56.7	41	14	US-10-072-438-44	Sequence

56.7	43	9	US-09-962-628B-40	Sequence 40, Appl	C 892	10.2	56.7	60	10	US-09-908-975-13444	Sequenc
56.7	43	14	US-10-193-360-28	Sequence 28, Appl	893	10.2	56.7	60	10	US-09-908-975-15858	Sequenc
56.7	43	15	US-10-027-632-177267	Sequence 177267,	C 894	10.2	56.7	60	10	US-09-908-975-15877	Sequenc
56.7	44	9	US-09-988-899-60	Sequence 60, Appl	C 895	10.2	56.7	60	10	US-09-908-975-16317	Sequenc
56.7	44	9	US-09-822-688A-11	Sequence 11, Appl	896	10.2	56.7	60	10	US-09-908-975-16550	Sequenc
56.7	44	15	US-10-027-632-58555	Sequence 58555, A	897	10.2	56.7	60	10	US-09-908-975-17126	Sequenc
56.7	47	15	US-10-170-097-819	Sequence 819, App	C 898	10.2	56.7	60	10	US-09-908-975-17235	Sequenc
56.7	47	15	US-10-349-143-258	Sequence 258, App	C 899	10.2	56.7	60	10	US-09-908-975-17449	Sequenc
56.7	47	15	US-10-349-143-422	Sequence 422, App	900	10.2	56.7	60	10	US-09-908-975-17892	Sequenc
56.7	47	15	US-10-349-143-477	Sequence 477, App	C 901	10.2	56.7	60	10	US-09-908-975-18915	Sequenc
56.7	47	15	US-10-349-143-855	Sequence 855, App	902	10.2	56.7	60	10	US-09-908-975-19358	Sequenc
56.7	47	15	US-10-349-143-899	Sequence 899, App	903	10.2	56.7	60	10	US-09-908-975-19739	Sequenc
56.7	47	15	US-10-349-143-2498	Sequence 2498, Ap	C 904	10.2	56.7	60	10	US-09-908-975-20314	Sequenc
56.7	47	15	US-10-349-143-2621	Sequence 2621, Ap	C 905	10.2	56.7	60	10	US-09-908-975-20342	Sequenc
56.7	47	15	US-10-349-143-2927	Sequence 2927, Ap	906	10.2	56.7	60	10	US-09-908-975-20387	Sequenc
56.7	47	15	US-10-349-143-3406	Sequence 3406, Ap	907	10.2	56.7	60	10	US-09-908-975-20466	Sequenc
56.7	47	15	US-10-349-143-3744	Sequence 3744, Ap	908	10.2	56.7	60	10	US-09-908-975-22281	Sequenc
56.7	50	15	US-10-131-827-237	Sequence 237, App	C 909	10.2	56.7	60	10	US-09-908-975-22684	Sequenc
56.7	50	15	US-10-131-827-892	Sequence 892, App	910	10.2	56.7	60	10	US-09-908-975-22939	Sequenc
56.7	50	15	US-10-131-827-1086	Sequence 1086, Ap	911	10.2	56.7	60	10	US-09-908-975-23270	Sequenc
56.7	50	15	US-10-131-827-2187	Sequence 2187, Ap	912	10.2	56.7	60	10	US-09-908-975-31687	Sequenc
56.7	50	15	US-10-131-827-2458	Sequence 2458, Ap	913	10.2	56.7	60	15	US-10-423-847-27	Sequenc
56.7	50	15	US-10-131-827-2526	Sequence 2526, Ap	C 914	10	55.6	19	9	US-09-881-012-125	Sequenc
56.7	50	15	US-10-131-827-3115	Sequence 3115, Ap	915	10	55.6	19	15	US-10-349-143-4876	Sequenc
56.7	50	15	US-10-131-827-3485	Sequence 3485, Ap	916	10	55.6	19	15	US-10-349-143-6312	Sequenc
56.7	50	15	US-10-131-827-3667	Sequence 3667, Ap	C 917	10	55.6	19	15	US-10-444-925-127	Sequenc
56.7	50	15	US-10-131-827-3933	Sequence 3933, Ap	C 918	10	55.6	20	9	US-09-734-188-6	Sequenc
56.7	50	15	US-10-131-827-4765	Sequence 4765, Ap	C 919	10	55.6	20	9	US-09-995-598-4	Sequenc
56.7	50	15	US-10-131-827-5202	Sequence 5202, Ap	920	10	55.6	20	14	US-09-828-344-60	Sequenc
56.7	50	15	US-10-131-827-5369	Sequence 5369, Ap	921	10	55.6	20	14	US-10-007-010-77	Sequenc
56.7	50	15	US-10-131-827-5435	Sequence 5435, Ap	C 922	10	55.6	20	14	US-10-023-782A-84	Sequenc
56.7	50	15	US-10-131-827-6139	Sequence 6139, Ap	923	10	55.6	20	15	US-10-177-573-53	Sequenc
56.7	50	15	US-10-131-827-6346	Sequence 6346, Ap	924	10	55.6	20	15	US-10-104-047-3960	Sequenc
56.7	50	15	US-10-131-827-7898	Sequence 7898, Ap	925	10	55.6	20	15	US-10-349-143-6720	Sequenc
56.7	50	15	US-10-444-925-102	Sequence 102, App	926	10	55.6	20	15	US-10-447-136-186	Sequenc
56.7	51	10	US-09-747-377-402	Sequence 402, App	927	10	55.6	20	15	US-10-199-221-62	Sequenc
56.7	51	10	US-09-922-225A-37	Sequence 37, Appl	928	10	55.6	21	10	US-09-932-300-64	Sequenc
56.7	51	14	US-10-105-613-402	Sequence 402, App	929	10	55.6	21	14	US-10-058-597-2	Sequenc
56.7	51	15	US-10-321-039-393	Sequence 393, App	C 930	10	55.6	21	15	US-10-349-143-11600	Sequenc
56.7	54	9	US-09-938-744-11	Sequence 11, Appl	C 931	10	55.6	21	15	US-10-452-510-178	Sequenc
56.7	54	12	US-10-403-676-37	Sequence 37, Appl	932	10	55.6	22	14	US-10-246-581-20	Sequenc
56.7	54	12	US-10-403-676-39	Sequence 39, Appl	933	10	55.6	22	14	US-10-032-585-4669	Sequenc
56.7	54	15	US-10-449-548-37	Sequence 37, Appl	934	10	55.6	22	15	US-10-374-077-88	Sequenc
56.7	54	15	US-10-449-548-39	Sequence 39, Appl	C 935	10	55.6	22	15	US-10-457-839-63	Sequenc
56.7	55	15	US-09-866-925-243	Sequence 243, App	C 936	10	55.6	23	9	US-09-950-046A-3	Sequenc
56.7	55	15	US-10-040-539-4	Sequence 4, Appli	C 937	10	55.6	23	14	US-10-308-460-9	Sequenc
56.7	55	15	US-10-444-925-106	Sequence 106, App	938	10	55.6	23	16	US-10-309-290-222	Sequenc
56.7	55	15	US-10-444-925-108	Sequence 108, App	939	10	55.6	24	10	US-09-940-185-2492	Sequenc
56.7	55	15	US-10-444-925-108	Sequence 108, App	C 940	10	55.6	24	10	US-09-940-185-3382	Sequenc
56.7	56	8	US-08-781-986A-2085	Sequence 2085, Ap	941	10	55.6	24	14	US-10-072-094-104	Sequenc
56.7	56	14	US-10-219-227-12	Sequence 12, Appl	C 942	10	55.6	24	14	US-10-024-648-2	Sequenc
56.7	59	13	US-10-013-737-10	Sequence 10, Appl	943	10	55.6	24	14	US-10-172-094-104	Sequenc
56.7	59	15	US-10-027-632-176095	Sequence 176095,	C 944	10	55.6	25	9	US-09-834-956-17	Sequenc
56.7	60	9	US-09-922-261-4	Sequence 4, Appli	C 945	10	55.6	25	14	US-10-081-119-5	Sequenc
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56.7	60	10	US-09-908-975-7495	Sequence 7495, Ap	954	10	55.6	25	14	US-10-098-263B-59974	Sequenc
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56.7	60	10	US-09-908-975-12128	Sequence 12128, A	C 961	10	55.6	25	14	US-10-098-263B-86937	Sequenc
56.7	60	10	US-09-908-975-12843	Sequence 12843, A	C 962	10	55.6	25	14	US-10-098-263B-86938	Sequenc
56.7	60	10	US-09-908-975-13068	Sequence 13068, A	C 963	10	55.6	25	14	US-10-098-263B-96434	Sequenc
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55.6 25 14 US-10-098-263B-115475  
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 55.6 25 14 US-10-098-263B-127403  
 55.6 25 15 US-10-285-061-39  
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 55.6 25 15 US-10-300-683-500  
 55.6 27 9 US-09-814-661A-23  
 55.6 28 9 US-09-037-657-31  
 55.6 28 9 US-09-851-129A-11  
 55.6 30 9 US-09-727-311-61  
 55.6 30 9 US-09-760-574-91  
 55.6 30 10 US-09-766-442A-91  
 55.6 30 14 US-10-287-919-1904  
 55.6 30 14 US-10-287-919-1905  
 55.6 31 10 US-09-862-393-16  
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 55.6 37 14 US-10-133-133A-2  
 55.6 37 14 US-10-133-133A-3  
 55.6 38 10 US-09-780-533A-4747  
 55.6 39 10 US-09-155-106-45  
 55.6 39 10 US-09-969-748C-84  
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 55.6 39 14 US-10-423-828-58  
 55.6 39 14 US-10-005-956-1446  
 55.6 39 15 US-10-457-839-80  
 55.6 41 14 US-10-005-956-934  
 55.6 43 9 US-09-753-574-1  
 55.6 44 9 US-09-968-355-9  
 55.6 45 9 US-09-912-787-50  
 55.6 45 9 US-09-957-641-10  
 55.6 45 9 US-09-957-641-18  
 55.6 45 10 US-09-884-465A-275

# ALIGNMENTS

13 Application US/10351157  
 3. US20030215838A1  
 WATION:  
 recher, Cindy A.  
 ao, Zeren  
 Kuipper, Joseph L.  
 Jasovich, Maria M.  
 Grant, Francis J.  
 Presnell, Scott R.  
 Whitmore, Theodore E.  
 Hammond, Angela K.  
 No. US20030215838A1ak, Julia E.  
 Gross, Jane A.  
 Dillon, Stacey R.  
 ENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS  
 CS: 02-02  
 ICATION NUMBER: US/10351,157  
 NG DATE: 2003-01-21  
 ATION NUMBER: US 60/435,361  
 DATE: 2003-12-19  
 ATION NUMBER: US 60/389,108  
 DATE: 2002-06-14  
 ATION NUMBER: US 60/350,325  
 DATE: 2002-01-18  
 Q ID NOS: 183  
 st-SEQ for Windows Version 4.0

rtificial Sequence

FEATURE:  
 ; OTHER INFORMATION: Primer ZC40574  
 US-10-351-157-143  
 Query Match 100.0%; Score 18; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 50; Indels 0;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0;  
 QY 1 CTCATTGGGAATTTTGGC 18  
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 Db 1 CTCATTGGGAATTTTGGC 18  
 |||||  
 RESULT 2  
 US-10-367-438-198  
 ; Sequence 198, Application US/10367438  
 ; Publication No. US20030180773A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COHEN, Daniel  
 ; BLUMENFELD, Marta  
 ; TCHOUMAKOV, Ilia  
 ; TITLE OF INVENTION: Biallelic markers for use in  
 ; constructing a high density disequilib  
 ; the human genome.  
 ; NUMBER OF SEQUENCES: 336  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Knobbe, Martens, Olson & Bear  
 ; STREET: 550 West C Street  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: Win95  
 ; SOFTWARE: Word  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/367,438  
 ; FILING DATE: 14-Feb-2003  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/463,075A  
 ; FILING DATE: 14-Jan-2000  
 ; INFORMATION FOR SEQ ID NO: 198:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 base pairs  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: SINGLE  
 ; TOPOLOGY: LINEAR  
 ; MOLECULE TYPE: DNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: downstream amplification primer for SEQ ID:  
 ; LOCATION: 1..20  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 198:  
 US-10-367-438-198  
 Query Match 77.8%; Score 14; DB 14; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 CATTGGGAATTTTG 16  
 |||||  
 Db 3 CATTGGGAATTTTG 16  
 |||||  
 RESULT 3  
 US-10-349-143-11109  
 ; Sequence 11109, Application US/10349143  
 ; Publication No. US20040005584A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cohen, Daniel

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us-10-090-326-16.max.rnpb

```
lumenfeld, Marta
humakov, Ilya
NTION: Biallelic markers for use in constructing a high density...
E: GENSET.020CPI
CATION NUMBER: US/10/349,143
G DATE: 2003-01-21
TION NUMBER: US/09/422,978
DATE: 1999-10-20
TION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
DATE: EARLIER FILING DATE: 1999-04-21
TION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
DATE: EARLIER FILING DATE: 1998-11-23
TION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
DATE: EARLIER FILING DATE: 1998-04-21
; ID NOS: 11796
;
imo Sapiens
imer_bind
.20
ATTION: downstream amplification primer 99-2645 for SEQ 3244, in compleme
109
77.8%; Score 14; DB 15; Length 20;
ilarity 100.0%; Pred. No. 3.8e+03;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TTTGGAAATTG 16
|||||
TTTGGAAATTG 16
C
plication US/10193960
. US20030104477A1
ATTION:
echler, Joe
alkirs, Gunars
ray, Jeff
iosite Diagnostics Inc.
NTION: Chimeric Polyclonal Antibodies
E: 014907-0027000US
CATION NUMBER: US/10/193,960
G DATE: 2002-07-12
TION NUMBER: US/09/410,903
DATE: 1999-10-02
TION NUMBER: US 08/832,985
DATE: 1997-04-04
TION NUMBER: US 08/835,159
DATE: 1997-04-04
TION NUMBER: WO PCT/US98/06704
DATE: 1998-04-03
ID NOS: 100
tSEQ for Windows Version 3.0
tifical Sequence
ATTION: oligo 50
73.3%; Score 13.2; DB 14; Length 43;
ilarity 83.3%; Pred. No. 1e+04;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CATTGGAAATTTGCC 18
|||||
CATTTCGGCTTTGCC 11
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RESULT 5
US-09-908-975-22707
; Sequence 22707, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRA
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 22707
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-22707
Query Match 73.3%; Score 13.2; DB 10; Length 60;
Best Local Similarity 83.3%; Pred. No. 1e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0;
QY 1 CTCATTGGAAATTTGCC 18
|||||
DB 38 CTCATTGGAAATTCCTCC 55
RESULT 6
US-10-032-585-4803/c
; Sequence 4803, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4803
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4803
Query Match 72.2%; Score 13; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0;
QY 5 TTTGGAAATTTGC 17
|||||
DB 14 TTTGGAAATTTGC 2
RESULT 7
US-09-902-563-46/c
; Sequence 46, Application US/09902563
; Publication No. US20030099654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
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ENTION: Methods of Modulating Immune Coagulation  
CE: 9579-37  
ICATION NUMBER: US/09/902,563  
NG DATE: 2002-09-09  
ATION NUMBER: US 09/442,143  
DATE: 1999-11-15  
Q ID NOS: 53  
tentin version 3.1

## rtificial Sequence

MATION: Primer

5

71.1%; Score 12.8; DB 10; Length 19;  
milarity 87.5%; Pred. No. 1.4e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ATTGGAATTTGCCC 18

||||| ||||| |||||  
ATTAGATTTTGGC 4

## s/c

Application US/10096255  
US20030103974A1

MATION:

svy, Gary

Clark, David A.

ENTION: Methods of Modulating Immune Coagulation

CE: 9579-52

ICATION NUMBER: US/10/096,255

NG DATE: 2002-03-13

ATION NUMBER: US 60/046,537

DATE: 1997-05-17

ATION NUMBER: US 60/061,684

DATE: 1997-10-10

Q ID NOS: 53

tentin version 3.1

## rtificial Sequence

MATION: Primer

6

71.1%; Score 12.8; DB 14; Length 19;  
milarity 87.5%; Pred. No. 1.4e+04;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ATTGGAATTTGCCC 18

||||| ||||| |||||  
ATTAGATTTTGGC 4

## 6

Application US/09863806  
US20020197609A1

ORMATION:

ANT: Sidransky, David

OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA

OF SEQUENCES: 195

PONDENCE ADDRESS:

DRESSEE: Fish &amp; Richardson P.C.

TREET: 4225 Executive Square, Suite 1400

ITY: La Jolla

TATE: CA

OUNTRY: USA

ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/863,806  
FILING DATE: 22-May-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/038,637  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/152,313  
FILING DATE: 12-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/146001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 66:  
US-09-863-806-66

Query Match 71.1%; Score 12.8; DB 9; Length 22;  
Best Local Similarity 87.5%; Pred. No. 1.4e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

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Db ||||| ||||| |||||  
6 CATCTGAATTTGCC 21

## RESULT 10

US-09-908-975-6713  
Sequence 6713, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Liat  
APPLICANT: FAIGLER, Simchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TR  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6713  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-6713

Query Match 71.1%; Score 12.8; DB 10; Length 60;  
Best Local Similarity 87.5%; Pred. No. 1.6e+04;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 3 CATTGGAATTTGCC 18

||||| ||||| |||||

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TTTGGAACTTTGCC 49

987  
Application US/09908975  
US20030165843A1

ATION:

OSHAN, Avi

ASSERMAN, Alon

INTZ, Eli

INTZ, Liat

ALGER, Simchon

ATION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

ATION: THAT POPULATE A TRANSCRIPTOME

IE: 36688-0005

CATION NUMBER: US/09/908,975

IG DATE: 2001-07-20

ATION NUMBER: US 60/287,724

DATE: 2001-05-02

ATION NUMBER: US 60/221,607

DATE: 2000-07-28

ID NOS: 32337

entIn version 3.0

7

mo sapiens

987

71.1%; Score 12.8; DB 10; Length 60;

ilarity 87.5%; Pred. No. 1.6e+04;

Conservative 2; Mismatches 2; Indels 0; Gaps 0;

TTTGGAACTTTGCC 18

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TTTGGTATTTGCC 37

04995

5. Application US/10098263B

US2003010410A1

ATION:

ttman, Michael

ATION: Human Microarray

IE: 3118.1

CATION NUMBER: US/10/098,263B

IG DATE: 2003-01-08

ATION NUMBER: 60/276,759

DATE: 2001-03-16

ID NOS: 131066

roarray Probe Sequence Listing Generator V 1.1

95

mo sapien

.04995

68.9%; Score 12.4; DB 14; Length 25;

ilarity 92.9%; Pred. No. 2.2e+04;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TCATTGGAATTT 14

TTTTTTTTTTTT

TCATTGGAATTT 19

.034

Application US/09754853A

US20030005491A1

ATION:

; APPLICANT: Hauge, Brian M.  
; APPLICANT: Parnell, Laurence D.  
; APPLICANT: Parsons, Jeremy D.  
; APPLICANT: Wang, Ming Li  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules A  
; TITLE OF INVENTION: Soybean Cyst Nematode Resistance  
; FILE REFERENCE: 38-10(15810)B  
; CURRENT APPLICATION NUMBER: US/09/754,853A  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 60/174,880  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 1119  
; SEQ ID NO 1034  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 515002\_region\_G2\_70595\_13\_Reverse\_  
US-03-754-853A-1034

Query Match 68.9%; Score 12.4; DB 10; Length 27;  
Best Local Similarity 92.9%; Pred. No. 2.2e+04;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

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Db 14 TCATTGGAATTTAT 27

RESULT 14

US-10-131-827-958

; Sequence 958, Application US/10131827

; Publication No. US20040009479A1

; GENERAL INFORMATION:

; APPLICANT: Wohlgenuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND

; FILE REFERENCE: 506612000120

; CURRENT APPLICATION NUMBER: US/10/131,827

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764

; PRIOR FILING DATE: 2001-06-08

; NUMBER OF SEQ ID NOS: 9090

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 958

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-131-827-958

Query Match 68.9%; Score 12.4; DB 15; Length 50;

Best Local Similarity 92.9%; Pred. No. 2.4e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 5 TTTGGAATTTTGGC 18

TTTTTTTTTTTT

Db 32 TTTGGAATTTTGGC 45

RESULT 15

US-10-131-827-2943

; Sequence 2943, Application US/10131827

; Publication No. US20040009479A1

; GENERAL INFORMATION:

; APPLICANT: Wohlgenuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

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ENTN: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
ENTN: CHRONIC INFLAMMATORY DISEASES
TE: 506612000120
[CAUTION NUMBER: US/10/131,827
NG DATE: 2002-09-06
ATION NUMBER: US 10/006,290
DATE: 2001-10-22
ATION NUMBER: US 60/296,764
DATE: 2001-06-08
) ID NOS: 9090
entIn version 3.1
;
ymo sapiens
143
    68.9%; Score 12.4; DB 15; Length 50;
ilarity 92.9%; Pred.No.2.4e+04;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;
TATTGGGAATTTT 15
|||||
TATTGGGAATTTT 43
;
1473/c
3, Application US/09908975
3, US20030165843A1
ATION:
HOSHAN, Avi
WASSERMAN, Alon
MINTZ, Eli
MINTZ, Eliat
FAIGLER, Simchon
ENTN: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
ENTN: THAT POPULATE A TRANSCRIPTOME
TE: 36688-0005
[CAUTION NUMBER: US/09/908,975
NG DATE: 2001-07-20
ATION NUMBER: US 60/287,724
DATE: 2001-05-02
ATION NUMBER: US 60/221,607
DATE: 2000-07-28
) ID NOS: 32337
entIn version 3.0
73
ymo sapiens
1473
    68.9%; Score 12.4; DB 10; Length 60;
ilarity 92.9%; Pred.No.2.5e+04;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;
TATTGGGAATTTT 15
|||||
TATTGGGAATTTT 31
;
1262/c
2, Application US/09908975
2, US20030165843A1
ATION:
HOSHAN, Avi
WASSERMAN, Alon
MINTZ, Eli
MINTZ, Eliat
FAIGLER, Simchon
ENTN: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
```

```

; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21262
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-21262

Query Match      68.9%; Score 12.4; DB 10; Length 60;
Best Local Similarity 92.9%; Pred.No.2.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY      5 TTTGGGAATTTTGGCC 18
        |||||
DB      43 TTGGGAATTTTGGCC 30
        |||||

RESULT 18
US-09-784-674-379
; Sequence 379, Application US/09784674
; Publication No. US20030054346A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; Wolber, Paul K.
; Delenstarr, Glenda C.
; Webb, Peter G.
; Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; probe sequences
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Records Manager, Legal Department, Hewlett-
; Company M/S 2080
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,674
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: No. US20030054346A1 available
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/021,701
; FILING DATE: 10-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
```

NSF: NO  
E DESCRIPTION: SEQ ID NO: 379:  
9

ilarity 67.8%; Score 12.2; DB 10; Length 20;  
Conservative 82.4%; Pred. No. 2.7e+04; Mismatches 3; Indels 0; Gaps 0;

CAATTGGAATTTGC 17  
|||||  
ACTTGGAAATTTGC 20

10  
Application US/09784674  
US20030054346A1

INVENTOR: Shannon, Karen W.  
Wolber, Paul K.  
Delenstarr, Glenda C.  
Webb, Peter G.  
Kincaid, Robert H.

OF INVENTION: Methods for evaluating oligonucleotide  
probe sequences

OF SEQUENCES: 1165

ADDRESS: 3000 Hanover Street

RESSEE: Records Manager, Legal Department, Hewlett-Packard  
Company M/S 20B0  
REET: 3000 Hanover Street  
TY: Palo Alto

ATE: CA

UNTRY: USA

P: 94304

R READABLE FORM:

DIUM TYPE: Floppy disk

PUTER: IBM PC compatible

ERATING SYSTEM: PC-DOS/MS-DOS

FTWARE: Patent In Release #1.0, Version #1.30

APPLICATION DATA:

PLICATION NUMBER: US/09/784, 674

LING DATE: 15-Feb-2001

ASSIFICATION: No. US20030054346A1 available

PLICATION DATA:

LING DATE: 10-FEB-1998

Y/AGENT INFORMATION:

ME: Choi, Wendy A.

REGISTRATION NUMBER: 36,697

REFERENCE/DOCKET NUMBER: 10971464-1

MUNICATION INFORMATION:

LEPHONE: 650-236-2386

LEFAX: 650-852-8063

FOR SEQ ID NO: 380:

E CHARACTERISTICS:

NGTH: 20 base pairs

PE: nucleic acid

RANDEDNESS: single

POLOGY: linear

E TYPE: cDNA

TICAL: NO

NSF: NO

E DESCRIPTION: SEQ ID NO: 380:

0

ilarity 67.8%; Score 12.2; DB 10; Length 20;  
Conservative 82.4%; Pred. No. 2.7e+04; Mismatches 3; Indels 0; Gaps 0;

CAATTGGAATTTGC 17  
|||||  
ACTTGGAAATTTGC 19

## RESULT 20

US-09-784-674-381  
; Sequence 381, Application US/09784674  
; Publication No. US20030054346A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Karen W.  
; Wolber, Paul K.  
; Delenstarr, Glenda C.  
; Webb, Peter G.  
; Kincaid, Robert H.  
; TITLE OF INVENTION: Methods for evaluating oligonucleotide  
; probe sequences  
; NUMBER OF SEQUENCES: 1165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Records Manager, Legal Department, Hewlett-  
; STREET: 3000 Hanover Street  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/784, 674  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: No. US20030054346A1 available  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/021,701  
; FILING DATE: 10-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Choi, Wendy A.  
; REGISTRATION NUMBER: 36,697  
; REFERENCE/DOCKET NUMBER: 10971464-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-236-2386  
; TELEFAX: 650-852-8063  
; INFORMATION FOR SEQ ID NO: 381:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 381:  
US-09-784-674-381

Query Match 67.8%; Score 12.2; DB 10; Length 20;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CTCATTTGGAATTTGC 17

Db 2 CTACTTTGGAATATTGC 18

## RESULT 21

US-09-784-674-382  
; Sequence 382, Application US/09784674  
; Publication No. US20030054346A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Karen W.  
; Wolber, Paul K.  
; Delenstarr, Glenda C.  
; Webb, Peter G.  
; Kincaid, Robert H.  
; TITLE OF INVENTION: Methods for evaluating oligonucleotide

1 09:38:22 2004

us-10-090-326-16.max.rnpb

probe sequences

OF SEQUENCES: 1165  
PONDENSE ADDRESS:  
DRESSENSE: Records Manager, Legal Department, Hewlett-Packard  
Company M/S 20BO  
TREET: 3000 Hanover Street  
ITY: Palo Alto  
TATE: CA  
COUNTRY: USA

IP: 94304  
ER READABLE FORM:  
EDIU TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
PERATING SYSTEM: PC-DOS/MS-DOS  
FTWARE: Patentin Release #1.0, Version #1.30  
T APPLICATION DATA:

PLICATION NUMBER: US/09/784,674  
ILING DATE: 15-Feb-2001  
LASSIFICATION: No. US20030054346A1 available  
APPLICATION DATA:  
PLICATION NUMBER: 09/021,701  
ILING DATE: 10-FEB-1998  
Y/AGENT INFORMATION:  
AME: Choi, Wendy A.  
EGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
MMUNICATION INFORMATION:  
ELEPHONE: 650-236-2386  
ELEFAX: 650-852-8063  
FOR SEQ ID NO: 382:  
CE CHARACTERISTICS:  
ENGTH: 20 base pairs  
YPE: nucleic acid  
TRANDEDNESS: single  
OLOLOGY: linear  
LE TYPE: cDNA  
ETICAL: NO

ENSE: NO  
CE DESCRIPTION: SEQ ID NO: 382:  
82

67.8%; Score 12.2; DB 10; Length 20;  
nilarity 82.4%; Pred. No. 2.7e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGGAATTTGCC 17  
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TACTTGGGAATTTGCC 17

Application US/10177573  
S. US20030236206A1  
ATION:

asan M. Freier  
ENTION: ANTISENSE MODULATION OF PPP3R1 EXPRESSION  
TE: PTS-0364  
ICATION NUMBER: US/10/177,573  
NG DATE: 2002-06-20  
Q ID NOS: 104

rtificial Sequence  
ATION: Antisense Oligonucleotide

67.8%; Score 12.2; DB 15; Length 20;  
nilarity 82.4%; Pred. No. 2.7e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGGAATTTGCC 18  
|||||  
TCTTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

Query Match 67.8%; Score 12.2; DB 14; Length 22;  
Best Local Similarity 82.4%; Pred. No. 2.7e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGGAATTTGCC 18  
Db 2 TCGTTTGTAAATTTGCC 18

plication US/10082546  
US20030165868A1  
RMATION:

NT: Lacroix, Jean-Michel

F INVENTION: METHOD AND KIT FOR QUANTITATION AND  
NUCLEIC ACID SEQUENCING OF NUCLEIC ACID ANALYTES IN A SAMPL

OF SEQUENCES: 7

DRESSEE: Oppedahl & Larson

REET: PO Box 5088

TY: Dillon

ATE: CO

UNTRY: US

P: 80435-5068

DUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage

MPUTER: IBM compatible

ERATING SYSTEM: MS DOS

FTWARE: Word Perfect

APPLICATION DATA:

PLICATION NUMBER: US/10/082,546

LING DATE: 25-Feb-2002

ASSIFICATION: <Unknown>

PLICATION DATA:

PLICATION NUMBER: <Unknown>

LING DATE: <Unknown>

Y/AGENT INFORMATION:

ME: Larson, Marina T.

ISTRATION NUMBER: 32,038

ERENCE/DOCKET NUMBER: VGEN.P-054

MUNICATION INFORMATION:

LEPHONE: 970 468 6600

LEFAX: 970 468 0104

LEX: <Unknown>

FOR SEQ ID NO: 5:

E CHARACTERISTICS:

NGTH: 27

PE: nucleic acid

RANDEDNESS: single

POLOGY: linear

E TYPE: other nucleic acid

TICAL: NO

NSE: NO

T TYPE: internal

L SOURCE:

GANISM: HIV-1

E DESCRIPTION: SEQ ID NO: 5:

67.8%; Score 12.2; DB 14; Length 27;  
ilarity 82.4%; Pred. No. 2.8e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTGGGAATTTCG 17  
|||||  
ACTTTGGGATATTGC 18

plication US/09766095  
0020062016A1  
RMATION:

NT: Sherrol H. McDonough, Thomas B. Ryder,

Yeastang Yang

F INVENTION: NUCLEIC ACID AMPLIFICATION  
OLIGONUCLEOTIDES AND PROBES

TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

OF SEQUENCES: 139

ONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,095

FILING DATE: 18-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/013,406

FILING DATE: 26-JAN-01

APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07

FILING DATE: 10-Jul-90

APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07

FILING DATE: 11-Jul-89

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 196/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-766-095-16

Query Match 67.8%; Score 12.2; DB 9; Length 36;  
Best Local Similarity 82.4%; Pred. No. 2.9e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CTCATTGGGAATTTCG 17  
|||  
Db 1 CTACTTTGGGATATTGC 17  
|||

RESULT 27

US-09-766-095-96/c

; Sequence 96, Application US/09766095

; Patent No. US20020062016A1

; GENERAL INFORMATION:

; APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,

; Yeasing Yang

; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION  
OLIGONUCLEOTIDES AND PROBES

; TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

; NUMBER OF SEQUENCES: 139

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 611 West Sixth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: USA

; ZIP: 90017

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,095



BILLING DATE: 18-Jan-2001  
 CLASSIFICATION: <Unknown>  
 APPLICATION DATA:  
 APPLICATION NUMBER: 09/013,406  
 BILLING DATE: 26-JAN-01  
 APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/550,837  
 BILLING DATE: 10-JUL-90  
 APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501  
 BILLING DATE: 11-Jul-89  
 APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501  
 AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 196/189  
 COMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELETYPE: 67-3510  
 FOR SEQ ID NO: 96:  
 CE CHARACTERISTICS:  
 LENGTH: 36  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 CE DESCRIPTION: SEQ ID NO: 96:

67.8%; Score 12.2; DH 9; Length 36;  
milarity 82.4%; Pred. No. 2.9e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGAATTTC 17  
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TACTTGGAATATTC 20

33 Application US/09766095  
20020062016A1  
PRIORITY:  
INVENTOR: SHERIOL H. McDONOUGH, Thomas B. Ryder,  
ANT: Yeasing Yang  
OF INVENTION: OLIGONUCLEOTIDES AND PROBES  
TO HUMAN IMMUNODEFICIENCY VIRUS  
OF SEQUENCES: 139  
PONDENCE ADDRESS:  
ADDRESS: Lyon & Lyon  
FREET: 611 West Sixth Street  
ITY: Los Angeles  
TATE: California  
UNTRY: USA  
IP: 90017

```

3R READABLE FORM:
3DIUM TYPE: 3.5" Diskette, 1.44 Mb storage
3MPUTER: IBM PS/2 Model 502 or 55SX
3REATING SYSTEM: IBM P.C. DOS (Version 3.30)
3FTWARE: WordPerfect (Version 5.0)
3 APPLICATION DATA:
3 APPLICATION NUMBER: US/09/766,095
3ILING DATE: 18-Jan-2001
3ASSIFICATION: <Unknown>
3 APPLICATION DATA:
3 APPLICATION NUMBER: 09/013,406
3ILING DATE: 26-JAN-01
3ILING NUMBER: U.S. Serial No. US20020062016A1 07/550,837
3ILING DATE: 10-Jul-90
3 APPLICATION NUMBER: U.S. Serial No. US20020062016A1 07/379,501
3ILING DATE: 11-Jul-89
3Y/AGENT INFORMATION:
3AME: Warburg, Richard J.
3GISTRATION NUMBER: 32,327
3REFERENCE/DOCKET NUMBER: 196/189

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-09-766-095-133

Query Match 67.8%; Score 12.2; DB 9; Length 36;
Best Local Similarity 41.2%; Pred. No. 2.9e+04;
Matches 7; Conservative 7; Mismatches 3; Indels 0;

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**OY**

1 CTCATTGTGGAATTTTGC 17  
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**D<sub>b</sub>**

1 CUACUUUGGAAUAUUGC 17

RESULT 29

US-09-766-095-137/c  
; Sequence 137, Application US/09766095  
; Patent No. US20020062016A1  
; GENERAL INFORMATION:

APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,  
Yeasing Yang

Accession Number	Title of Invention: Nucleic Acid Amplification Oligonucleotides and Probes to Human Immunodeficiency Virus Type 1	Number of Sequences: 139
U00001		

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CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/766,095  
 FILING DATE: 10 FEB 2001

FILING DATE: 18-Jan-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/013,406

REFLECTION NUMBER: 097013,408  
FILING DATE: 26-JAN-01  
APPLICATION NUMBER: U.S. Serial

;;	FILING DATE:	10-Jul-90
;;	APPLICATION NUMBER:	U.S. Serial No. US20020062016A1
;;	APPLICATION NUMBER:	U.S. Serial No. US20020062016A1

APPLICATION NUMBER: U.S. Serial N  
FILING DATE: 11-Jul-89

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J

NAME: WALDUIG, RICHARD O.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 196/189

REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 480-1600

TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 137:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36

LENGTH: 36  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE	DESCRIPTION	SEQ ID NO
137		

US-C9-766-095-137

67.8%; Score 12.2; DB 9; Length 36;  
ilarity 82.4%; Pred. No. 2.9e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
TCATTGGAATTTGTC 17  
|||||  
ACTTTGGAATTTGTC 20  
/c  
application US/10379836  
US20030215850A1  
ATION:  
iscol-Kyers Squibb Company  
ATION: NOVEL NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING BABOON  
ATION: TAFI  
E: D0214NP  
CATION NUMBER: US/10/379,836  
G DATE: 2003-03-04  
ATION NUMBER: U.S. 60/361,523  
DATE: 2002-03-04  
ID NOS: 24  
entIn version 3.2

## pio hamadryas

67.8%; Score 12.2; DB 15; Length 37;  
ilarity 82.4%; Pred. No. 2.9e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ATTGGAATTTGCC 18  
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ATTAGGAATTTGTC 10

2/c  
Application US/09747377  
US20030022255A1  
ATION:

ris, David  
ATION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER

E: A-69959/RMS/DCF  
CATION NUMBER: US/09/747,377  
3 DATE: 2000-12-22  
ID NOS: 493

entIn version 3.0

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67.8%; Score 12.2; DB 10; Length 39;  
ilarity 82.4%; Pred. No. 2.9e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGAATTTGTC 17  
|||||  
CATTATAATTTGTC 14

2/c  
Application US/10105613  
US2003009963A1  
ATION:

ris, David  
ATION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER

FILE REFERENCE: A-69959/RMS/DCF  
CURRENT APPLICATION NUMBER: US/10/105,613  
CURRENT FILING DATE: 2002-03-20  
PRIOR APPLICATION NUMBER: US/09/747,377  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 493  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 472  
LENGTH: 39  
TYPE: DNA  
ORGANISM: Mus sp.  
US-10-105-613-472

Query Match 67.8%; Score 12.2; DB 14; Length 39;  
Best Local Similarity 82.4%; Pred. No. 2.9e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAAATTTGTC 17  
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Db 30 CACATTATAATTTGTC 14

## RESULT 33

US-10-443-694-80  
Sequence 80, Application US/10443694  
Publication No. US20040001846A1  
GENERAL INFORMATION:  
APPLICANT: Israeli, Ron S  
APPLICANT: Heston, Warren D.W.  
APPLICANT: Fair, William R  
APPLICANT: Overfelli, Ouathak  
APPLICANT: Pinto, John  
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES T  
FILE REFERENCE: 1769/41426-GB  
CURRENT APPLICATION NUMBER: US/10/443,694  
CURRENT FILING DATE: 2003-05-21  
PRIOR APPLICATION NUMBER: US 08/705,477  
PRIOR FILING DATE: 1996-08-29  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 80  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-443-694-80

Query Match 67.8%; Score 12.2; DB 15; Length 40;  
Best Local Similarity 82.4%; Pred. No. 2.9e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 2 TCATTGGAAATTTGCC 18  
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Db 8 TCATTGGTATGTACC 24

## RESULT 34

US-10-131-827-2575/c  
Sequence 2575, Application US/10131827  
Publication No. US20040009479A1  
GENERAL INFORMATION:  
APPLICANT: Wohlgenuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND M  
FILE REFERENCE: 506612000120  
CURRENT APPLICATION NUMBER: US/10/131,827  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US 10/006,290  
PRIOR FILING DATE: 2001-10-22  
PRIOR APPLICATION NUMBER: US 60/296,764  
PRIOR FILING DATE: 2001-06-08

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us-10-090-326-16.max.rnpb

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; ID NOS: 9090
; entIn version 3.1

mo sapiens
175
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;CATTTGGAATTTGTC 17
| | | | | | | | | |
;CCTTTAGAAATTTTAC 25

;47
    Application US/10131827
    . US20040009479A1
    IATION:
    hlgemuth, Jay
    Fry, Kirk
    Woodward, Robert
    y, Ngoc
    IENT: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
    ENTION: CHRONIC INFLAMMATORY DISEASES
    E: 506612000120
    IATION NUMBER: US/10/131,827
    NG DATE: 2002-09-06
    IATION NUMBER: US 10/006,290
    DATE: 2001-10-22
    IATION NUMBER: US 60/296,764
    DATE: 2001-06-08
    ID NOS: 9090
    :entIn version 3.1
;

mo sapiens
347
    67.8%; Score 12.2; DB 15; Length 50;
    ilarity 82.4%; Pred. No. 3e+04; 3; Indels 0; Gaps 0;
    Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;CATTTGGAATTTGTC 17
| | | | | | | | | |
;CATTTGGAATTTGTC 46

182/c
    Application US/10131827
    . US20040009479A1
    IATION:
    hlgemuth, Jay
    Fry, Kirk
    Woodward, Robert
    y, Ngoc
    IENT: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
    ENTION: CHRONIC INFLAMMATORY DISEASES
    E: 506612000120
    IATION NUMBER: US/10/131,827
    NG DATE: 2002-09-06
    IATION NUMBER: US 10/006,290
    DATE: 2001-10-22
    IATION NUMBER: US 60/296,764
    DATE: 2001-06-08
    ID NOS: 9090
    :entIn version 3.1
;

mo sapiens
347
    67.8%; Score 12.2; DB 15; Length 50;
    ilarity 82.4%; Pred. No. 3e+04; 3; Indels 0; Gaps 0;
    Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;CATTTGGAATTTGTC 17
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;CATTTGGAATTTGTC 46
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; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-5482

Query Match      67.8%; Score 12.2; DB 15; Length 50;
Best Local Similarity 82.4%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTTCGAATTTGTC 17
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DB 49 CTCATTTCGCAGTTTTC 33

RESULT 37
US-10-131-827-6631
; Sequence 6631, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND
; FILE REFERENCE: 506612000120
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6631
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-6631

Query Match      67.8%; Score 12.2; DB 15; Length 50;
Best Local Similarity 82.4%; Pred. No. 3e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTTCGAATTTGTC 17
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DB 3 CTGATTTCGAATTTGTC 19

RESULT 38
US-10-131-827-7021/c
; Sequence 7021, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND
; FILE REFERENCE: 506612000120
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7021
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
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21

ilarity 67.8%; Score 12.2; DB 15; Length 50;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTGGGAATTTGC 17  
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3ATTTGGATTTCTGC 32

/c  
plication US/10298796

US20030220490A1  
ATION:  
RIYAMA, Shinichi  
ASEGAWA, Takashi  
NTION: CELL MEMBRANE DIRECTED DRUGS  
E: 1110-253P  
CATION NUMBER: US/10/298,796  
3 DATE: 2002-11-19  
TION NUMBER: US/09/331,793  
DATE: 1999-06-25  
ID NOS: 67  
entIn version 3.0

nthetic DNA Primers

ilarity 67.8%; Score 12.2; DB 15; Length 59;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTGGGAATTTGC 17  
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TTTTTGGGAATTTGC 37

79 Application US/09908975

US20030165843A1  
ATION:  
OSHAN, Avi  
ASSERMAN, Alon  
INTZ, Eli  
INTZ, Liat  
AIGLER, Simchon  
NTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
TION: THAT POPULATE A TRANSCRIPTOME  
E: 36688-0005  
CATION NUMBER: US/09/908,975  
G DATE: 2001-07-20  
TION NUMBER: US 60/287,724  
DATE: 2001-05-02  
TION NUMBER: US 60/221,607  
DATE: 2000-07-28  
ID NOS: 32337  
entIn version 3.0

mo sapiens  
79

ilarity 67.8%; Score 12.2; DB 10; Length 60;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTGGGAATTTGC 17

Db 34 CACCAATGGGAATTTGC 50  
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RESULT 41

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; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRA  
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 19813  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-19813

Query Match 67.8%; Score 12.2; DB 10; Length 60;  
Best Local Similarity 82.4%; Pred. No. 3.1e+04;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 2 TCATTTCGAATTTTGGC 18  
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Db 45 TCACTTAGAATTTTACC 29

RESULT 42

US-10-123-101-75/c  
; Sequence 75, Application US/10123101  
; Publication No. US20030148262A1  
; GENERAL INFORMATION:  
; APPLICANT: POLO, John  
; APPLICANT: PERRI, Silvia  
; APPLICANT: THUDIUM, Kent  
; TITLE OF INVENTION: CHIMERIC ALPHAVIRUS REPLICON PARTICLES  
; FILE REFERENCE: 2300-17924 / PFI7924.002  
; CURRENT APPLICATION NUMBER: US/10/123,101  
; CURRENT FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: 60/295,451  
; PRIOR FILING DATE: 2001-05-31  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.0  
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; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: WEE  
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Matches 14; Conservative 0; Mismatches 3; Indels 0;

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|||||  
Db 18 TCAGTTGGGAATTTGAC 2

09:38:22 2004

us-10-090-326-16.max.rnpb

ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,445  
REFERENCE/DOCKET NUMBER: PB248PP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 2738:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 53 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-2738  
Query Match 66.7%; Score 12; DB 8; Length 53;  
Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;

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Db 29 ATTTGGAAATTTT 40

Search completed: February 29, 2004, 13:42:55  
Job time : 121.571 secs

Application US/10298796  
US20030220490A1  
ATTON:  
RIYAMA, Shinichi  
ASEGAWA, Takashi  
NTION: CELL MEMBRANE DIRECTED DRUGS  
E: 1110-253P  
CATION NUMBER: US/10/298,796  
G DATE: 2002-11-19  
TION NUMBER: US/09/331,793  
DATE: 1999-06-25  
ID NOS: 67  
entIn version 3.0

nthetic Synthetic DNA Primers

67.8%; Score 12.2; DB 15; Length 60;  
ilarity 82.4%; Pred. No. 3.1e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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TTTTCGAATTTTGC 27

5/c  
Application US/10310734  
US20030232324A1  
ATTON:  
LO, John  
ERRI, Silvia  
HUDIUM, Kent  
ANG, Zequn  
NTION: CHIMERIC ALPHAVIRUS REPLICON PARTICLES  
E: CHR-17924/02US (2300-17924.20)  
CATION NUMBER: US/10/310,734  
G DATE: 2002-12-04  
TION NUMBER: 10/123,101  
DATE: 2002-04-11  
ID NOS: 125  
entIn Ver. 2.0

tificial Sequence

NTION: Description of Artificial Sequence: WEE  
35

67.8%; Score 12.2; DB 15; Length 60;  
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Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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CAGTTTGAATGTGAC 2

2738  
, Application US/08781986A  
O. US20030054436A1  
RMATION:  
Charles Kunsch  
NVENTION: Staphylococcus aureus Polynucleotides and Sequences  
SEQUENCES: 5255  
ENCE ADDRESS:

09:38:23 2004

us-10-090-326-16.max.rst

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

.eic search, using sw model

February 29, 2004, 08:43:19 ; Search time 1351.17 Seconds  
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397.818 Million cell updates/sec

JS-10-090-326-16

l ctcatattggaatttggcc 18

IDENTITY NUC

hapop 10.0 , Gapext 1.0

37513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 203984

anght: 0

anght: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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1: em\_estba:\*

2: em\_esthm:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vit:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

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64.4	49	28	CC040486	CC040486 3591.1.13	C 153	10.8	60.0	36	28	AZ767524	AZ767524
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64.4	57	10	AW638114	AW638114 B166C09.w	C 156	10.8	60.0	38	9	AU252860	AU252860
64.4	58	28	BH902719	BH902719 SALK_0988	C 157	10.8	60.0	40	28	AZ300900	AZ300900
64.4	59	28	AL940439	AL940439 Arabidops	C 158	10.8	60.0	42	28	AZ972457	AZ972457
64.4	59	12	BJ082885	BJ082885 BJ082885	C 159	10.8	60.0	43	9	AI867888	AI867888
64.4	24	13	BQ589506	BQ589506 E012561-0	C 160	10.8	60.0	43	28	AZ778538	AZ778538
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63.3	37	29	AL938056	AL938056 Arabidops	C 163	10.8	60.0	44	28	BH903740	BH903740
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63.3	48	28	BH814703	BH814703 SALK_0668	C 166	10.8	60.0	44	29	AL943922	AL943922
63.3	48	28	BH907079	BH907079 SALK_0380	C 167	10.8	60.0	45	28	BZ382481	BZ382481
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63.3	53	28	BH892901	BH892901 3526.1.22	C 171	10.8	60.0	46	14	H71330.Y	H71330.Y
63.3	53	28	BH910961	BH910961 SALK_0637	C 172	10.8	60.0	46	28	AZ822694	AZ822694
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62.2	29	28	BZ762504	BZ762504 SALK_1050	C 179	10.8	60.0	49	9	AA995234	AA995234
62.2	30	28	AZ437578	AZ437578 1M0225124	C 180	10.8	60.0	49	9	AI802512	AI802512
62.2	31	28	BH811601	BH811601 SALK_0591	C 181	10.8	60.0	49	12	BJ066503	BJ066503
62.2	31	28	BH856486	BH856486 SALK_0796	C 182	10.8	60.0	50	9	AU106907	AU106907
62.2	31	28	BZ356958	BZ356958 SALK_1300	C 183	10.8	60.0	50	28	BZ665284	BZ665284
62.2	31	28	BZ380225	BZ380225 SALK_1148	C 184	10.8	60.0	52	9	A1203654	A1203654
62.2	34	28	BH812106	BH812106 SALK_0611	C 185	10.8	60.0	52	13	BQ633508	BQ633508
62.2	35	28	AZ764339	AZ764339 1M0560C17	C 186	10.8	60.0	53	9	AU264971	AU264971
62.2	35	28	BH862829	BH862829 SALK_0906	C 187	10.8	60.0	53	13	BX558179	BX558179
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62.2	38	28	AZ632696	AZ632696 1M0487B03	C 190	10.8	60.0	53	29	AL771776	AL771776
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62.2	43	9	AI189940	AI189940 q33h08.x	C 193	10.8	60.0	55	14	H70860	H70860
62.2	45	29	CG796721	CG796721 SALK_1369	C 194	10.8	60.0	55	28	BZ381950	BZ381950
62.2	47	28	BZ763653	BZ763653 SALK_1200	C 195	10.8	60.0	55	28	AL754918	AL754918
62.2	49	9	AA699686	AA699686 zi78d08.s	C 196	10.8	60.0	55	29	AL754920	AL754920
62.2	50	13	BQ482029	BQ482029 ke48a10.Y	C 197	10.8	60.0	55	29	AL754922	AL754922
62.2	50	28	CC455184	CC455184 SALK_0621	C 198	10.8	60.0	55	29	BX659250	BX659250
62.2	51	9	AA529767	AA529767 vj12a02.r	C 200	10.8	60.0	56	28	BJ082374	BJ082374
62.2	51	12	BG650265	BG650265 sad04d07.r	C 201	10.8	60.0	56	28	AZ489069	AZ489069
62.2	52	10	BF650045	BF650045 NF084F07E	C 202	10.8	60.0	56	28	BZ380334	BZ380334
62.2	52	14	H94540	H94540 YW55903.r1	C 203	10.8	60.0	57	9	AV519777	AV519777
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62.2	54	29	TA85G06Q	TA85G06Q T. brucei	C 205	10.8	60.0	57	28	B03191	B03191
62.2	55	14	CF384789	CF384789 caa11C04.	C 206	10.8	60.0	58	10	AW513497	AW513497
62.2	55	28	BH640205	BH640205 1008034E0	C 207	10.8	60.0	58	12	BM186981	BM186981
62.2	56	28	CC887254	CC887254 SALK_1498	C 208	10.8	60.0	58	14	CB280990	CB280990
62.2	57	28	AZ400478	AZ400478 1M0166J13	C 209	10.8	60.0	58	28	AZ65186	AZ65186
62.2	57	28	BH812624	BH812624 SALK_0622	C 210	10.8	60.0	58	28	BH847562	BH847562
62.2	58	9	AA935194	AA935194 ty39b06.s	C 211	10.8	60.0	58	28	BH854716	BH854716
62.2	58	9	AI375271	AI375271 tcl1C09.x	C 212	10.8	60.0	58	29	CC795493	CC795493
62.2	59	9	AA913781	AA913781 ol35a06.s	C 213	10.8	60.0	58	29	BX242864	BX242864
62.2	59	14	CB337952	CB337952 laa31907.	C 214	10.8	60.0	59	12	B1749057	B1749057
62.2	60	29	CG720713	CG720713 1119063E1	C 215	10.8	60.0	59	13	BH700798	BH700798
61.1	45	28	BH811345	BH811345 SALK_0584	C 216	10.8	60.0	59	28	BH789276	BH789276
61.1	52	29	BX651475	BX651475 Arabidops	C 217	10.8	60.0	59	28	BZ770038	BZ770038
61.1	53	28	AQ050186	AQ050186 nbxb0003C	C 218	10.8	60.0	59	29	AG222255	AG222255
61.1	55	9	AA184777	AA184777 hum47d10.r	C 219	10.8	60.0	59	29	BX893417	BX893417
61.1	57	13	C02505	C02505 HUMGS001239	C 220	10.8	60.0	60	9	AA587501	AA587501
61.1	60	12	BM283609	BM283609 ki49906.Y	C 221	10.8	60.0	60	12	B1492703	B1492703
60.0	22	28	BH853424	BH853424 SALK_0769	C 222	10.8	60.0	60	29	AG212685	AG212685
60.0	24	28	AZ763574	AZ763574 1M0559P01	C 223	10.6	58.9	21	28	AZ442520	AZ442520
60.0	25	28	AZ794346	AZ794346 2M0048P01							

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58.9	30	28	BH814304	SALK_0661	BH814304	SALK_0661	10.4	57.8	42	29	AG227149	AG227149
58.9	33	28	BZ592037	SALK_0911	BZ592037	SALK_0911	10.4	57.8	43	28	BZ592815	BZ592815
58.9	33	28	BZ594009	SALK_0825	BZ594009	SALK_0825	10.4	57.8	45	9	AU007314	AU007314
58.9	34	28	BH810792	SALK_0512	BH810792	SALK_0512	10.4	57.8	45	29	AL942241	AL942241
58.9	35	28	BH813890	SALK_0654	BH813890	SALK_0654	10.4	57.8	45	29	BX651940	BX651940
58.9	35	28	BH864447	SALK_0960	BH864447	SALK_0960	10.4	57.8	46	28	AZ767539	AZ767539
58.9	37	28	BZ356214	SALK_1284	BZ356214	SALK_1284	10.4	57.8	46	28	BH810374	BH810374
58.9	37	28	BZ664670	SALK_0997	BZ664670	SALK_0997	10.4	57.8	46	28	BH909441	BH909441
58.9	39	29	CC987215	SALK_1497	CC987215	SALK_1497	10.4	57.8	47	29	TA290H07P	TA290H07P
58.9	42	9	AA936922	om55c08.s	AA936922	om55c08.s	10.4	57.8	48	14	D18685	D18685
58.9	42	28	BZ766600	SALK_1376	BZ766600	SALK_1376	10.4	57.8	48	28	BH903352	BH903352
58.9	45	28	BZ597593	SALK_1099	BZ597593	SALK_1099	10.4	57.8	48	28	BH903352	BH903352
58.9	46	9	AA015178	mh33h08.r	AA015178	mh33h08.r	10.4	57.8	48	29	AB004335	AB004335
58.9	46	9	AA023270	mh69g09.r	AA023270	mh69g09.r	10.4	57.8	48	29	AL761058	AL761058
58.9	46	9	AA291212	zsl8b12.s	AA291212	zsl8b12.s	10.4	57.8	49	9	AI003826	AI003826
58.9	46	29	BX651777	ArabiDops	BX651777	ArabiDops	10.4	57.8	49	13	BQ625383	BQ625383
58.9	47	28	BH792501	SALK_0646	BH792501	SALK_0646	10.4	57.8	49	29	BX658124	BX658124
58.9	47	28	BZ379658	SALK_1136	BZ379658	SALK_1136	10.4	57.8	50	29	AG245332	AG245332
58.9	48	28	BH807683	SALK_1008073A0	BH807683	SALK_1008073A0	10.4	57.8	50	29	BX247174	BX247174
58.9	48	28	BH851465	SALK_0730	BH851465	SALK_0730	10.4	57.8	51	28	AZ461131	AZ461131
58.9	48	29	TA373C08P	AL496396 T. brucei	TA373C08P	AL496396 T. brucei	10.4	57.8	51	28	BZ770848	BZ770848
58.9	49	9	AL747625	ul19d03.x	AL747625	ul19d03.x	10.4	57.8	52	9	AA989862	AA989862
58.9	49	29	AL767455	ArabiDops	AL767455	ArabiDops	10.4	57.8	52	10	AW168312	AW168312
58.9	49	29	BX661638	ArabiDops	BX661638	ArabiDops	10.4	57.8	52	28	AZ609402	AZ609402
58.9	50	28	BH904193	SALK_1041	BH904193	SALK_1041	10.4	57.8	53	12	BM513499	BM513499
58.9	50	28	CC020659	3591_1_20	CC020659	3591_1_20	10.4	57.8	53	13	BQ479354	BQ479354
58.9	50	29	BX004572	ArabiDops	BX004572	ArabiDops	10.4	57.8	53	13	BX569249	BX569249
58.9	52	12	BG153633	nag51h03	BG153633	nag51h03	10.4	57.8	54	12	B1101893	B1101893
58.9	52	12	BM432542	1JEF10F6	BM432542	1JEF10F6	10.4	57.8	54	28	BH903653	BH903653
58.9	52	14	H04947	yJ5id09.sl	H04947	yJ5id09.sl	10.4	57.8	54	29	AG227150	AG227150
58.9	53	28	BZ292415	SALK_1242	BZ292415	SALK_1242	10.4	57.8	55	9	AI202030	AI202030
58.9	53	28	CC458856	SALK_1222	CC458856	SALK_1222	10.4	57.8	55	9	AU011483	AU011483
58.9	53	29	AL767456	ArabiDops	AL767456	ArabiDops	10.4	57.8	55	12	BI946339	BI946339
58.9	53	28	BX890894	ArabiDops	BX890894	ArabiDops	10.4	57.8	55	29	CC486853	CC486853
58.9	54	28	BH848588	SALK_0685	BH848588	SALK_0685	10.4	57.8	55	29	AG218047	AG218047
58.9	55	10	AW168527	x188a12.x	AW168527	x188a12.x	10.4	57.8	55	29	CNS01185	CNS01185
58.9	55	12	BI451246	TI7618	BI451246	TI7618	10.4	57.8	56	13	BQ541507	BQ541507
58.9	56	14	AZ485389	LM0312H16	AZ485389	LM0312H16	10.4	57.8	56	14	CD683079	CD683079
58.9	56	28	AZ514492	LM0361G23	AZ514492	LM0361G23	10.4	57.8	56	28	AZ423790	AZ423790
58.9	56	29	AL760048	ArabiDops	AL760048	ArabiDops	10.4	57.8	56	28	BH415166	BH415166
58.9	56	29	BX002873	ArabiDops	BX002873	ArabiDops	10.4	57.8	56	28	AA389623	AA389623
58.9	57	9	AU264614	AU264614	AU264614	AU264614	10.4	57.8	57	9	AZ655595	AZ655595
58.9	57	12	BI676989	ic67h08.Y	BI676989	ic67h08.Y	10.4	57.8	57	28	B07121	B07121
58.9	57	28	BZ358275	SALK_1321	BZ358275	SALK_1321	10.4	57.8	57	28	AL760328	AL760328
58.9	58	9	AU007255	AU007255	AU007255	AU007255	10.4	57.8	57	29	BX892964	BX892964
58.9	58	12	B035240	B035240	B035240	B035240	10.4	57.8	58	14	T73609	T73609
58.9	58	28	B44722	HS-1059-B2-	B44722	HS-1059-B2-	10.4	57.8	58	14	AA683173	AA683173
58.9	58	28	BH229733	1006154A1	BH229733	1006154A1	10.4	57.8	59	9	AL847347	AL847347
58.9	58	28	BH813934	SALK_0654	BH813934	SALK_0654	10.4	57.8	59	14	CF801181	CF801181
58.9	58	28	BH852423	SALK_0746	BH852423	SALK_0746	10.4	57.8	59	28	BZ660742	BZ660742
58.9	60	10	B0203589	sm82e03.Y	B0203589	sm82e03.Y	10.4	57.8	59	29	AB081870	AB081870
58.9	60	14	CB298245	220026.re	CB298245	220026.re	10.4	57.8	60	13	BX742108	BX742108
58.9	60	28	BH789193	SALK_0009	BH789193	SALK_0009	10.4	57.8	60	14	CB827830	CB827830
58.9	60	28	BH863067	SALK_0930	BH863067	SALK_0930	10.4	57.8	60	29	BX293252	BX293252
58.9	60	28	BZ291651	SALK_1215	BZ291651	SALK_1215	10.4	57.8	60	29	BX655884	BX655884
58.9	60	28	BZ291392	AU013927	BZ291392	AU013927	10.4	57.8	60	28	AZ433830	AZ433830
58.9	60	28	AQ073689	EP(2)2563	AQ073689	EP(2)2563	10.2	56.7	21	9	AU013584	AU013584
58.9	60	28	AZ411545	LM0184H07	AZ411545	LM0184H07	10.2	56.7	21	13	BX551680	BX551680
58.9	60	28	BH853496	SALK_0770	BH853496	SALK_0770	10.2	56.7	25	9	AI000229	AI000229
58.9	60	28	AZ610538	LM0435E23	AZ610538	LM0435E23	10.2	56.7	25	28	AZ414362	AZ414362
58.9	60	28	AU243401	AU243401	AU243401	AU243401	10.2	56.7	25	28	AZ805210	AZ805210
58.9	60	28	BH814123	SALK_0657	BH814123	SALK_0657	10.2	56.7	25	28	AZ346666	AZ346666
58.9	60	28	CC798589	SALK_1465	CC798589	SALK_1465	10.2	56.7	26	28	AZ469300	AZ469300
58.9	60	28	BJ050429	BJ050429	BJ050429	BJ050429	10.2	56.7	26	28	BH810217	BH810217
58.9	60	28	CC792786	SALK_0010	CC792786	SALK_0010	10.2	56.7	27	28	TA55F11Q	TA55F11Q
58.9	60	28	BZ380454	SALK_1151	BZ380454	SALK_1151	10.2	56.7	27	28	AZ331611	AZ331611
58.9	60	28	BX568339	BX568339	BX568339	BX568339	10.2	56.7	28	28	AZ599541	AZ599541
58.9	60	28	AU259419	AU259419	AU259419	AU259419	10.2	56.7	29	28	AZ762588	AZ762588
58.9	60	28	BZ358737	SALK_1332	BZ358737	SALK_1332	10.2	56.7	29	28	BZ377688	BZ377688
58.9	60	28	BZ766230	SALK_1169	BZ766230	SALK_1169	10.2	56.7	29	28		
58.9	60	28	CC798587	SALK_1465	CC798587	SALK_1465	10.2	56.7	29	28		



56.7	30	13	BX625353	443	10.2	56.7	51	28	BZ380783	BZ380783
56.7	30	28	AZ401335	C 444	10.2	56.7	52	9	AI654461	AI654461
56.7	30	29	DM546253	C 445	10.2	56.7	52	10	BF636249	BF636249
56.7	31	9	AI057173	C 446	10.2	56.7	52	10	BF213416	BF213416
56.7	31	9	AI057173	C 447	10.2	56.7	52	14	T80648	T80648
56.7	32	28	BZ290702	C 448	10.2	56.7	52	28	AZ776478	AZ776478
56.7	32	29	DM545760	C 449	10.2	56.7	52	28	AZ447221	AZ447221
56.7	33	29	AG253538	C 450	10.2	56.7	53	28	AZ487502	AZ487502
56.7	33	29	AG253538	C 451	10.2	56.7	53	28	BH812711	BH812711
56.7	33	29	AI760357	C 452	10.2	56.7	53	28	BH849882	BH849882
56.7	34	9	AI12693	C 453	10.2	56.7	53	28	BZ355814	BZ355814
56.7	34	28	CC457308	C 454	10.2	56.7	53	28	BZ660680	BZ660680
56.7	35	10	BF531141	C 455	10.2	56.7	53	28	CC885074	CC885074
56.7	35	10	BF581828	C 456	10.2	56.7	53	28	AU269158	AU269158
56.7	35	29	BX654143	C 457	10.2	56.7	54	9	AA224858	AA224858
56.7	36	28	BH848146	C 458	10.2	56.7	54	9	AA279907	AA279907
56.7	36	28	BX890659	C 459	10.2	56.7	54	9	AA617305	AA617305
56.7	37	28	AZ466754	C 460	10.2	56.7	54	12	BM434926	BM434926
56.7	37	28	BZ665596	C 461	10.2	56.7	54	28	BH759557	BH759557
56.7	38	12	BJ077725	C 462	10.2	56.7	54	28	BH866169	BH866169
56.7	38	12	BJ077725	C 463	10.2	56.7	54	28	CC179501	CC179501
56.7	39	28	AZ417124	C 464	10.2	56.7	54	29	BX121288	BX121288
56.7	39	28	AZ417124	C 465	10.2	56.7	54	29	DR25224T	DR25224T
56.7	39	28	AZ431347	C 466	10.2	56.7	55	13	BQ548203	BQ548203
56.7	39	29	AI754813	C 467	10.2	56.7	55	13	BU663325	BU663325
56.7	40	9	AI153860	C 468	10.2	56.7	55	14	W89536	W89536
56.7	40	28	AZ336797	C 469	10.2	56.7	55	29	CG710511	CG710511
56.7	40	28	BH146179	C 470	10.2	56.7	55	29	EX531700	EX531700
56.7	40	29	AL937697	C 471	10.2	56.7	56	9	AA816098	AA816098
56.7	41	10	BF207504	C 472	10.2	56.7	56	9	AU258314	AU258314
56.7	41	28	AZ474055	C 473	10.2	56.7	56	9	AV557704	AV557704
56.7	41	28	BH911711	C 474	10.2	56.7	56	14	CB225832	CB225832
56.7	43	9	AI130593	C 475	10.2	56.7	56	14	CB258411	CB258411
56.7	43	28	AZ327870	C 476	10.2	56.7	56	14	CF358645	CF358645
56.7	43	28	AZ937730	C 477	10.2	56.7	56	28	AZ496413	AZ496413
56.7	44	28	AQ026331	C 478	10.2	56.7	56	28	AZ818221	AZ818221
56.7	44	28	AZ339849	C 479	10.2	56.7	56	28	BH758325	BH758325
56.7	44	28	BH910335	C 480	10.2	56.7	56	28	BZ594242	BZ594242
56.7	44	29	AI769592	C 481	10.2	56.7	56	28	CC458332	CC458332
56.7	45	10	BF665932	C 482	10.2	56.7	57	10	BF542036	BF542036
56.7	45	10	BF665932	C 483	10.2	56.7	57	10	AM424384	AM424384
56.7	45	28	AZ662681	C 484	10.2	56.7	57	14	CB931735	CB931735
56.7	45	28	BZ286360	C 485	10.2	56.7	57	28	BH908477	BH908477
56.7	45	28	BZ583559	C 486	10.2	56.7	57	28	BH911536	BH911536
56.7	46	9	AA922456	C 487	10.2	56.7	57	28	BZ590849	BZ590849
56.7	46	12	BG614289	C 488	10.2	56.7	57	29	EX891164	EX891164
56.7	46	14	H95347	C 489	10.2	56.7	58	9	AA139470	AA139470
56.7	46	14	H95347	C 490	10.2	56.7	58	9	AI560245	AI560245
56.7	46	28	AZ662482	C 491	10.2	56.7	58	9	AI828536	AI828536
56.7	46	28	BZ383830	C 492	10.2	56.7	58	10	BF634202	BF634202
56.7	46	28	CC057315	C 493	10.2	56.7	58	10	BE320889	BE320889
56.7	46	28	CC057317	C 494	10.2	56.7	58	14	CF099493	CF099493
56.7	47	28	CC455141	C 495	10.2	56.7	58	14	CK136840	CK136840
56.7	48	12	BJ062280	C 496	10.2	56.7	58	28	BH609701	BH609701
56.7	48	28	AZ598674	C 497	10.2	56.7	58	28	BZ379244	BZ379244
56.7	48	28	AZ656367	C 498	10.2	56.7	58	28	BX895854	BX895854
56.7	48	28	AZ782497	C 499	10.2	56.7	58	28	CB294111	CB294111
56.7	49	9	AI287232	C 500	10.2	56.7	59	28	AQ103610	AQ103610
56.7	49	9	AU268820	C 501	10.2	56.7	59	28	AZ484130	AZ484130
56.7	49	9	AV836810	C 502	10.2	56.7	59	28	AZ485555	AZ485555
56.7	49	12	BJ049535	C 503	10.2	56.7	59	28	AZ773992	AZ773992
56.7	49	28	AZ401521	C 504	10.2	56.7	59	28	AZ806084	AZ806084
56.7	49	28	BH846378	C 505	10.2	56.7	59	28	BH857040	BH857040
56.7	49	28	BZ770783	C 506	10.2	56.7	59	28	BH902574	BH902574
56.7	49	29	AL952708	C 507	10.2	56.7	59	28	BH906359	BH906359
56.7	50	9	AU103183	C 508	10.2	56.7	59	28	CG806861	CG806861
56.7	50	28	AZ801849	C 509	10.2	56.7	59	29	TA101F03P	TA101F03P
56.7	50	29	BX536405	C 510	10.2	56.7	60	12	BM568451	BM568451
56.7	51	10	BF208869	C 511	10.2	56.7	60	14	CD950504	CD950504
56.7	51	14	CB274969	C 512	10.2	56.7	60	14	CF025058	CF025058
56.7	51	28	AZ694064	C 513	10.2	56.7	60	14	CF776186	CF776186
56.7	51	28	AZ760001	C 514	10.2	56.7	60	14	CF776615	CF776615
56.7	51	28	AZ836163	C 515	10.2	56.7	60	14	CF776672	CF776672
56.7	51	28	B00433							
56.7	51	28	BH909805							

56.7	60	14	CF776686	CF776686 jaa33f01.	589	10	55.6	56	13	BQ666073	BQ666073
56.7	60	28	AZ778391	AZ778391 2M0013006	590	10	55.6	56	14	CD683163	CD683163
56.7	60	29	CC888759	CC888759 SALK_1523	591	10	55.6	56	28	B01312	B01312
55.6	23	28	BH846934	BH846934 SALK_0120	C 592	10	55.6	56	28	BH229493	BH229493
55.6	24	28	AZ355269	AZ355269 1M0054E03	C 593	10	55.6	57	29	CG917991	CG917991
55.6	24	28	AZ514241	AZ514241 1M0360H21	C 594	10	55.6	57	29	TA356E01P	TA356E01P
55.6	25	28	AZ391004	AZ391004 1M0152U17	595	10	55.6	58	9	AA179009	AA179009
55.6	25	28	AZ504995	AZ504995 1M0345A02	596	10	55.6	58	9	BH906702	BH906702
55.6	25	29	PCH304007	AJ304007 Plasmodi	597	10	55.6	59	28	AU255386	AU255386
55.6	28	29	CG724685	CG724685 1119082C0	598	10	55.6	59	28	AZ630895	AZ630895
55.6	28	29	AZ833718	AZ833718 2M0116D04	599	10	55.6	59	28	BH853618	BH853618
55.6	30	14	CF269581	CF269581 Fcy1col17	600	10	55.6	59	28	BH853683	BH853683
55.6	30	28	AZ664841	AZ664841 1M0545P19	601	10	55.6	59	28	BH904715	BH904715
55.6	34	28	AZ762569	AZ762569 1M0557004	602	10	55.6	59	29	CC471273	CC471273
55.6	34	29	BZ768900	BZ768900 SALK_1412	C 603	10	55.6	59	29	AL766857	AL766857
55.6	34	29	CG723119	CG723119 1119074G1	C 604	10	55.6	60	9	AV833379	AV833379
55.6	35	28	BH852456	BH852456 SALK_0746	605	10	55.6	60	12	BM126375	BM126375
55.6	36	28	AZ499855	AZ499855 1M0337G22	C 606	10	55.6	60	12	BM513770	BM513770
55.6	37	9	AU263716	AU263716 AU263716	C 607	10	55.6	60	28	BH895321	BH895321
55.6	38	9	AV840044	AV840044 AV840044	C 608	10	55.6	60	29	CNS02FJ2	CNS02FJ2
55.6	38	28	BZ425325	BZ425325 100029638	C 609	9.8	54.4	22	28	AZ799717	AZ799717
55.6	39	9	AU259565	AU259565 AU259565	C 610	9.8	54.4	23	28	BH846974	BH846974
55.6	39	29	AG256137	AG256137 Lotus cor	C 611	9.8	54.4	24	28	AZ415688	AZ415688
55.6	40	28	CC025737	CC025737 3591_1_47	612	9.8	54.4	24	28	AZ443637	AZ443637
55.6	41	12	BJ049370	BJ049370 BJ049370	613	9.8	54.4	25	9	AA916478	AA916478
55.6	42	10	AW455805	AW455805 2DZ Neuro	614	9.8	54.4	25	29	CC886538	CC886538
55.6	42	14	D67708	D67708 CELK076G7F	C 615	9.8	54.4	27	28	AZ345858	AZ345858
55.6	42	28	BZ586955	BZ586955 3590_1_24	C 616	9.8	54.4	27	28	AZ782590	AZ782590
55.6	42	29	BX897196	BX897196 Arabidops	C 617	9.8	54.4	27	29	TA129H02P	TA129H02P
55.6	43	9	AA509550	AA509550 vH50403.Y	C 618	9.8	54.4	28	28	AZ346727	AZ346727
55.6	43	14	CA851085	CA851085 D10A01_B0	C 619	9.8	54.4	28	28	BH904375	BH904375
55.6	43	29	CG724749	CG724749 1119082E0	C 620	9.8	54.4	29	9	AU256382	AU256382
55.6	43	29	BX170734	BX170734 Danilo rer	C 621	9.8	54.4	29	28	AZ313355	AZ313355
55.6	44	9	AU006731	AU006731 AU006731	C 622	9.8	54.4	31	28	AZ345457	AZ345457
55.6	44	14	CD029205	CD029205 mgn5007XA	623	9.8	54.4	31	28	BH903720	BH903720
55.6	44	28	BZ384717	BZ384717 SALK_1359	624	9.8	54.4	32	9	AU007928	AU007928
55.6	45	28	BH789555	BH789555 SALK_0378	625	9.8	54.4	32	28	BH907230	BH907230
55.6	45	28	BH865166	BH865166 SALK_0974	626	9.8	54.4	33	14	CF269589	CF269589
55.6	46	9	AI667606	AI667606 fdi6ell.x	627	9.8	54.4	33	28	AZ483388	AZ483388
55.6	46	28	BZ352539	BZ352539 SALK_0809	C 628	9.8	54.4	33	29	BX532756	BX532756
55.6	47	28	BZ783942	BZ783942 2M0026P03	C 629	9.8	54.4	33	29	TA61D02P	TA61D02P
55.6	47	28	BH633020	BH633020 1007058D0	C 630	9.8	54.4	34	12	B1145382	B1145382
55.6	47	28	CC022052	CC022052 3591_1_27	C 631	9.8	54.4	34	12	BJ055305	BJ055305
55.6	47	29	CG724664	CG724664 1119082B1	632	9.8	54.4	34	14	CF333374	CF333374
55.6	47	29	CL002272	CL002272 02S0105-0	633	9.8	54.4	34	29	AL944704	AL944704
55.6	48	28	BH814607	BH814607 SALK_0667	634	9.8	54.4	34	29	AL72216	AL72216
55.6	48	28	BZ762779	BZ762779 SALK_1069	C 635	9.8	54.4	35	28	BH906663	BH906663
55.6	48	29	TA263H04Q	TA263H04Q T. brucei	636	9.8	54.4	35	29	CG893855	CG893855
55.6	49	9	AA123717	AA123717 mq76d09.x	637	9.8	54.4	35	29	AL753362	AL753362
55.6	49	9	AI889232	AI889232 wms3609.x	C 638	9.8	54.4	35	29	AL065861	AL065861
55.6	49	28	BH641431	BH641431 1008047F0	C 639	9.8	54.4	36	28	CNSC06SA	CNSC06SA
55.6	49	28	BH911354	BH911354 SALK_0678	C 640	9.8	54.4	36	28	AZ807406	AZ807406
55.6	49	28	BZ356313	BZ356313 SALK_1287	C 641	9.8	54.4	36	28	BH904644	BH904644
55.6	49	29	DME546797	AJ546797 Drosophil	C 642	9.8	54.4	36	29	AG217240	AG217240
55.6	50	9	AI988040	AI988040 sc33a11.x	643	9.8	54.4	36	29	AG218041	AG218041
55.6	50	29	CG427403	CG427403 01S0749-0	C 644	9.8	54.4	37	14	R02052	R02052
55.6	51	9	AA614531	AA614531 np49c06.s	645	9.8	54.4	37	28	AQ254776	AQ254776
55.6	51	14	CD682301	CD682301 r749d02.Y	646	9.8	54.4	37	28	BZ287003	BZ287003
55.6	51	28	AZ633366	AZ633366 1M048L03	C 647	9.8	54.4	37	29	AL751513	AL751513
55.6	51	28	BZ377421	BZ377421 SALK_0808	648	9.8	54.4	38	9	AA910311	AA910311
55.6	52	9	AI789302	AI789302 uk53e04.y	C 649	9.8	54.4	38	28	AZ837547	AZ837547
55.6	52	14	CA955020	CA955020 kl34fil1.Y	650	9.8	54.4	38	28	BH792610	BH792610
55.6	52	14	CD683281	CD683281 r741f08.Y	C 651	9.8	54.4	38	29	BX001766	BX001766
55.6	52	28	BH629312	BH629312 1007070C0	652	9.8	54.4	38	29	BX662374	BX662374
55.6	52	29	CC796941	CC796941 SALK_1442	C 653	9.8	54.4	38	29	DR102FIS	DR102FIS
55.6	53	9	AV856132	AV856132 AV856132	C 654	9.8	54.4	39	9	AV853005	AV853005
55.6	53	28	BH411420	BH411420 1007022F0	C 655	9.8	54.4	39	13	C21308	C21308
55.6	53	28	BH902250	BH902250 SALK_0915	656	9.8	54.4	39	28	AZ775786	AZ775786
55.6	53	29	AL770198	AL770198 Arabidops	C 657	9.8	54.4	39	28	BH906670	BH906670
55.6	54	28	AQ902860	AQ902860 O661117-T	C 658	9.8	54.4	40	12	BJ033972	BJ033972
55.6	54	28	CC182349	CC182349 02S0205-0	659	9.8	54.4	40	14	CF328543	CF328543
55.6	55	9	AJ914859	AJ914859 tr26c02.x	660	9.8	54.4	40	14	H92455	H92455
55.6	55	28	BH910550	BH910550 SALK_0601	C 661	9.8	54.4	40	28	AZ424144	AZ424144

54.4	40	28	AZ590926	1M0400G15	100400G15	9.8	54.4	52	28	BZ765415	BZ765415
54.4	40	28	AZ848456	AZ848456	2M0149020	9.8	54.4	52	29	BX536573	BX536573
54.4	40	28	BH864615	SALK_0963	BH864615	9.8	54.4	53	14	H53365	H53365
54.4	40	28	BZ588133	3590_1.5	BZ588133	9.8	54.4	53	29	BX565614	BX565614
54.4	40	29	CC886423	SALK_1485	CC886423	9.8	54.4	53	29	BX661868	BX661868
54.4	40	29	AG218522	Drosophila	AG218522	9.8	54.4	54	9	AU255002	AU255002
54.4	40	29	AG218577	Drosophila	AG218577	9.8	54.4	54	9	AV833768	AV833768
54.4	41	28	BH901464	SALK_0793	BH901464	9.8	54.4	54	9	AA621269	AA621269
54.4	41	28	BH906771	SALK_0357	BH906771	9.8	54.4	54	10	BE249013	BE249013
54.4	42	14	T17555	mps v112	Th	9.8	54.4	54	12	BM529183	BM529183
54.4	42	28	AZ826326	2M0102A03	AZ826326	9.8	54.4	54	14	CF776279	CF776279
54.4	42	28	BH791460	SALK_0599	BH791460	9.8	54.4	54	28	BH863218	BH863218
54.4	42	28	BH847647	SALK_0551	BH847647	9.8	54.4	54	28	BH902316	BH902316
54.4	42	28	CC455293	SALK_0802	CC455293	9.8	54.4	54	28	BH902317	BH902317
54.4	43	9	AA921819	om40d12.s	AA921819	9.8	54.4	54	28	BH902323	BH902323
54.4	43	28	AZ432623	1M0218D08	AZ432623	9.8	54.4	54	28	BH909991	BH909991
54.4	43	28	BZ662828	SALK_0263	BZ662828	9.8	54.4	54	28	BZ384156	BZ384156
54.4	43	28	BZ662833	SALK_0263	BZ662833	9.8	54.4	54	28	BZ596694	BZ596694
54.4	43	29	AG216392	Drosophila	AG216392	9.8	54.4	55	9	AU254157	AU254157
54.4	43	29	BX656823	Arabidops	BX656823	9.8	54.4	55	9	AV742610	AV742610
54.4	44	9	AA508066	ng92f11.s	AA508066	9.8	54.4	55	12	B051885	B051885
54.4	44	9	AA545630	vj65g10.r	AA545630	9.8	54.4	55	13	BQ568246	BQ568246
54.4	44	14	CF333059	JMT--04-J	CF333059	9.8	54.4	55	14	CB098745	CB098745
54.4	44	28	BH908609	SALK_0495	BH908609	9.8	54.4	55	14	D19548	D19548
54.4	44	28	BX534980	Arabidops	BX534980	9.8	54.4	55	14	D19548	D19548
54.4	45	28	AZ661549	1M0540M06	AZ661549	9.8	54.4	55	14	D19548	D19548
54.4	45	29	BX891955	Arabidops	BX891955	9.8	54.4	55	14	D19548	D19548
54.4	46	9	AI636188	tz06e08.x	AI636188	9.8	54.4	55	14	D19548	D19548
54.4	46	12	B1083327	602875594	B1083327	9.8	54.4	55	14	D19548	D19548
54.4	46	28	BZ596536	SALK_0927	BZ596536	9.8	54.4	55	29	CC795056	CC795056
54.4	46	28	BZ665286	SALK_1109	BZ665286	9.8	54.4	55	29	AL761596	AL761596
54.4	46	28	BZ768917	SALK_1413	BZ768917	9.8	54.4	55	29	AL952570	AL952570
54.4	46	29	AG232605	Lotus cor	AG232605	9.8	54.4	56	9	AA634526	AA634526
54.4	47	9	AV956026	AV956026	AV956026	9.8	54.4	56	10	AA74036	AA74036
54.4	47	28	AZ321991	1M0040204	AZ321991	9.8	54.4	56	13	BQ72299	BQ72299
54.4	47	28	AZ386189	1M0145H04	AZ386189	9.8	54.4	56	13	BQ762054	BQ762054
54.4	47	28	AZ804274	2M0065N07	AZ804274	9.8	54.4	56	13	BX718070	BX718070
54.4	47	29	AL770737	Arabidops	AL770737	9.8	54.4	56	13	C21239	C21239
54.4	48	28	AZ458214	1M0262A08	AZ458214	9.8	54.4	56	14	CF358797	CF358797
54.4	48	28	BH909255	SALK_0526	BH909255	9.8	54.4	56	28	AQ025208	AQ025208
54.4	48	28	CC458944	SALK_1230	CC458944	9.8	54.4	56	29	CC794651	CC794651
54.4	49	9	AU260260	AU260260	AU260260	9.8	54.4	57	10	BF057873	BF057873
54.4	49	12	B1701273	8495605	B1701273	9.8	54.4	57	12	BG885365	BG885365
54.4	49	14	CA995110	rg24c03.y	CA995110	9.8	54.4	57	12	BM128852	BM128852
54.4	49	14	CF312600	ABF--08-G	CF312600	9.8	54.4	57	14	CB274909	CB274909
54.4	49	28	AZ786047	2M0030D19	AZ786047	9.8	54.4	57	14	CF801546	CF801546
54.4	49	28	BZ382085	SALK_1178	BZ382085	9.8	54.4	57	28	AZ463500	AZ463500
54.4	49	29	CC886429	SALK_1485	CC886429	9.8	54.4	57	28	BH812817	BH812817
54.4	49	29	AL941925	Arabidops	AL941925	9.8	54.4	57	28	BZ287127	BZ287127
54.4	49	29	BX531176	Arabidops	BX531176	9.8	54.4	57	28	BZ384117	BZ384117
54.4	50	9	AU102299	AU102299	AU102299	9.8	54.4	57	29	AL765755	AL765755
54.4	50	9	AU102299	AU102299	AU102299	9.8	54.4	57	29	BX286419	BX286419
54.4	50	9	AU103189	AU103189	AU103189	9.8	54.4	57	29	BX533727	BX533727
54.4	50	9	AA615310	vo01h08.r	AA615310	9.8	54.4	58	10	AW246501	AW246501
54.4	50	10	AW783902	5.AL2.Gil	AW783902	9.8	54.4	58	12	B1438036	B1438036
54.4	50	12	BM069725	ie88d07.y	BM069725	9.8	54.4	58	13	BX549853	BX549853
54.4	50	13	BQ125541	rc69f06.y	BQ125541	9.8	54.4	58	14	BH416669	BH416669
54.4	50	14	CA795302	Cac.BL.23	CA795302	9.8	54.4	58	28	BH791190	BH791190
54.4	50	14	CF301799	7LEAF--06	CF301799	9.8	54.4	58	28	BH862804	BH862804
54.4	50	28	BH636136	1008009D0	BH636136	9.8	54.4	58	28	BZ287603	BZ287603
54.4	50	29	CC493346	CH240_327	CC493346	9.8	54.4	58	29	BX535617	BX535617
54.4	51	9	AL644395	AL644395	AL644395	9.8	54.4	59	29	BX660313	BX660313
54.4	51	12	B1174734	OSTF052F1	B1174734	9.8	54.4	59	29	AA458427	AA458427
54.4	51	28	AZ838224	2M0133018	AZ838224	9.8	54.4	59	10	BF036854	BF036854
54.4	52	9	AI326324	ml57g04.x	AI326324	9.8	54.4	59	28	BH790538	BH790538
54.4	52	9	AL872200	AL872200	AL872200	9.8	54.4	59	28	BZ768804	BZ768804
54.4	52	10	BF631825	NF026C09D	BF631825	9.8	54.4	59	29	BX534620	BX534620
54.4	52	10	BM692095	NF026B07S	BM692095	9.8	54.4	60	9	AV521053	AV521053
54.4	52	10	BE320772	NF028E03R	BE320772	9.8	54.4	60	9	AV833768	AV833768
54.4	52	12	BM893619	1j27d05.x	BM893619	9.8	54.4	60	10	BF638495	BF638495
54.4	52	13	BU497340	PfESToab6	BU497340	9.8	54.4	60	10	BF639003	BF639003
54.4	52	28	AZ576597	AST-TD1.2	AZ576597	9.8	54.4	60	14	D18195	D18195
54.4	52	28	BZ288336	SALK_0217	BZ288336	9.8	54.4	60	14	D18195	D18195

54.4	60	28	AZ7822310	AZ7822310	2M0222C03	C 881	3.6	53.3	41	28	AZ467036
54.4	60	28	BZ354346	BZ354346	SALK_1248	882	9.6	53.3	41	28	AZ762719
54.4	60	28	BZ762244	BZ762244	SALK_0925	883	9.6	53.3	41	28	BZ381303
54.4	60	29	AL940665	AL940665	ArabiDops	884	9.6	53.3	41	29	AG217208
53.3	19	28	AZ769438	AZ769438	1M0570F09	C 885	9.6	53.3	42	28	AZ309889
53.3	19	28	AZ973582	AZ973582	2M0247C20	C 886	9.6	53.3	42	28	BH906566
53.3	20	28	AZ421329	AZ421329	1M0399J003	C 887	9.6	53.3	43	28	AZ378285
53.3	21	9	AL585535	AL585535	AL585535	888	9.6	53.3	43	28	AZ992855
53.3	22	28	AZ366186	AZ366186	1M0115L21	889	9.6	53.3	43	28	BH809878
53.3	22	28	AZ479849	AZ479849	1M0300E20	890	9.6	53.3	43	28	BZ352990
53.3	23	14	CF312348	CF312348	ABF--08-A	C 891	9.6	53.3	43	28	BZ763952
53.3	23	28	AZ345552	AZ345552	1M0808E15	C 892	9.6	53.3	43	29	CG722753
53.3	23	28	AZ826455	AZ826455	2M0102P09	893	9.6	53.3	44	9	AA926720
53.3	24	28	AZ320835	AZ320835	1M0041I17	894	9.6	53.3	44	10	BE311212
53.3	24	28	AZ345509	AZ345509	1M0808I03	895	9.6	53.3	44	28	AZ492304
53.3	24	29	TA208D09P	TA208D09P	AL479446 T. brucei	896	9.6	53.3	44	28	AZ601755
53.3	25	28	AZ427760	AZ427760	1M0209P22	C 897	9.6	53.3	44	28	BH789833
53.3	25	28	AZ829708	AZ829708	2M0107G19	C 898	9.6	53.3	45	9	AA778766
53.3	25	28	AZ950699	AZ950699	2M0214F20	C 899	9.6	53.3	45	9	AI471721
53.3	25	28	BH792245	BH792245	SALK_0631	900	9.6	53.3	45	28	AZ387836
53.3	25	29	TA62D04Q	TA62D04Q	AL464606 T. brucei	901	9.6	53.3	45	28	AZ954848
53.3	26	28	AZ309024	AZ309024	1M0012H07	902	9.6	53.3	45	28	BH789570
53.3	26	28	AZ410119	AZ410119	1M0182P08	C 903	9.6	53.3	45	29	CC883051
53.3	26	28	AZ478344	AZ478344	1M0298A22	C 904	9.6	53.3	46	9	AA654894
53.3	27	28	AZ443035	AZ443035	1M0237G06	C 905	9.6	53.3	46	9	AI033006
53.3	27	28	AZ949965	AZ949965	2M0213L16	C 906	9.6	53.3	46	9	AI744366
53.3	28	28	AZ343935	AZ343935	1M0077K12	907	9.6	53.3	46	10	BF123084
53.3	28	28	AZ774261	AZ774261	2M0003N21	908	9.6	53.3	46	28	AZ336053
53.3	28	28	BH905737	BH905737	SALK_1076	C 909	9.6	53.3	46	28	AZ418890
53.3	28	28	BZ664534	BZ664534	SALK_0759	C 910	9.6	53.3	46	28	AZ595876
53.3	29	28	AZ419920	AZ419920	1M0196E12	911	9.6	53.3	46	28	AZ808188
53.3	29	28	BZ596327	BZ596327	SALK_0923	912	9.6	53.3	46	28	BH906372
53.3	30	9	AV856232	AV856232	AV856232	913	9.6	53.3	46	29	EX125703
53.3	30	13	C01051	HUMGS000720	C01051 HUMGS000720	914	9.6	53.3	46	29	EX534722
53.3	30	28	AQ025784	AQ025784	1(2)k0620	C 915	9.6	53.3	47	28	AZ633235
53.3	30	28	AQ025785	AQ025785	1(2)k0620	916	9.6	53.3	47	28	AZ946143
53.3	30	28	AZ428907	AZ428907	1M0212C15	C 917	9.6	53.3	47	28	BH813635
53.3	31	9	AI002013	AI002013	ot40e08.s	C 918	9.6	53.3	47	28	BH906478
53.3	31	28	AZ827463	AZ827463	2M0103H19	C 919	9.6	53.3	47	29	AG019636
53.3	31	28	BH906412	BH906412	SALK_1098	920	9.6	53.3	47	29	BX654811
53.3	31	28	BZ597449	BZ597449	SALK_1050	C 921	9.6	53.3	48	14	D12328
53.3	31	28	BZ763070	BZ763070	SALK_1118	C 922	9.6	53.3	48	14	D12328
53.3	31	29	AL761476	AL761476	ArabiDops	C 923	9.6	53.3	48	29	BZ595002
53.3	31	29	AL943189	AL943189	ArabiDops	924	9.6	53.3	48	29	CC795453
53.3	32	28	AZ485437	AZ485437	1M0312H19	925	9.6	53.3	49	9	AA496619
53.3	32	28	AZ602044	AZ602044	1M0420B12	C 926	9.6	53.3	49	9	AA594397
53.3	34	28	AZ462024	AZ462024	1M0269E12	C 927	9.6	53.3	49	12	BM281964
53.3	34	28	BH792264	BH792264	SALK_0632	C 928	9.6	53.3	49	14	CB277378
53.3	34	29	TA202F08P	TA202F08P	T. brucei	929	9.6	53.3	49	28	BH846326
53.3	35	28	BZ353611	BZ353611	SALK_1205	C 930	9.6	53.3	49	29	AB082215
53.3	35	29	TA336F08Q	TA336F08Q	T. brucei	C 931	9.6	53.3	50	9	AI126970
53.3	36	9	AU258465	AU258465	AU258465	932	9.6	53.3	50	9	AI102957
53.3	36	28	AZ425719	AZ425719	1M0205N21	C 933	9.6	53.3	50	9	AU103002
53.3	37	28	AZ423769	AZ423769	1M0203G22	C 934	9.6	53.3	50	12	BG526086
53.3	37	28	AZ586716	AZ586716	1M0392B19	C 935	9.6	53.3	50	12	BI749153
53.3	37	28	DR6805T	DR6805T	Dario rer	C 936	9.6	53.3	50	12	BM183051
53.3	37	29	TA35D05P	TA35D05P	AL953874 T. brucei	937	9.6	53.3	50	13	BQ590343
53.3	38	28	AZ334854	AZ334854	1M0064K20	C 938	9.6	53.3	50	14	CB274908
53.3	38	28	AZ453551	AZ453551	1M0255E06	C 939	9.6	53.3	50	14	CB858064
53.3	38	28	BH847845	BH847845	SALK_0605	C 940	9.6	53.3	50	28	AZ427184
53.3	38	28	BH863567	BH863567	SALK_0941	941	9.6	53.3	50	28	AZ769352
53.3	38	28	BH903283	BH903283	SALK_0527	942	9.6	53.3	50	28	BH900918
53.3	38	28	CC456487	CC456487	SALK_0987	943	9.6	53.3	50	28	CC182113
53.3	38	28	BX659120	BX659120	ArabiDops	944	9.6	53.3	50	29	CC795807
53.3	38	29	TA115F10Q	TA115F10Q	AL463791 T. brucei	C 945	9.6	53.3	50	29	CC941572
53.3	38	29	AZ798493	AZ798493	2M0055P15	946	9.6	53.3	50	29	CG400426
53.3	39	28	BZ593768	BZ593768	SALK_0820	947	9.6	53.3	50	29	CG400440
53.3	40	9	AI032824	AI032824	ot17f07.x	948	9.6	53.3	50	29	CG729919
53.3	40	9	AV845525	AV845525	AV845525	949	9.6	53.3	50	29	AL763583
53.3	40	28	AZ775335	AZ775335	2M0007G07	950	9.6	53.3	50	29	BX897057
53.3	40	28	BZ358998	BZ358998	SALK_1336	951	9.6	53.3	51	29	CC884509
53.3	41	9	AU013901	AU013901	AU013901	952	9.6	53.3	52	9	AI307707
53.3	41	28	AZ457981	AZ457981	1M0261B12	C 953	9.6	53.3	52	9	AI598081

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53.3 52 9 AT805242 tc90e01.x
53.3 52 9 AA173932 zp01e02.s
53.3 52 9 AU007260 AU007260
53.3 52 10 BF635986 BF635986
53.3 52 10 AW683560 AW683560
53.3 52 10 BE320905 BE320905
53.3 52 13 C02368 C02368
53.3 52 14 CA844637 CA844637
53.3 52 14 CA935080 CA935080
53.3 52 28 AZ427438 AZ427438
53.3 52 28 AZ759984 AZ759984
53.3 52 28 B00446 B00446
53.3 52 29 AL935915 AL935915
53.3 53 9 AA071155 AA071155
53.3 53 9 AV952063 AV952063
53.3 53 13 BQ075816 BQ075816
53.3 53 13 BX557466 BX557466
53.3 53 14 T81497 T81497
53.3 53 28 AZ303904 AZ303904
53.3 53 28 AZ346829 AZ346829
53.3 53 28 AZ401594 AZ401594
53.3 53 28 AZ623780 AZ623780
53.3 53 28 BZ592770 BZ592770
53.3 53 28 CC457296 CC457296
53.3 53 9 AA566129 AA566129
53.3 54 12 BJ080031 BJ080031
53.3 54 14 CB212351 CB212351
53.3 54 28 B32318 B32318
53.3 54 28 BH849558 BH849558
53.3 54 28 BH853866 BH853866
53.3 54 28 BH906072 BH906072
53.3 54 28 BZ290279 BZ290279
53.3 55 9 AI001973 AI001973
53.3 55 9 AI678370 AI678370
53.3 55 9 AI698400 AI698400
53.3 55 9 AA526459 AA526459
53.3 55 14 CD012170 CD012170
53.3 55 14 R38350 R38350
53.3 55 28 AZ321753 AZ321753
53.3 55 28 AZ333386 AZ333386
53.3 55 28 AZ443755 AZ443755
53.3 55 28 AZ943318 AZ943318
53.3 55 28 B03439 B03439
53.3 55 28 BZ596819 BZ596819
53.3 55 28 BZ596820 BZ596820
53.3 55 29 CC794226 CC794226
53.3 55 29 AL759691 AL759691

ALIGNMENTS

70903 29 bp DNA linear GSS 13-MAR-2003
       143911.26.30.x Arabidopsis thaliana TDNA insertion lines
       bidopsis thaliana genomic clone SALK_143911.26.30.x, genomic
       rev sequence.
70903
70903.1 GI:28944587

       bidopsis thaliana (thale cress)
       bidopsis thaliana
       arykta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
       rnatophyta; Magnoliophyta; eudicotyledons; core eudicots;
       ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
       (bases 1 to 29)
       nso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
       rinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
       nn,P., Zimmerman,J. and Ecker,J.R.
       sequence-Indexed Library of Insertion Mutations in the
       bidopsis Genome
       ublished (2001)

COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left bor
TDNA. This sequence lies within an annotated exon of Atl
Class: TDNA tagged.

FEATURES
source
1..29
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_143911.26.30.x"
/notes="PCR was performed on Arabidopsis thalian
each of which contains one or more TDNA insert
elements. The resultant fragment for each line
directly sequenced to determine the genomic seq
the site of insertion. Details of the protocol
be found at http://signal.salk.edu/tdna_protoc

ORIGIN
Query Match 74.4%; Score 13.4; DB 28; Length 29;
Best Local Similarity 93.3%; Pred. No. 6.9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0;

QY 2 TCATTGGCAATTTG 16
DB 17 TCTTTGGCAATTTG 3

RESULT 2
AZ345478/c
LOCUS AZ345478 40 bp DNA linear GSS
DEFINITION lM0080A01F Mouse 10kb plasmid UUC1M library Mus muscult
clone UUC1M0080A01 F, genomic survey sequence.
ACCESSION AZ345478
VERSION AZ345478.1 GI:10424715
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Han
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,J
Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads fr
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: A column: 01
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
1..40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

FEATURES
source
1..40
Location/Qualifiers

```

/db\_xref="taxon:10090"  
 /clone="UUGC1M0080A01"  
 /sex="Male"  
 /lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

74.4%; Score 13.4; DB 28; Length 40;  
 ilarity 93.3%; Pred. No. 6.8e+04;  
 Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ATTGGAATTTCG 16  
 |||||  
 ATTGGAATTTCG 17

2501 56 bp DNA linear GSS 17-JUN-2002  
 idopsis thaliana T-DNA flanking sequence GK-013F10-011902,  
 mic survey sequence.

2501 GI:21484999

idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 db; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

zhov.N., Li.Y., Rosso.M., Viehoveer.P., Dekker.K., Saedler.H.  
 Weisshaar,B.  
 peline for automated high-throughput generation of FSTs  
 nking sequence tags) from Arabidopsis thaliana T-DNA  
 sformed lines  
 blished

O.M., Strizhov.N., Li.Y., Reiss.B., Dekker.K. and Weisshaar,B.  
 w Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 flanking sequence tag based reverse genetics  
 blished  
 bases 1 to 56)  
 zhov.N., Li.Y., Rosso.M. and Weisshaar,B.  
 ct Submission  
 itted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer  
 hungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 cates an insertion close to or within gene Atg08400. The  
 ences are generated at the MPI for Plant Breeding Research in  
 context of the GABI-Kat project. GABI-Kat is part of the German  
 t Genomics program designated 'GABI'. Information on line  
 liability can be found at:  
 ://www.mpiz-koeln.mpg.de/GABI-Kat/  
 Location/Qualifiers

source  
 1. .56  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-013F10-011902"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertio  
 /note="PCR was performed on DNA from Arabidopsi  
 plants (T1) which were transformed with the T-D  
 vector pAC106. The lines contain one or more T-  
 insertions. The DNA fragment(s) resulting from  
 were directly sequenced to determine the genom  
 flanking the insertion. Sequences displaying si  
 similarity to the A. thaliana nuclear genome se  
 processed for submission. T-DNA derived sequenc  
 removed"

## ORIGIN

Query Match 74.4%; Score 13.4; DB 29; Length 56;  
 Best Local Similarity 93.3%; Pred. No. 6.7e+04;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0;

Qy 3 CATTTGGAATTTCG 17

Db 43 CATTTGGAATTTCG 29

RESULT 4  
 BE491325  
 LOCUS 60 bp mRNA linear EST  
 DEFINITION db71e06.y1 Wellcome CRC psk egg Xenopus laevis cDNA clon  
 IMAGE:3378466 5' similar to SW:TRCB\_XENLA\_Q91854 BETA-TR  
 sequence.

ACCESSION BE491325

VERSION BE491325.1 GI:9610858

KEYWORDS EST.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pip  
 Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 60)

AUTHORS

Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,  
 Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B.,  
 Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y.,  
 Waterston,R. and Wilson,R.  
 WashU Xenopus EST project, 1999  
 Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Sandy Clifton, Ph.D.  
 WashU Xenopus EST project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Library constructed by N. Garrett, P. LeMaire, A.M. Zorn  
 Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Wash  
 University Genome Sequencing Center  
 Clone distribution: Xenopus clones from this library ar  
 through the I.M.A.G.E. Consortium/LLNL at: info@image.ll  
 Seq primer: -40RP from Gibco.

Location/Qualifiers

source

1. .60  
 /organism="Xenopus laevis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8355"  
 /clone="IMAGE:3378466"  
 /tissue\_type="egg"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="Wellcome CRC psk egg"  
 /note="Vector: pBluescript SK-; Site 1: NotI; S  
 EcoRI; cDNAs were oligo-dT primed and direction  
 cloned. Library was constructed by N. Garrett,

A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute).  
Note: This is a Xenopus Gene Collection (XGC) library."

74.4%; Score 13.4; DB 10; Length 60;  
ilarity 93.3%; Pred. No. 6.7e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
TCATTGGAAATTTT 15  
|||||  
TCATTGGGAATTTT 38

13284 37 bp DNA linear GSS 04-SEP-2002  
102372.19.30.x Arabidopsis thaliana TDNA insertion lines  
idopsis thaliana genomic clone SALK\_102372.19.30.x, genomic  
ey sequence.  
13284  
13284.1 GI:22714450

idopsis thaliana (thale cress)  
idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
(bases 1 to 37)  
iso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
cinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
m,P., Zimmerman,J., and Ecker,J.R.  
quence-Indexed Library of Insertion Mutations in the  
idopsis Genome  
inished (2001)

act: Joseph R. Ecker  
c Institute Genomic Analysis Laboratory (SIGNAL)  
Salk Institute for Biological Studies  
10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
: 858 453 4300 x1752  
: 858 558 6379  
li: ecker@salk.edu  
s is single pass sequence recovered from the left border of  
A. This sequence lies within an annotated exon of At3g23970.  
ss: TDNA tagged.

Location/Qualifiers  
1..37  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_102372.19.30.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

73.3%; Score 13.2; DB 28; Length 37;  
ilarity 83.3%; Pred. No. 8.4e+04;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGAAATTTGCC 18  
|||||  
TCATTGGGAATTTGCC 26

11561  
4a01.x1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1916136 3',  
EST 02-FEB-1999

similar to TR:014597 O14597 NON-FUNCTIONAL FOLATE BINDIN  
/, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AI3111561  
AI3111561.1 GI:4006432  
EST.  
Homo sapiens (human)  
Homo sapiens  
Mammalia; Euthera; Primates; Catarrhini; Homidae; Hom  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Euthera; Primates; Catarrhini; Homidae; Hom  
1 (bases 1 to 52)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project  
Tumor Gene Index  
Unpublished (1997)

REFERENCE  
AUTHORS  
TITLE

JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,  
Emmerit-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequenc  
Clone distribution: NCI-CGAP clone distribution inform  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 539 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source

1..52  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1916136"  
/tissue\_type="2 pooled tumors (clear cell type  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Kid5"  
/note="Organ: kidney; Vector: pT73D-Pac (Phar  
a modified polylinker; Site 1: Not I; Site 2:  
strand cDNA was primed with a Not I - oligo(dT  
RACCTGGAAGATTCGCGCGCAATATTTTATTTTATTTT  
double-stranded cDNA was ligated to Eco RI ada  
(Pharmacia), digested with Not I and cloned in  
and Eco RI sites of the modified pT73 vector.  
went through one round of normalization. Libra  
constructed by Bento Soares and M. Fatima Bona

ORIGIN

Query Match 73.3%; Score 13.2; DB 9; Length 52;  
Best Local Similarity 83.3%; Pred. No. 8.3e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CTCATTGGGAATTTGCC 18

Db 50 CCATTGGGAAGTTGCC 33

RESULT 7

BH902184

LOCUS  
DEFINITION  
BH902184 57 bp DNA linear GSS  
SALK\_091427.17.20.x Arabidopsis thaliana TDNA insertion  
Arabidopsis thaliana genomic clone SALK\_091427.17.20.x,  
survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BH902184  
BH902184.1 GI:22713065  
GSS.  
Arabidopsis thaliana (thale cress)

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi  
rosids; eurosids II; Brassicales; Brassicaceae; Arabido  
1 (bases 1 to 57)

O.J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 nab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 P., Zimmerman,J. and Ecker,J.R.  
 nence-Indexed Library of Insertion Mutations in the  
 dopsis Genome  
 lished (2001)  
 ict: Joseph R. Ecker  
 nstitute Genomic Analysis Laboratory (SIGnAL)  
 alk Institute for Biological Studies  
 ) N. Torrey Pines Road, La Jolla, CA 92037, USA  
 858 453 4100 x1752  
 858 558 6379  
 .: ecker@salk.edu  
 is single pass sequence recovered from the left border of  
 . This sequence lies within an annotated exon of At3g23970.  
 : TDNA tagged.  
 : Location/Qualifiers  
 1. 57  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:3702"  
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 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /notes="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
 73.3%; Score 13.2; DB 28; Length 57;  
 ilarity 83.3%; Pred. No. 8.3e+04;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 TATTGGGAATTTGCG 18  
 |||||  
 TATTGGGATGATTGCC 25

0275 25 bp DNA linear GSS 26-NOV-2002  
 114881.40.40.x Arabidopsis thaliana TDNA insertion lines  
 idopsis thaliana genomic clone SALK\_114881.40.40.x, genomic  
 y sequence.  
 0275  
 0275.1 GI:25472978  
 idopsis thaliana (thale cress)  
 idopsis thaliana  
 cyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 natophyta; Magnoliophyta; eudicotyledons; core eudicot;  
 3s; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 ases 1 to 25)  
 so,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 inab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 a.P., Zimmerman,J. and Ecker,J.R.  
 nence-Indexed Library of Insertion Mutations in the  
 dopsis Genome  
 blished (2001)  
 act: Joseph R. Ecker  
 nstitute Genomic Analysis Laboratory (SIGnAL)  
 Salk Institute for Biological Studies  
 0 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 858 453 4100 x1752  
 858 558 6379  
 l: ecker@salk.edu  
 is single pass sequence recovered from the left border of  
 . This sequence lies within 300 bases of the 5' end of  
 44370.  
 s: TDNA tagged.

FEATURES  
 source  
 Location/Qualifiers  
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 /organism="Arabidopsis thaliana"  
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 /db\_xref="taxon:3702"  
 /clone="SALK\_114881.40.40.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /notes="PCR was performed on Arabidopsis thaliana  
 each of which contains one or more TDNA insert:  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

ORIGIN  
 Query Match 72.2%; Score 13; DB 28; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0;  
 QY 1 CTCATTGGGAATT 13  
 |||||  
 Db 13 CTCATTGGGAATT 25

RESULT 9  
 BZ380283 59 bp DNA linear GSS  
 SALK\_114889.22.40.x Arabidopsis thaliana TDNA insertion  
 Arabidopsis thaliana genomic clone SALK\_114889.22.40.x,  
 survey sequence.  
 BZ380283  
 BZ380283.1 GI:25472995  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 (bases 1 to 59)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P  
 Shinn,P., Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGnAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left bor  
 TDNA. This sequence lies within 300 bases of the 5' end  
 At2g44370  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1. 59  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
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 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /notes="PCR was performed on Arabidopsis thalian  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

FEATURES  
 source  
 Location/Qualifiers  
 1. 59  
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 /clone="SALK\_114889.22.40.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /notes="PCR was performed on Arabidopsis thalian  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

ORIGIN



72.2%; Score 13; DB 28; Length 59;  
 ilarity 100.0%; Pred. No. 1e+05;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CATTGGGAATT 13  
 |||||  
 CATTGGGAATT 59

4722 57 bp DNA linear GSS 15-DEC-2003  
 idopsis thaliana T-DNA flanking sequence GK-682C08-023963,  
 mic survey sequence.  
 4722.1 GI:39927217

idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 natophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

zhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.  
 Weisshaar,B.  
 eline for automated high-throughput generation of FSTs  
 nking sequence tags) from Arabidopsis thaliana T-DNA  
 ublished lines  
 ublished

30,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
 w Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 flanking sequence tag based reverse genetics  
 ublished  
 (bases 1 to 57)  
 f., Strizhov,N., Rosso,M. and Weisshaar,B.  
 ct Submission  
 itted (15-DEC-2003) Weisshaar B., Max-Planck-Institut fuer  
 htungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 s sequence is recovered from the left border of the T-DNA. It  
 icates an insertion close to or within gene Atlg79000. The  
 nences are generated at the MPI for Plant Breeding Research in  
 context of the GABI-Kat project. GABI-Kat is part of the German  
 it Genomics program designated 'GABI'. Information on line  
 liability can be found at:  
 p://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers  
 1. 57  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-682C08-023963"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /notes="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

71.1%; Score 12.8; DB 29; Length 57;  
 ilarity 87.5%; Pred. No. 1.3e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TATTGGGAATTGCC 18  
 |||||  
 TATTAAAAATTTGCC 53

RESULT 11  
 AZ477130 58 bp DNA linear GSS  
 LOCUS  
 DEFINITION  
 1M0296021F Mouse 10kb plasmid UUGC1M library Mus musculus  
 clone UUGC1M0296021 F, genomic survey sequence.  
 AZ477130  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur  
 1 (bases 1 to 58)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Ham  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads fir  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0296 Row: 0 Column: 21  
 Seq primer: CTTGTAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 58.  
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 1. 58  
 /organism="Mus musculus"  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0296021"  
 /sex="Male"  
 /lab\_host="W. Coli strain XL10-Gold, T1-resist  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: FWD42rv; Purified genomic DNA f  
 musculus C57BL/6J (male) was obtained from th  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares  
 was hydrodynamically sheared by repeated passa  
 0.005 inch orifice at constant velocity. The s  
 was blunt end-repaired with T4 DNA polymerase  
 polynucleotide kinase. Adaptor oligonucleotide  
 ligated to the blunt ends in high molar excess  
 adaptor DNA was purified and size-selected f  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from  
 of pMD42 (G14732114|9b|AF129072.1), a copy-nu  
 inducible derivative of plasmid R1. The vector  
 with adaptors complementary to the insert adap  
 purified. The sheared, adaptor mouse DNA was  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Strata  
 and selected for ampicillin resistance."

Query Match 71.1%; Score 12.8; DB 28; Length 58;  
 Best Local Similarity 87.5%; Pred. No. 1.3e+05;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 2 TCATTGGGAATTTGCC 17  
 |||||  
 Db 25 TGAGTTGGAATTTGCC 40

## ORIGIN

775 58 bp DNA linear GSS 03-SEP-2002  
phila melanogaster DNA, clone:NP6401-5-1, flanking P(GAWB)  
poson insertion, genomic survey sequence.

775.1 GI:22764775

phila melanogaster (fruit fly)

phila melanogaster  
yota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
era; Endopterygota; Diptera; Brachycera; Muscomorpha;  
roidea; Drosophilidae; Drosophila.

hi,S., Ito,K., Sado,Y., Taniguchi,M., Akimoto,A., Takeuchi,H.,  
i,T., Matsuzaki,F., Nakagoshi,H., Tanimura,T., Ueda,R.,  
a,T., Yoshihara,M. and Goto,S.  
a database compiling expression patterns and molecular  
ions of a collection of Gal4 enhancer traps  
is (2002) In press  
ases 1 to 58)

hi,S.

Submission  
tted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for  
limental Biology, Laboratory for Morphogenetic Singaling;  
-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan  
il:shayashi@cdb.riken.go.jp, Tel:81-78-301-3184,  
91-78-301-3183)

clone was isolated from genomic DNA flanking an insertion of  
p element vector P(GAWB) of a Drosophila strain.

Location/Qualifiers

1..58  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/strain="NP6401"  
/db\_xref="taxon:7227"  
/chromosome="2"  
/map="50D1"  
/clone="NP6401-5-1"  
/note="Flanking P(GAWB) transposon insertion"

71.1%; Score 12.8; DB 29; Length 58;  
ilarity 87.5%; Pred. No. 1.3e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CATTGGAAATTTG 16

|||||

CATTTGGATTTG 15

1979 59 bp DNA linear GSS 09-OCT-2003  
idopsis thaliana T-DNA flanking sequence GK-682C08-023112,  
mic survey sequence.

1979.1 GI:37618401

idopsis thaliana (thale cress)

idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

zhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Siedler,H.  
Weisshaar,B.

pipeline for automated high-throughput generation of FSTs  
inking sequence tags) from Arabidopsis thaliana T-DNA

transformed lines

ublished

AUTHORS  
TITLE

JOURNAL

REFERENCE

AUTHORS

JOURNAL

COMMENT

FEATURES

source

Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Wei  
A new Arabidopsis thaliana T-DNA mutagenised population  
for flanking sequence tag based reverse genetics

Unpublished

3 (bases 1 to 59)

Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.

Direct Submission

Submitted (06-OCT-2003) Weisshaar B., Max-Planck-Institut  
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829,  
This sequence is recovered from the left border of the T-  
indicates an insertion close to or within gene Atlg79000  
sequences are generated at the MPI for Plant Breeding Re-  
the context of the GABI-Kat project. GABI-Kat is part of  
Plant Genomics program designated 'GABI'. Information on  
availability can be found at:  
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1..59

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-682C08-023112"

/clone\_lib="Arabidopsis thaliana T-DNA insertion"  
/note="PCR was performed on DNA from Arabidopsis  
plants (T1) which were transformed with the T-DNA  
vector pAC161. The lines contain one or more T-  
insertions. The DNA fragment(s) resulting from  
were directly sequenced to determine the genomic  
flanking the insertion. Sequences displaying si-  
milarity to the A. thaliana nuclear genome se-  
processed for submission. T-DNA derived sequence  
removed"

ORIGIN

Query Match 71.1%; Score 12.8; DB 29; Length 59;

Best Local Similarity 87.5%; Pred. No. 1.3e+05;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 3 CATTGGAAATTTGCC 18

|||||

40 CATTTACATTTGCC 55

Db

RESULT 14

AL758081

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-155F02-0  
genomic survey sequence.

ACCESSION AL758081

VERSION AL758081.1 GI:21496429

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra-  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic-  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidop-  
1

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institi

htungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 states an insertion within the locus defined by clone t31e10.  
 sequences are generated at the MPI for Plant Breeding Research  
 he context of the GABI-Kat project. GABI-Kat is part of the  
 an Plant Genomics program designated 'GABI'. Information on  
 availability can be found at:  
 ://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers  
 1. 50

/organism="Arabidopsis thaliana"  
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 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

71.1%; Score 12.8; DB 29; Length 60;  
 ilarity 87.5%; Pred. No. 1.3e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

'CATTTGGAATTTG 16  
 |||||  
 'CTTTGCAATTTG 57

7315 45 bp mRNA linear EST 31-JUL-1998  
 7315 Schizosaccharomyces pombe late log phase cDNA  
 izosaccharomyces pombe cDNA clone spc01747, mRNA sequence.

7315  
 7315.1 GI:3343773

izosaccharomyces pombe (fission yeast)  
 izosaccharomyces pombe  
 ryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 izosaccharomycetales; Schizosaccharomycetaceae;  
 izosaccharomycetes.  
 (bases 1 to 45)  
 lmyo.M. and Mita, K.  
 atification of expressed sequence tags of Schizosaccharomyces  
 e  
 blished (1998)  
 act: Mitsuoki Morimyo  
 me Research Group  
 ional Institute of Radiological Sciences  
 , Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
 il: morimyo@nirs.go.jp

Location/Qualifiers

1. 45  
 /organism="Schizosaccharomyces pombe"  
 /mol\_type="mRNA"  
 /strain="972"  
 /db\_xref="taxon:4896"  
 /clone="spc01747"  
 /sex="a minus"  
 /note="lib="Schizosaccharomyces pombe late log phase cDNA"  
 /clone="vector: M13mp19; The cDNA library of  
 Schizosaccharomyces pombe was prepared by cloning cDNA  
 into the SmaI site of M13mp19 DNA and the direction of DNA  
 sequences was not always from 5' to 3'. The cDNA data of  
 Schizosaccharomyces pombe are available for searching on

the World Wide Web. (URL, <http://www.nirs.go.jp>)

ORIGIN  
 Query Match 68.9%; Score 12.4; DB 9; Length 45;  
 Best Local Similarity 92.9%; Pred. No. 1.9e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;

Oy 2 TCATTGGAATTTT 15  
 |||||  
 Db 28 TCATTGGAATTTT 15

RESULT 16  
 AUI03941/c

LOCUS  
 DEFINITION AUI03941 Sugano Homo sapiens cDNA library Homo sapiens c  
 HEP17626, mRNA sequence.

ACCESSION AUI03941

VERSION AUI03941.1 GI:13553462

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Hom

REFERENCE  
 AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Se  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Ok  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S., Ok  
 Diverse transcriptional initiation revealed by fine, lar  
 mapping of mRNA start sites  
 EMBO Rep. 2 (5), 388-393 (2001)

21270072

11375929

COMMENT

Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A.  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gen  
 149-156 (1997).

FEATURES  
 source

1..50  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HEP17626"  
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ORIGIN

Query Match 68.9%; Score 12.4; DB 9; Length 50;  
 Best Local Similarity 92.9%; Pred. No. 1.9e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0;

Oy 5 TTTTGGAAATTTGCC 18  
 |||||

Db 30 TTTTGGAAATTTCCC 17

RESULT 17

CC85817

LOCUS

DEFINITION CC85817 30 bp DNA linear GSS  
 SALK\_147877.15.70.x Arabidopsis thaliana TDNA insertion  
 Arabidopsis thaliana genomic clone SALK\_147877.15.70.X,  
 survey sequence.

ACCESSION CC85817

VERSION CC85817.1 GI:33362173

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudi

is; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 bases 1 to 30)  
 o,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 nab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 P., Zimmerman,J. and Ecker,J.R.  
 quence-Indexed Library of Insertion Mutations in the  
 idopsis Genome  
 ublished (2001)  
 act: Joseph R. Ecker  
 Institute Genomic Analysis Laboratory (SIGNAL)  
 Salk Institute for Biological Studies  
 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 858 453 4100 x1752  
 858 558 6379  
 l: ecker@salk.edu  
 is single pass sequence recovered from the left border of

3: TDNA tagged.  
 Location/Qualifiers  
 1. .30  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
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 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

67.8%; Score 12.2; DB 29; Length 30;  
 ilarity 82.4%; Pred. No. 2.4e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TATTGGGAATTTTGC 17  
 ||||| ||||| |||||  
 TATATGGAGTTTGGC 18

3850 34 bp DNA linear GSS 13-JUN-2002  
 078369.50.70.x Arabidopsis thaliana TDNA insertion lines  
 idopsis thaliana genomic clone SALK\_078369.50.70.x, genomic  
 ey sequence.  
 3850  
 3850.1 GI:21424721

idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 bases 1 to 34)  
 so,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 inab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 n.P., Zimmerman,J. and Ecker,J.R.  
 quence-Indexed Library of Insertion Mutations in the  
 idopsis Genome  
 ublished (2001)  
 act: Joseph R. Ecker  
 Institute Genomic Analysis Laboratory (SIGNAL)  
 Salk Institute for Biological Studies  
 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 858 453 4100 x1752  
 858 558 6379  
 l: ecker@salk.edu  
 is single pass sequence recovered from the left border of  
 . This sequence lies within an annotated exon of At3g33056.

Class: TDNA tagged.  
 Location/Qualifiers  
 1. .34  
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 /note="PCR was performed on Arabidopsis thalian  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 34;  
 Best Local Similarity 82.4%; Pred. No. 2.4e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTTGC 17  
 ||||| ||||| |||||  
 Db 3 CTCATATGGAGTTTGGC 19

RESULT 19  
 BZ379829 36 bp DNA linear GSS  
 SALK\_114073.15.70.x Arabidopsis thaliana TDNA insertion  
 Arabidopsis thaliana genomic clone SALK\_114073.15.70.x,  
 survey sequence.

ACCESSION BZ379829  
 VERSION BZ379829.1 GI:25472068  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Arabidopsis thaliana  
 Rukarya; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 (bases 1 to 36)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P  
 Shinn,P., Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGNAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left bor  
 TDNA.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1. .36  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
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 /clone="SALK\_114073.15.70.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /note="PCR was performed on Arabidopsis thalian  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

ORIGIN

SOURCE ORGANISM	Arabidopsis thaliana (thale cress)
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL COMMENT	Unpublished (2001) Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (STGrNL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379

**JOURNAL  
COMMENT**

Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGnAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379

```

Email: ecker@salk.edu
This is single pass sequence recovered from the left box.
TDNA. This sequence lies within an annotated exon of AtrS.
Class: TDNA tagged.
      Location/Qualifiers
1. 37
   /organism="Arabidopsis thaliana"
   /mol_type="genomic DNA"
   /strain="Columbia 0"
   /db_xref="taxon:3702"
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   /clone_lib="Arabidopsis thaliana TDNA insertion"
   /note="PCR was performed on Arabidopsis thalian
each of which contains one or more TDNA insert
elements. the resultant fragment for each line
directly sequenced to determine the genomic seq
the site of insertion. Details of the protocol
be found at http://signal.salk.edu/tdna\_protoc

```

Matches	14;	Conservative	0;	Mismatches	3;	Indels	0;
Qy	1	CTCATTTGGAATTTTGC	17				
Db	9	CTCATATGGAGTTTGC	25				
RESULT 22							
BZ355646							
LOCUS		BZ355646		40 bp	DNA	linear	GSS
DEFINITION		SALK_127150.32.95.x Arabidopsis thaliana					TDNA insertion
		Arabidopsis thaliana genomic clone SALK_127150.32.95.x,					
		survey sequence.					
ACCESSION		BZ355646					
VERSION		BZ355646.1					GI:24946805
KEYWORDS		GSS.					
SOURCE		Arabidopsis thaliana (thale cress)					
ORGANISM		Arabidopsis thaliana					
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra					

REFERENCE  
1. (bases 1 to 40)  
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
AUTHORS

Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGnAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

09:38:23 2004

us-10-090-326-16.max.rst

```
858 558 6379
: ecker@salk.edu
is single pass sequence recovered from the left border of

:: TDNA tagged.
Location/Qualifiers
1. .40
/organism="Arabidopsis thaliana"
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/strain="Columbia 0"
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

        67.8%; Score 12.2; DB 28; Length 40;
        82.4%; Pred. No. 2.4e+05;
Conservative 0; Mismatches 3; Indels 0;

ATTGTGGAATTTGC 17
|||||
ATATGGACTTTGGC 25

:201
086477.45.50.x Arabidopsis thaliana TDNA insertion lines
[dopsis thaliana genomic clone SALK_086477.45.50.x, genomic
sequence.
:201.1 GI:21704791

dopsis thaliana (thale cress)
.dopsis thaliana
yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; eudicotyledons; core eudicots;
is; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
ases 1 to 41)
so J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
inab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
l, P., Zimmerman, J. and Ecker, J.R.
pence-Indexed Library of Insertion Mutations in the
dopsis Genome
lished (2001)
ct: Joseph R. Ecker
nstitute Genomic Analysis Laboratory (SIGnAL)
alk Institute for Biological Studies
) N. Torrey Pines Road, La Jolla, CA 92037, USA
858 453 4100 x1752
858 558 6379
l: ecker@salk.edu
is single pass sequence recovered from the left border of
. This sequence lies within an annotated exon of At3g33056.
s: TDNA tagged.
Location/Qualifiers
1. .41
/organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_086477.45.50.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
```

```
the site of insertion. Details of the protocols
be found at http://signal.salk.edu/tdna\_protoc

ORIGIN
Query Match 67.8%; Score 12.2; DB 28; Length 41;
Best Local Similarity 82.4%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTGCG 17
|||||
5 CTCATATGGACTTTGGC 21

Db

RESULT 24
CC887116
LOCUS
DEFINITION
SALK_149581.42.50.x Arabidopsis thaliana TDNA insertion
Arabidopsis thaliana genomic clone SALK_149581.42.50.x,
survey sequence.
CC887116
CC887116.1 GI:33363472
GSS.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
rosids; eurosids II; Brassicales; Brassicaceae; Arabidop
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., P
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left bor
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. .41
/organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_149581.42.50.x"
/clone_lib="Arabidopsis thaliana TDNA insertion
/note="PCR was performed on Arabidopsis thalian
each of which contains one or more TDNA insert
elements. The resultant fragment for each line
directly sequenced to determine the genomic seq
the site of insertion. Details of the protocols
be found at http://signal.salk.edu/tdna\_protoc

ORIGIN
Query Match 67.8%; Score 12.2; DB 29; Length 41;
Best Local Similarity 82.4%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGGAATTTGCG 17
|||||
10 CTCATATGGACTTTGGC 26

Db

RESULT 25
AU012201/c
LOCUS
DEFINITION
AU012201 Schizosaccharomyces pombe late log phase cDNA
42 bp mRNA linear EST
```

zosaccharomyces pombe cDNA clone spc06480, mRNA sequence.

```

2201      1 GI:3357110
2201.1    GI:3357110

zosaccharomyces pombe (fission yeast)
zosaccharomyces pombe
ryota; Fungi; Ascomycota; Schizosaccharomycetes;
zosaccharomycetales; Schizosaccharomycetaceae;
zosaccharomycetes.
cases 1 to 42)
Mito, Mita, K.
fication of expressed sequence tags of Schizosaccharomyces
published (1998)
act: Mitsuoki Morimyo
me Research Group
onal Institute of Radiological Sciences
Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
1: morimyo@nirs.go.jp.
Location/Qualifiers
1..42
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc06480"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
67.8%; Score 12.2; DB 9; Length 42;
ilarity 82.4%; Pred. No. 2.4e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

'CATTTGGAATTTC 17
|||||
'CATTTGGAATTTC 8

14071      42 bp      DNA      linear      GSS 20-OCT-2003
162C05.2EL_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
rey sequence.
14071
14071.1    GI:37776563

mays
mays
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
le; Panicoideae; Andropogoneae; Zea.
(bases 1 to 42)
oot, V.
ze genomic sequences found using engineered RescueMu transposon
ublished (2001)
tact: Walbot V
artment of Biological Sciences
nford University
California Ave, Palo Alto, CA 94304, USA
: 650 723 2227
: 650 725 8221
il: walbot@stanford.edu
sible ligation site of ends cut by 2 different endonucleases.
erse complemented post-ligation sequence from source sequence.
te: 1119162 column: 1
ss: transposon-tagged.

```

#### FEATURES

source

```

Location/Qualifiers
1..42
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered
pBluescript backbone); Site 1: BamHI; Site 2: B
RescueMu is a 4.9 kb, modified maize Mu transpo
designed to allow plasmid rescue from total gen
Mu elements insert preferentially into transcri
units. For more information on RescueMu, go to
site 'www.zmdb.iastate.edu' and follow the link
'RescueMu.' Grid AA was grown at UC San Diego i
was extracted from leaf strips, double digested
BamHI and BglII, and ligated to form circular p
DH10B cells were transformed and then screened
plates with ampicillin."

```

#### ORIGIN

```

Query Match      67.8%; Score 12.2; DB 29; Length 42;
Best Local Similarity 82.4%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

```

QY 1 CTATTGGAAATTTC 17

DB 10 CTCATTGGAATTTC 26

#### RESULT 27

BZ765054

LOCUS

#### DEFINITION

BZ765054 43 bp DNA linear GSS  
SALK\_128153.35.60.n Arabidopsis thaliana TDNA insertion  
Arabidopsis thaliana genomic clone SALK\_128153.35.60.n,  
survey sequence.

#### ACCESSION

BZ765054

#### VERSION

BZ765054.1 GI:28937607

#### KEYWORDS

GSS.

#### SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra

Spermatophyta; Magnoliophyta; eudicotyledons; core eudic

rosids; eurosids II; Brassicales; Brassicaceae; Arabidoi

1 (bases 1 to 43)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., I

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left bo:

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..43

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_128153.35.60.n"

/clone\_lib="Arabidopsis thaliana TDNA insertio

/note="PCR was performed on Arabidopsis thalia

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

67.8%; Score 12.2; DB 28; Length 43;  
 ilarity 82.4%; Pred. No. 2.4e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTTGTC 17  
 |||||  
 CATATGACTTTGTC 28

9777 47 bp DNA linear GSS 13-JUN-2002  
 070271.47.05.x Arabidopsis thaliana TDNA insertion lines  
 idopsis thaliana genomic clone SALK\_070271.47.05.x, genomic  
 ey sequence.

9777.1 GI:21420648

idopsis thaliana (thale cress)

Arabidopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 bases 1 to 47)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 inab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 n, P., Zimmerman, J. and Ecker, J.R.

quence-Indexed Library of Insertion Mutations in the  
 idopsis Genome

blished (2001)

act: Joseph R. Ecker  
 Institute Genomic Analysis Laboratory (SIGnAL)  
 Salk Institute for Biological Studies  
 0 N. Torrey Pines Road, La Jolla, CA 92037, USA

858 453 4100 x1752  
 858 558 6379  
 l: ecker@salk.edu

is single pass sequence recovered from the left border of  
 .. This sequence lies within an annotated exon of At3g33056.  
 s: TDNA tagged.

Location/Qualifiers

1. 47  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_070271.47.05.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

67.8%; Score 12.2; DB 28; Length 47;  
 ilarity 82.4%; Pred. No. 2.4e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTTGTC 17  
 |||||  
 CATATGGAATTTGTC 32

BZ761387

LOCUS

DEFINITION  
 SALK\_000303.29.60.x Arabidopsis thaliana TDNA insertion  
 Arabidopsis thaliana genomic clone SALK\_000303.29.60.x,  
 survey sequence.

ACCESSION

VERSION BZ761387.1 GI:28933940

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 (bases 1 to 47)

REFERENCE

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., I  
 Shinn, P., Zimmerman, J. and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)

JOURNAL

COMMENT

Contact: Joseph R. Ecker

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The Salk Institute for Biological Studies

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Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 47  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_000303.29.60.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /note="PCR was performed on Arabidopsis thalian  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 47;  
 Best Local Similarity 82.4%; Pred. No. 2.4e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTTGGAATTTGTC 17

|||||

Db 11 CTCATATGGGATTTGTC 27

RESULT 30

BZ765317

LOCUS

DEFINITION  
 SALK\_130130.43.05.x Arabidopsis thaliana TDNA insertion  
 Arabidopsis thaliana genomic clone SALK\_130130.43.05.x,  
 survey sequence.

ACCESSION

VERSION BZ765317

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidop  
 1 (bases 1 to 47)

REFERENCE

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., P  
 Shinn, P., Zimmerman, J. and Ecker, J.R.



quence-Indexed Library of Insertion Mutations in the  
idopsis Genome  
blished (2001)  
at: Joseph R. Ecker  
Institute Genomic Analysis Laboratory (SIGNAL)  
Salk Institute for Biological Studies  
10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
858 453 4100 x1752  
858 558 6379  
il: ecker@salk.edu  
is single pass sequence recovered from the left border of

s: TDNA tagged.  
Location/Qualifiers  
1. .47  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_lib="SALK\_130130.43.05.x"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

67.8%; Score 12.2; DB 28; Length 47;  
ilarity 82.4%; Pred.No. 2.4e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTATTGGAATTTCG 17  
|||||  
CATATGACCTTTGGC 32

11466 48 bp DNA linear GSS 02-APR-2002  
\_060006.39.50.x Arabidopsis thaliana TDNA insertion lines  
idopsis thaliana genomic clone SALK\_060006.39.50.x, genomic  
ey sequence.

11466  
11466.1 GI:19885359

idopsis thaliana (thale cress)  
idopsis thaliana  
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
(bases 1 to 48)  
iso.J.M., Leisbe, T.J., Barajas, P., Chen, H., Cheuk, R.,  
cinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
an, P., Zimmerman, J., and Ecker, J.R.  
sequence-Indexed Library of Insertion Mutations in the  
idopsis Genome  
blished (2001)

act: Joseph R. Ecker  
k Institute Genomic Analysis Laboratory (SIGNAL)  
Salk Institute for Biological Studies  
10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
: 858 453 4100 x1752  
: 858 558 6379  
il: ecker@salk.edu

s is single pass sequence recovered from the left border of  
A.

ss: TDNA tagged.  
Location/Qualifiers  
1. .48  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"

/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_060006.39.50.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion  
/note="PCR was performed on Arabidopsis thalian  
each of which contains one or more TDNA inser  
elements. The resultant fragment for each line  
directly sequenced to determine the genomic seq  
the site of insertion. Details of the protocol  
be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

## ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 48;  
Best Local Similarity 82.4%; Pred.No. 2.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAAATTTGCG 17  
|||||  
DB 17 CTCATATGGACTTTGGC 33

## RESULT 32

BZ765295 48 bp DNA linear GSS  
SALK\_129795.21.75.x Arabidopsis thaliana TDNA insertion  
Arabidopsis thaliana genomic clone SALK\_129795.21.75.x,  
survey sequence.

ACCESSION BZ765295  
VERSION BZ765295.1 GI:28937848

## KEYWORDS

Arabidopsis thaliana (thale cress)

## SOURCE

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidoi

## REFERENCE

1 (bases 1 to 48)  
Alonso, J.M., Leisbe, T.J., Barajas, P., Chen, H., Cheuk, R.,  
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., i  
Shinn, P., Zimmerman, J., and Ecker, J.R.

## TITLE

A sequence-indexed library of insertion mutations in the  
Arabidopsis Genome

## JOURNAL

Unpublished (2001)

## COMMENT

Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left bo  
TDNA.

Class: TDNA tagged.

Location/Qualifiers

## FEATURES

source  
1. .48  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_129795.21.75.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion  
/note="PCR was performed on Arabidopsis thalian  
each of which contains one or more TDNA inser  
elements. The resultant fragment for each lin  
directly sequenced to determine the genomic se  
the site of insertion. Details of the protocol  
be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

## ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 48;  
Best Local Similarity 82.4%; Pred.No. 2.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGAAATTTGCG 17

|||||  
 ATATGGACTTTGGC 45

392 50 bp DNA linear GSS 02-APR-2002  
 056948.49.55.x Arabidopsis thaliana TDNA insertion lines  
 dopsis thaliana genomic clone SALK\_056948.49.55.x, genomic  
 y sequence.  
 392  
 392.1 GI:19883490

dopsis thaliana (thale cress)

yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 atophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 s; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 ases 1 to 50)

O.J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 nab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednits, L.,  
 P., Zimmerman, J., and Ecker, J.R.

quence-Indexed Library of Insertion Mutations in the  
 dopsis Genome

lished (2001)

ct: Joseph R. Ecker

Institute Genomic Analysis Laboratory (SIGNAL)

alk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

858 453 4100 x1752

858 558 6379

.. ecker@salk.edu

is single pass sequence recovered from the left border of

:: TDNA tagged.

Location/Qualifiers

1. .50

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_056948.49.55.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

ilarity 67.8%; Score 12.2; DB 28; Length 50;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTGGCAATTTCG 17

|||||

CATATGGACTTTGGC 35

6964 51 bp DNA linear GSS 07-JAN-2003

097916.43.45.x Arabidopsis thaliana TDNA insertion lines

idopsis thaliana genomic clone SALK\_097916.43.45.x, genomic

ey sequence.

6964

6964.1 GI:27537676

idopsis thaliana (thale cress)

idopsis thaliana

ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

matophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidops  
 1 (bases 1 to 51)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., P

Shinn, P., Zimmerman, J., and Ecker, J.R.

A sequence-indexed library of insertion mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left bord

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .51

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_097916.43.45.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion

/note="PCR was performed on Arabidopsis thaliana

each of which contains one or more TDNA inserti

elements. The resultant fragment for each line

directly sequenced to determine the genomic seq

the site of insertion. Details of the protocol

be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

# ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 51;

Best Local Similarity 82.4%; Pred. No. 2.4e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGCAATTTCG 17

|||||

Db 20 CTCATATGGACTTTGGC 36

RESULT 35

BZ766946

LOCUS

DEFINITION

Arabidopsis thaliana genomic clone SALK\_138093.30.10.n,

survey sequence.

ACCESSION

BZ766946

VERSION

BZ766946.1

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress).

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra

Spermatophyta; Magnoliophyta; eudicotyledons; core eudic

rosids; eurosids II; Brassicales; Brassicaceae; Arabidop

1 (bases 1 to 51)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., P

Shinn, P., Zimmerman, J., and Ecker, J.R.

A sequence-indexed library of insertion mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left bor

TDNA.

09:38:23 2004

us-10-090-326-16.max.rst

```
s: TDNA tagged.
Location/Qualifiers
1..51
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/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_138093.30.10.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

67.8%; Score 12.2; DB 28; Length 51;
ilarity 82.4%; Pred. NO. 2.4e+05;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CATTTGGAATTTGTC 17
|||||
CATATGGACTTTGCC 48

5493
098653 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_098653, genomic survey sequence.
5493
5493.1 GI:22101391

idopsis thaliana (thale cress)
idopsis thaliana
idopsis thaliana
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; eudicotyledons; core eudicots;
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
(bases 1 to 52)
iso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
cinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
m,P., Zimmerman,J. and Ecker,J.R.
sequence-Indexed Library of Insertion Mutations in the
idopsis Genome
ublished (2001)
act: Joseph R. Ecker
c Institute Genomic Analysis Laboratory (SIGAL)
Salk Institute for Biological Studies
10 N. Torrey Pines Road, La Jolla, CA 92037, USA
: 858 453 4100 x1752
: 858 558 6379
l: ecker@salk.edu
s is single pass sequence recovered from the left border of
a. This sequence lies within an annotated exon of At3g3056.
ss: TDNA tagged.
Location/Qualifiers
1..52
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_098653"
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

67.8%; Score 12.2; DB 28; Length 52;
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Best Local Similarity 82.4%; Pred. NO. 2.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CTCATTTGGAAATTTGTC 17
|||||
Db 21 CTCATATGGAACTTTGCC 37

RESULT 37
CF048724
LOCUS QCU26f05.yg QCL Zea mays cDNA clone QCU26f05, mRNA sequ 54 bp mRNA linear EST
DEFINITION CF048724
ACCESSION CF048724
VERSION CF048724.1 GI:32943905
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poace
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 54)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the
plant genomics programme 'Genoplante' (http://www.genopl)
and http://genoplante-info.inbio.gen.fr.
FEATURES
Location/Qualifiers
1..54
Source
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QCU26f05"
/tissue type="apex"
/clone_lib="QCL"

Query Match 67.8%; Score 12.2; DB 14; Length 54;
Best Local Similarity 82.4%; Pred. NO. 2.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 2 TCATTTGGAATTTGTC 18
|||||
Db 12 TCATTTGGAATTTGCC 28

RESULT 38
CF053832
LOCUS QCN2ic11.yg QCN Zea mays cDNA clone QCN2ic11, mRNA sequ 54 bp mRNA linear EST
DEFINITION CF053832
ACCESSION CF053832
VERSION CF053832.1 GI:33093838
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poace
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 54)
AUTHORS Genoplante.
TITLE Genoplante, a major partnership french program in plant
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
```

sequence has been generated in the framework of the french genomics programme 'genoplante' (<http://www.genoplante.com>)  
<http://genoplante-info.infobiogen.fr/>.

Location/Qualifiers  
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 /clone\_lib="QC21"  
 57.8%; Score 12.2; DB 14; Length 54;  
 larity 82.4%; Pred. No. 2.4e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 TTTCGAAATTTGGC 18  
 |||||  
 TTTCGATTTTCCC 28  
 |||||  
 '961 55 bp DNA linear GSS 13-MAR-2003  
 139587.40.90.x Arabidopsis thaliana TDNA insertion lines  
 dopsis thaliana genomic clone SALK\_139587.40.90.x, genomic  
 y sequence.  
 '961 GI:28940903  
 dopsis thaliana (thale cress)  
 dopsis thaliana  
 yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 natophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 is; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 ases 1 to 55)  
 o.J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 nab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 l,P., Zimmerman,J. and Ecker,J.R.  
 uence-Indexed Library of Insertion Mutations in the  
 dopsis Genome  
 lished (2001)  
 ct: Joseph R. Ecker  
 Institute Genomic Analysis Laboratory (SIGnAL)  
 alk Institute for Biological Studies  
 ) N. Torrey Pines Road, La Jolla, CA 92037, USA  
 858 453 4100 x1752  
 858 558 6379  
 l: ecker@salk.edu  
 is single pass sequence recovered from the left border of  
 s: TDNA tagged.  
 Location/Qualifiers  
 1..55  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_139587.40.90.x"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
 67.8%; Score 12.2; DB 28; Length 55;  
 ilarity 82.4%; Pred. No. 2.4e+05;  
 Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTCATTTGGAATTTGTC 17  
 |||||  
 Db 24 CTCATATGGACTTTGGC 40  
 |||||

RESULT 40  
 BZ352570  
 LOCUS  
 DEFINITION  
 Arabidopsis thaliana genomic clone SALK\_081150.33.65.x, 9  
 survey sequence.  
 BZ352570  
 BZ352570.1 GI:24943432  
 GSS.  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicc  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidops  
 1 (bases 1 to 56)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P;  
 Shinn,P., Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGnAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left bord  
 TDNA.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1..56  
 /organism="Arabidopsis thaliana"  
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 /clone\_lib="Arabidopsis thaliana TDNA insertion  
 /note="PCR was performed on Arabidopsis thalian  
 each of which contains one or more TDNA insert  
 elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

## ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 56;  
 Best Local Similarity 82.4%; Pred. No. 2.4e+05;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTTGGAATTTTGC 17  
 |||||  
 Db 25 CTCATATGGACTTTGGC 41  
 |||||

RESULT 41  
 AU007849/c  
 LOCUS  
 DEFINITION  
 Schizosaccharomyces pombe cDNA clone spc02572, mRNA sequ  
 Schizosaccharomyces pombe  
 AU007849  
 AU007849.1 GI:3344307  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Schizosaccharomyces pombe (fission yeast)  
 Schizosaccharomyces pombe  
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

zooaccharomycetales; Schizosaccharomycetaceae;  
zooaccharomycetes.

bases 1 to 58)

myo.M. and Mita.K.

ification of expressed sequence tags of Schizosaccharomycetes

ublished (1998)

act: Mitsuoki Morimyo

me Research Group

onal Institute of Radiological Sciences

Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan

l: morimyo@nirs.go.jp.

Location/Qualifiers

1. 58

/organism="Schizosaccharomycetes pombe"

/mol\_type="mRNA"

/strain="972"

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/sex="h minus"

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/note="Vector: M13mp19; The cDNA library of

Schizosaccharomycetes pombe was prepared by cloning cDNA

into the SmaI site of M13mp19 DNA and the direction of DNA

sequences was not always from 5' to 3'. The cDNA data of

Schizosaccharomycetes pombe are available for searching on

the World Wide Web. (URL, <http://www.nirs.go.jp>)"

67.8%; Score 12.2; DB 9; Length 58;

ilarity 82.4%; Pred. NO. 2.3e+05;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATTGGCAATTTCG 17

|||||

TCATTGAATATTTCG 26

18039 58 bp mRNA linear EST 31-JUL-1998

18039 Schizosaccharomycetes pombe late log phase cDNA

zooaccharomycetes pombe cDNA clone spc02795, mRNA sequence.

18039

18039.1 GI:3344497

zooaccharomycetes pombe (fission yeast)

zooaccharomycetes pombe

ryota; Fungi; Ascomycota; Schizosaccharomycetes;

zooaccharomycetales; Schizosaccharomycetaceae;

zooaccharomycetes.

(bases 1 to 58)

myo.M. and Mita.K.

ification of expressed sequence tags of Schizosaccharomycetes

ublished (1998)

act: Mitsuoki Morimyo

me Research Group

ional Institute of Radiological Sciences

Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan

l: morimyo@nirs.go.jp.

Location/Qualifiers

1. 58

/organism="Schizosaccharomycetes pombe"

/mol\_type="mRNA"

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/note="Vector: M13mp19; The cDNA library of

Schizosaccharomycetes pombe was prepared by cloning cDNA

into the SmaI site of M13mp19 DNA and the direction of DNA

# ORIGIN

Query Match 67.8%; Score 12.2; DB 9; Length 58;  
Best Local Similarity 82.4%; Pred. NO. 2.3e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGCAATTTCG 17

|||||

DB 42 CTCATTGAATATTTCG 26

RESULT 43

BZ769782

LOCUS

DEFINITION BZ769782 58 bp DNA linear GSS

SALK\_142715.38.60.x Arabidopsis thaliana TDNA insertion

Arabidopsis thaliana genomic clone SALK\_142715.38.60.x,

survey sequence.

ACCESSION BZ769782

VERSION BZ769782.1 GI:28943466

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (chale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra

Spermatophyta; Magnoliophyta; eudicotyledons; core eudic

rosids; eurosids II; Brassicales; Brassicaceae; Arabido

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., I

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

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Unpublished (2001)

Contact: Joseph R. Ecker

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The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left bo

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 58

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

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/clone\_lib="Arabidopsis thaliana TDNA insertion

/note="PCR was performed on Arabidopsis thalian

each of which contains one or more TDNA insert

elements. The resultant fragment for each line

directly sequenced to determine the genomic se

the site of insertion. Details of the protoc

be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)

# ORIGIN

Query Match 67.8%; Score 12.2; DB 28; Length 58;  
Best Local Similarity 82.4%; Pred. NO. 2.3e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CTCATTGGCAATTTCG 17

|||||

DB 25 CTCATATGCAATTTCG 41

RESULT 44

BZ765982

LOCUS

BZ765982 59 bp DNA linear GSS

sequences was not always from 5' to 3'. The cD  
Schizosaccharomycetes pombe are available for sea  
the World Wide Web. (URL, <http://www.nirs.go>;

09:38:23 2004

us-10-090-326-16.max.rst

136100.47.80.x Arabidopsis thaliana TDNA insertion lines  
idopsis thaliana genomic clone SALK\_136100.47.80.x, genomic  
ey sequence.  
5982.1 GI:28938535  
idopsis thaliana (thale cress)  
idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
bases 1 to 59)  
so, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
inab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
n, P., Zimmerman, J. and Ecker, J.R.  
quence-Indexed Library of Insertion Mutations in the  
idopsis Genome  
blished (2001)  
act: Joseph R. Ecker  
Institute Genomic Analysis Laboratory (SIGnAL)  
Salk Institute for Biological Studies  
O N. Torrey Pines Road, La Jolla, CA 92037, USA  
958 453 4100 x1752  
858 558 6379  
l: ecker@salk.edu  
is single pass sequence recovered from the left border of  
s: TDNA tagged.  
Location/Qualifiers  
l. 59  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
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each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
67.8%; Score 12.2; DB 28; Length 59;  
ilarity 82.4%; Pred. No. 2.3e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
'CATTTGGAAATTTTGC 17  
|||||  
CATATGGACTTTGGC 44  
1034  
1034.1 GI:19884457  
idopsis thaliana (thale cress)  
idopsis thaliana  
ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
bases 1 to 60)  
iso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
inab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
n, P., Zimmerman, J. and Ecker, J.R.  
quence-Indexed Library of Insertion Mutations in the  
idopsis Genome

JOURNAL  
COMMENT  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGnAL)  
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10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left bor  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
l. 60  
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/note="PCR was performed on Arabidopsis thalian  
each of which contains one or more TDNA insert  
elements. The resultant fragment for each line  
directly sequenced to determine the genomic seq  
the site of insertion. Details of the protocol  
be found at [http://signal.salk.edu/tdna\\_protoc](http://signal.salk.edu/tdna_protoc)  
Query Match 67.8%; Score 12.2; DB 28; Length 60;  
Best Local Similarity 82.4%; Pred. No. 2.3e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;  
Qy 1 CTCATTTGGAAATTTTGC 17  
|||||  
Db 28 CTCATATGGACTTTGGC 44  
Search completed: February 29, 2004, 11:21:24  
Job time : 1391.17 secs



09:38:23 2004

us-10-090-326-17.max.rge

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

elic search, using sw model

February 29, 2004, 08:42:24 ; Search time 530.753 Seconds  
(without alignments)  
1388.275 Million cell updates/sec

JS-10-090-326-17

cgagtgaagatccctt 17

IDENTITY NUC  
Japop 10.0 , Gapext 1.0

3470272 seqs, 21671516995 residues

hits satisfying chosen parameters: 1685580

length: 0  
length: 60

Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*

30: em.htg.hum.\*

31: em.htg.inv.\*

32: em.htg.other.\*

33: em.htg.mus.\*

34: em.htg.pln.\*

35: em.htg.rtd.\*

36: em.htg.mam.\*

37: em.htg.vrt.\*

38: em.sy.\*

39: em.htgo.hum.\*

40: em.htgo.mus.\*

41: em.htgo.other.\*

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being p  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Descripti
C 1	13.4	78.8	20	6	AR315288	AR315288
C 2	12.4	72.9	17	6	BD197525	BD197525
C 3	12.4	72.9	17	6	BD197526	BD197526
C 4	12.4	72.9	32	6	I24919	I24919 Se
C 5	12.4	72.9	41	6	AX518499	AX518499
C 6	12.2	71.8	17	6	AX215216	AX215216
C 7	12.2	71.8	24	6	AX443791	AX443791
C 8	12.2	71.8	25	6	AX447772	AX447772
C 9	12.2	71.8	25	6	AX467554	AX467554
C 10	12.2	71.8	36	6	AR285893	AR285893
C 11	12.2	71.8	36	6	AX815952	AX815952
C 12	12.2	71.8	37	6	AR397883	AR397883
C 13	12.2	71.8	38	6	AR286827	AR286827
C 14	12.2	71.8	38	6	AR286885	AR286885
C 15	12.2	71.8	38	6	AR286931	AR286931
C 16	12.2	71.8	38	6	AR286960	AR286960
C 17	12.2	71.8	38	6	AR398817	AR398817
C 18	12.2	71.8	38	6	AR398875	AR398875
C 19	12.2	71.8	38	6	AR398921	AR398921
C 20	12.2	71.8	38	6	AR398950	AR398950
C 21	12.2	71.8	38	6	AX220484	AX220484
C 22	12.2	71.8	38	6	AX228757	AX228757
C 23	12.2	71.8	38	6	AX273935	AX273935
C 24	12.2	71.8	38	6	AX425294	AX425294
C 25	12.2	71.8	38	6	AX463628	AX463628
C 26	12.2	71.8	40	6	AX805954	AX805954
C 27	12.2	71.8	46	6	AR126440	AR126440
C 28	12	70.6	17	6	AX759214	AX759214
C 29	12	70.6	17	6	AX762760	AX762760
C 30	12	70.6	26	6	AX753432	AX753432
C 31	12	70.6	31	6	E59836	E59836 Me
C 32	12	70.6	31	6	AR340181	AR340181
C 33	12	70.6	38	6	AX135624	AX135624
C 34	12	70.6	43	6	I71937	I71937 Se
C 35	11.8	69.4	17	6	AX216871	AX216871
C 36	11.8	69.4	20	6	AX296625	AX296625
C 37	11.8	69.4	20	6	AX537893	AX537893
C 38	11.8	69.4	24	6	AX291992	AX291992
C 39	11.8	69.4	27	6	A57409	A57409 Se
C 40	11.8	69.4	27	6	AR131454	AR131454
C 41	11.8	69.4	33	6	BD273188	BD273188
C 42	11.8	69.4	33	6	AR381516	AR381516
C 43	11.8	69.4	33	6	AX474382	AX474382
C 44	11.8	69.4	33	6	BD073213	BD073213
C 45	11.8	69.4	33	6	BD181899	BD181899
C 46	11.8	69.4	35	11	C75890	C75890 H
C 47	11.8	69.4	46	6	A01315	A01315 H.
C 48	11.8	69.4	46	6	A01316	A01316 H.
C 49	11.8	69.4	50	6	AR210368	AR210368
C 50	11.8	69.4	52	6	AR356147	AR356147
C 51	11.8	69.4	57	6	BD074138	BD074138
C 52	11.4	67.1	17	6	I37628	I37628 Se
C 53	11.4	67.1	17	6	I94478	I94478 Se
C 54	11.4	67.1	17	6	AX217232	AX217232
C 55	11.4	67.1	17	6	AX217233	AX217233
C 56	11.4	67.1	17	6	BD197527	BD197527
C 57	11.4	67.1	20	6	AR312818	AR312818
C 58	11.4	67.1	20	6	AR314161	AR314161
C 59	11.4	67.1	20	6	AR315815	AR315815
C 60	11.4	67.1	21	6	AR263717	AR263717
C 61	11.4	67.1	21	6	AX282174	AX282174
C 62	11.4	67.1	21	6	AX282283	AX282283
C 63	11.4	67.1	21	6	AX322934	AX322934
C 64	11.4	67.1	22	6	AX454914	AX454914
C 65	11.4	67.1	23	6	AX211678	AX211678



67.1	26	6	AR122725	Sequence	139	11.2	65.9	38	6	AR399019	AR399019
67.1	29	6	BD270473	Synthetic	140	11.2	65.9	38	6	AR399043	AR399043
67.1	29	6	AX039225	Sequence	141	11.2	65.9	38	6	AR399071	AR399071
67.1	29	6	AX039306	Sequence	142	11.2	65.9	38	6	AR399080	AR399080
67.1	29	6	AX039515	Sequence	143	11.2	65.9	38	6	AX220488	AX220488
67.1	29	6	BD103468	Methods a	144	11.2	65.9	38	6	AX220521	AX220521
67.1	30	6	AX698766	Sequence	145	11.2	65.9	38	6	AX223173	AX223173
67.1	33	6	BD266668	Death dom	146	11.2	65.9	38	6	AX273941	AX273941
67.1	33	6	AR183734	Sequence	147	11.2	65.9	38	6	AX273987	AX273987
67.1	33	6	AR235742	Sequence	148	11.2	65.9	38	6	AX274016	AX274016
67.1	33	6	BD056815	Death dom	149	11.2	65.9	38	6	AX425318	AX425318
67.1	35	6	BD247628	A method	150	11.2	65.9	38	6	AX425438	AX425438
67.1	35	6	AR345097	Sequence	151	11.2	65.9	38	6	AX425447	AX425447
67.1	36	6	I74525	Sequence 29	152	11.2	65.9	39	6	AR018945	AR018945
67.1	37	6	AX481790	Sequence	153	11.2	65.9	39	6	AR066573	AR066573
67.1	40	6	E13253	Oligonucleo	154	11.2	65.9	39	6	I72290	I72290
67.1	41	6	AR161440	Sequence	155	11.2	65.9	39	6	I76857	I76857
67.1	41	6	I81456	Sequence 15	156	11.2	65.9	42	6	AX614944	AX614944
67.1	42	6	AR161439	Sequence	157	11.2	65.9	43	6	AX6303	AX6303
67.1	42	6	I81455	Sequence 14	158	11.2	65.9	43	6	AX6307	AX6307
67.1	42	6	AR263729	Sequence	159	11.2	65.9	43	6	AR0184	AR0184
67.1	42	6	AX282186	Sequence	160	11.2	65.9	43	6	AR0188	AR0188
67.1	42	6	AX282295	Sequence	161	11.2	65.9	47	6	AR2317	AR2317
67.1	42	6	AX322946	Sequence	162	11.2	65.9	51	6	AR404988	AR404988
67.1	45	6	I45552	Sequence 1	163	11.2	65.9	51	6	AX158926	AX158926
67.1	45	6	I45561	Sequence 10	164	11.2	65.9	51	6	AX441334	AX441334
67.1	47	6	AR288849	Sequence	165	11.2	65.9	51	6	BD171635	BD171635
67.1	47	6	AR292007	Sequence	166	11.2	65.9	54	6	AX776474	AX776474
65.9	20	6	AR297233	Sequence	167	11.2	65.9	55	6	AX485766	AX485766
65.9	20	6	AR312449	Sequence	168	11.2	65.9	56	9	HUMTCRVJ22	HUMTCRVJ22
65.9	20	6	AX297421	Sequence	169	11.2	65.9	58	4	AF330204	AF330204
65.9	20	6	BD102630	L-Glutama	170	11.2	65.9	60	6	AR118197	AR118197
65.9	22	6	I46707	Sequence 68	171	11.2	65.9	60	6	AR337357	AR337357
65.9	22	6	I46708	Sequence 68	172	11.2	65.9	60	6	AR372205	AR372205
65.9	22	6	I46710	Sequence 68	173	11.2	65.9	60	6	BD130717	BD130717
65.9	22	6	I46711	Sequence 69	174	11	64.7	15	6	AR180491	AR180491
65.9	24	6	I07719	Sequence 24	175	11	64.7	17	6	AX649518	AX649518
65.9	24	6	AX292788	Sequence	176	11	64.7	17	6	AX649519	AX649519
65.9	26	6	A23966	Vacuolar AT	177	11	64.7	17	6	AX649520	AX649520
65.9	28	6	AX252348	Sequence	178	11	64.7	17	6	AX649521	AX649521
65.9	30	6	A97150	Sequence 6	179	11	64.7	17	6	AX649522	AX649522
65.9	30	6	I29845	Sequence 31	180	11	64.7	17	6	AX649523	AX649523
65.9	30	6	AX792853	Sequence	181	11	64.7	17	6	AX649524	AX649524
65.9	31	6	AR018946	Sequence	182	11	64.7	17	6	AX725133	AX725133
65.9	31	6	AR066574	Sequence	183	11	64.7	17	6	AX726680	AX726680
65.9	31	6	I72291	Sequence 74	184	11	64.7	17	6	AX761621	AX761621
65.9	31	6	I76858	Sequence 74	185	11	64.7	17	6	BD168809	BD168809
65.9	33	6	AX611962	Sequence	186	11	64.7	17	6	BD178165	BD178165
65.9	36	6	A29215	Oligonucleo	187	11	64.7	20	6	AR315439	AR315439
65.9	37	6	E36454	DNA polymer	188	11	64.7	21	6	AX033430	AX033430
65.9	37	6	I13355	Sequence 12	189	11	64.7	21	6	BD088182	BD088182
65.9	37	6	AR286801	Sequence	190	11	64.7	21	12	AB069005	AB069005
65.9	38	6	AR286806	Sequence	191	11	64.7	25	6	AX651022	AX651022
65.9	38	6	AR286846	Sequence	192	11	64.7	25	6	AX651023	AX651023
65.9	38	6	AR286864	Sequence	193	11	64.7	25	6	AX651024	AX651024
65.9	38	6	AR286900	Sequence	194	11	64.7	25	6	AX651025	AX651025
65.9	38	6	AR286903	Sequence	195	11	64.7	25	6	AX651026	AX651026
65.9	38	6	AR286905	Sequence	196	11	64.7	25	6	AX651027	AX651027
65.9	38	6	AR286929	Sequence	197	11	64.7	25	6	AX651028	AX651028
65.9	38	6	AR287020	Sequence	198	11	64.7	25	6	AX651029	AX651029
65.9	38	6	AR287029	Sequence	199	11	64.7	25	6	AX651030	AX651030
65.9	38	6	AR287053	Sequence	200	11	64.7	25	6	AX651031	AX651031
65.9	38	6	AR287081	Sequence	201	11	64.7	25	6	AX651032	AX651032
65.9	38	6	AR287090	Sequence	202	11	64.7	25	6	AX651033	AX651033
65.9	38	6	AR398791	Sequence	203	11	64.7	25	6	AX651034	AX651034
65.9	38	6	AR398796	Sequence	204	11	64.7	25	6	AX651035	AX651035
65.9	38	6	AR398836	Sequence	205	11	64.7	25	6	AX651036	AX651036
65.9	38	6	AR398854	Sequence	206	11	64.7	28	6	AR170364	AR170364
65.9	38	6	AR398890	Sequence	207	11	64.7	28	6	BD233814	BD233814
65.9	38	6	AR398893	Sequence	208	11	64.7	28	6	BD237164	BD237164
65.9	38	6	AR398895	Sequence	209	11	64.7	28	6	I19818	I19818
65.9	38	6	AR398919	Sequence	210	11	64.7	28	6	I19819	I19819
65.9	38	6	AR399010	Sequence	211	11	64.7	28	6	I19869	I19869

64.7	28	6	I19870	I19870 Sequence 10	285	10.8	63.5	33	6	AR126131	AR126131
64.7	28	6	I20278	I20278 Sequence 48	c 286	10.8	63.5	33	6	AX062294	AX062294
64.7	28	6	I20279	I20279 Sequence 49	287	10.8	63.5	34	6	AX283668	AX283668
64.7	28	6	I20329	I20329 Sequence 99	c 288	10.8	63.5	38	6	A23776	A23776 C
64.7	28	6	I20330	I20330 Sequence 10	289	10.8	63.5	38	6	A41604	A41604 S
64.7	28	6	AR199695	AR199695 Sequence	290	10.8	63.5	38	6	A95666	A95666 S
64.7	28	6	AR221340	AR221340 Sequence	291	10.8	63.5	38	6	A95708	A95708 S
64.7	28	6	BD075106	BD075106 MAGE-3 pe	292	10.8	63.5	38	6	A95750	A95750 S
64.7	33	6	A69040	A69040 Sequence 28	293	10.8	63.5	38	6	A95792	A95792 S
64.7	33	6	AR193490	AR193490 Sequence	294	10.8	63.5	38	6	AR116283	AR116283
64.7	33	6	BD006117	BD006117 Feline po	c 295	10.8	63.5	38	6	I26306	I26306 S
64.7	41	6	AX517090	AX517090 Sequence	c 296	10.8	63.5	38	6	I47762	I47762 S
64.7	41	6	AX519619	AX519619 Sequence	c 297	10.8	63.5	38	6	I47762	I47762 S
64.7	42	6	BD266496	BD266496 Universal	298	10.8	63.5	38	6	I64634	I64634 S
64.7	48	6	AX426329	AX426329 Sequence	299	10.8	63.5	39	6	A28775	A28775 O
64.7	50	6	AR032527	AR032527 Sequence	300	10.8	63.5	40	6	AR053634	AR053634
64.7	50	6	I29267	I29267 Sequence 13	301	10.8	63.5	40	6	AR258569	AR258569
64.7	50	6	I90941	I90941 Sequence 13	302	10.8	63.5	41	6	AX514068	AX514068
64.7	50	6	AR209191	AR209191 Sequence	c 303	10.8	63.5	41	6	AX514189	AX514189
63.5	17	6	I82053	I82053 Sequence 3	c 304	10.8	63.5	41	6	AX519048	AX519048
63.5	17	6	AR191860	AR191860 Sequence	c 305	10.8	63.5	41	6	AX520222	AX520222
63.5	18	6	AR325755	AR325755 Sequence	306	10.8	63.5	42	6	BD209218	BD209218
63.5	18	6	E32527	E32527 Scavenger r	c 307	10.8	63.5	43	6	AR035251	AR035251
63.5	20	6	AR085483	AR085483 Sequence	c 308	10.8	63.5	43	6	AR035252	AR035252
63.5	20	6	E40657	E40657 Antihuman F	c 309	10.8	63.5	43	6	AR107121	AR107121
63.5	20	6	AR281890	AR281890 Sequence	c 310	10.8	63.5	43	6	AR107122	AR107122
63.5	20	6	AR312525	AR312525 Sequence	c 311	10.8	63.5	43	6	AR112712	AR112712
63.5	20	6	AR315443	AR315443 Sequence	c 312	10.8	63.5	43	6	AR112713	AR112713
63.5	20	6	AR315544	AR315544 Sequence	c 313	10.8	63.5	43	6	AR169883	AR169883
63.5	20	6	AR427881	AR427881 Sequence	c 314	10.8	63.5	43	6	I73533	I73533 S
63.5	20	6	AX018881	AX018881 Sequence	c 315	10.8	63.5	43	6	I73534	I73534 S
63.5	20	6	AX018896	AX018896 Sequence	c 316	10.8	63.5	45	6	A40305	A40305 S
63.5	20	6	AX018913	AX018913 Sequence	c 317	10.8	63.5	45	6	A84478	A84478 S
63.5	20	6	AX018928	AX018928 Sequence	c 318	10.8	63.5	45	6	A95463	A95463 S
63.5	20	6	AX019042	AX019042 Sequence	c 319	10.8	63.5	45	6	AR144895	AR144895
63.5	20	6	AX117394	AX117394 Sequence	c 320	10.8	63.5	45	6	AR177526	AR177526
63.5	20	6	AX295460	AX295460 Sequence	c 321	10.8	63.5	45	6	BD267924	BD267924
63.5	20	6	AX329282	AX329282 Sequence	c 322	10.8	63.5	45	6	AR279936	AR279936
63.5	20	6	AX394375	AX394375 Sequence	c 323	10.8	63.5	45	6	AR361783	AR361783
63.5	20	6	AX590794	AX590794 Sequence	c 324	10.8	63.5	45	6	AX010327	AX010327
63.5	20	6	AX741290	AX741290 Sequence	c 325	10.8	63.5	45	6	AX329066	AX329066
63.5	20	6	BD091320	BD091320 Dull1 cod	c 326	10.8	63.5	45	6	AX427377	AX427377
63.5	20	6	BD170190	BD170190 Method of	c 327	10.8	63.5	45	6	BD082558	BD082558
63.5	21	6	AX094962	AX094962 Sequence	c 328	10.8	63.5	45	6	BD124117	BD124117
63.5	21	6	BD134579	BD134579 Method fo	c 329	10.8	63.5	45	6	BD177969	BD177969
63.5	22	6	AR207707	AR207707 Sequence	c 330	10.8	63.5	46	6	E63262	E63262 Co
63.5	22	6	AR265033	AR265033 Sequence	c 331	10.8	63.5	46	6	AX612094	AX612094
63.5	22	6	AX696164	AX696164 Sequence	c 332	10.8	63.5	46	6	AX612095	AX612095
63.5	23	6	BD094035	BD094035 A novel p	c 333	10.8	63.5	46	6	AX612096	AX612096
63.5	24	6	A49391	A49391 Sequence 9	334	10.8	63.5	46	6	AX612097	AX612097
63.5	24	6	A65736	A65736 Sequence 17	335	10.8	63.5	46	6	AX612099	AX612099
63.5	24	6	AR176297	AR176297 Sequence	336	10.8	63.5	46	6	AX614571	AX614571
63.5	24	6	AX290827	AX290827 Sequence	c 337	10.8	63.5	46	6	BD133457	BD133457
63.5	25	6	AR170299	AR170299 Sequence	c 338	10.8	63.5	46	6	BD133468	BD133468
63.5	25	6	E51073	E51073 Novel Esche	339	10.8	63.5	47	6	AR288782	AR288782
63.5	25	6	AX007127	AX007127 Sequence	c 340	10.8	63.5	47	6	AX194947	AX194947
63.5	25	6	AX521586	AX521586 Sequence	c 341	10.8	63.5	47	6	AX302472	AX302472
63.5	29	6	AR146958	AR146958 Sequence	c 342	10.8	63.5	48	6	AR007502	AR007502
63.5	29	6	I24909	I24909 Sequence 50	343	10.8	63.5	48	6	AX614572	AX614572
63.5	29	6	AR222155	AR222155 Sequence	344	10.8	63.5	50	6	AX199566	AX199566
63.5	30	6	I35737	I35737 Sequence 1	345	10.8	63.5	50	6	AX485734	AX485734
63.5	30	6	I95599	I95599 Sequence 1	346	10.8	63.5	50	6	AX697162	AX697162
63.5	30	6	AR211352	AR211352 Sequence	c 347	10.8	63.5	50	6	AX923414	AX923414
63.5	30	6	AR430800	AR430800 Sequence	c 348	10.8	63.5	51	6	E14328	E14328 P
63.5	30	6	AX235827	AX235827 Sequence	349	10.8	63.5	51	6	AX116621	AX116621
63.5	30	6	AX791760	AX791760 Sequence	c 350	10.8	63.5	51	6	AX157031	AX157031
63.5	30	6	AX793046	AX793046 Sequence	c 351	10.8	63.5	51	6	AX157032	AX157032
63.5	30	6	BD016830	BD016830 Novel cyt	c 352	10.8	63.5	51	6	AX157033	AX157033
63.5	30	6	BD161108	BD161108 N-Acetyl	c 353	10.8	63.5	51	6	AX199084	AX199084
63.5	31	6	AR022300	AR022300 Sequence	354	10.8	63.5	51	6	AX199565	AX199565
63.5	31	6	AX615155	AX615155 Sequence	c 355	10.8	63.5	51	6	AX204077	AX204077
63.5	31	6	AX754987	AX754987 Sequence	c 356	10.8	63.5	51	6	AX612493	AX612493
63.5	32	6	A10251	A10251 Oligonucleo	357	10.8	63.5	54	6	A01255	A01255 Nu

63.5	54	6	A01256	A01256 (reverse co	431	10.6	62.4	38	6	AR287084	AR287084
63.5	54	6	A01268	A01268 Nucleotide	432	10.6	62.4	38	6	AR287105	AR287105
63.5	54	6	A01269	A01269 (reverse co	433	10.6	62.4	38	6	AR398582	AR398582
63.5	54	6	A01302	A01302 Nucleotide	434	10.6	62.4	38	6	AR398693	AR398693
63.5	54	6	A13103	A13103 Nucleotide	435	10.6	62.4	38	6	AR398713	AR398713
63.5	54	6	A18344	A18344 BIN19 polyI	436	10.6	62.4	38	6	AR398730	AR398730
63.5	55	6	A18345	A28185 Primer DNA	437	10.6	62.4	38	6	AR398806	AR398806
63.5	55	6	AR365150	AR365150 Sequence	438	10.6	62.4	38	6	AR398811	AR398811
63.5	55	6	AX521528	AX521528 Sequence	439	10.6	62.4	38	6	AR398822	AR398822
63.5	55	11	BF296254	BF296254 Arabidops	440	10.6	62.4	38	6	AR398826	AR398826
63.5	58	10	AF357503	AF357503 Mus muscu	441	10.6	62.4	38	6	AR398874	AR398874
63.5	60	6	A33490	A33490 Synthetic p	442	10.6	62.4	38	6	AR398903	AR398903
63.5	60	6	AR118183	AR118183 Sequence	443	10.6	62.4	38	6	AR398909	AR398909
63.5	60	6	BD232441	BD232441 Antibodie	444	10.6	62.4	38	6	AR398974	AR398974
63.5	60	6	I42386	I42386 Sequence 15	445	10.6	62.4	38	6	AR399024	AR399024
63.5	60	6	AR337343	AR337343 Sequence	446	10.6	62.4	38	6	AR399029	AR399029
63.5	60	6	AR372191	AR372191 Sequence	447	10.6	62.4	38	6	AR399045	AR399045
63.5	60	6	AX010631	AX010631 Sequence	448	10.6	62.4	38	6	AR399074	AR399074
63.5	60	6	AX657142	AX657142 Sequence	449	10.6	62.4	38	6	AR399095	AR399095
63.5	60	6	BD130703	BD130703 High-affi	450	10.6	62.4	38	6	AX220166	AX220166
63.5	60	6	BD134501	BD134501 Lipopolys	451	10.6	62.4	38	6	AX220225	AX220225
63.5	60	12	SYNLTKSD	MI3108 Mouse L cel	452	10.6	62.4	38	6	AX220302	AX220302
62.4	18	6	I66349	I66349 Sequence 8	453	10.6	62.4	38	6	AX220335	AX220335
62.4	19	6	AR298314	AR298314 Sequence	454	10.6	62.4	38	6	AX220379	AX220379
62.4	20	6	AR016139	AR016139 Sequence	455	10.6	62.4	38	6	AX220392	AX220392
62.4	20	6	AR019137	AR019137 Sequence	456	10.6	62.4	38	6	AX220395	AX220395
62.4	20	6	E14591	E14591 PCR primer	457	10.6	62.4	38	6	AX220414	AX220414
62.4	20	6	AR350258	AR350258 Sequence	458	10.6	62.4	38	6	AX220420	AX220420
62.4	21	6	AX096571	AX096571 Sequence	459	10.6	62.4	38	6	AX220454	AX220454
62.4	21	6	AX153989	AX153989 Sequence	460	10.6	62.4	38	6	AX220455	AX220455
62.4	22	6	AR211944	AR211944 Sequence	461	10.6	62.4	38	6	AX220507	AX220507
62.4	22	6	AX244545	AX244545 Sequence	462	10.6	62.4	38	6	AX220512	AX220512
62.4	23	6	BD078733	BD078733 B type DN	463	10.6	62.4	38	6	AX223075	AX223075
62.4	23	6	BD170322	BD170322 Novel pol	464	10.6	62.4	38	6	AX223086	AX223086
62.4	24	6	A48486	A48486 Sequence 7	465	10.6	62.4	38	6	AX223101	AX223101
62.4	24	6	AR206737	AR206737 Sequence	466	10.6	62.4	38	6	AX223156	AX223156
62.4	24	6	AX166709	AX166709 Sequence	467	10.6	62.4	38	6	AX228654	AX228654
62.4	25	6	AX241132	AX241132 Sequence	468	10.6	62.4	38	6	AX228673	AX228673
62.4	25	6	AX486739	AX486739 Sequence	469	10.6	62.4	38	6	AX228712	AX228712
62.4	27	6	I04705	I04705 sequence 29	470	10.6	62.4	38	6	AX228713	AX228713
62.4	28	6	BD176660	BD176660 Promoter.	471	10.6	62.4	38	6	AX228778	AX228778
62.4	31	6	AR211939	AR211939 Sequence	472	10.6	62.4	38	6	AX273921	AX273921
62.4	31	6	AX248207	AX248207 Sequence	473	10.6	62.4	38	6	AX273924	AX273924
62.4	33	6	AR169342	AR169342 Sequence	474	10.6	62.4	38	6	AX273973	AX273973
62.4	33	6	I66358	I66358 Sequence 17	475	10.6	62.4	38	6	AX274017	AX274017
62.4	34	6	AR242786	AR242786 Sequence	476	10.6	62.4	38	6	AX425201	AX425201
62.4	34	6	AR261523	AR261523 Sequence	477	10.6	62.4	38	6	AX425213	AX425213
62.4	34	6	AR285929	AR285929 Sequence	478	10.6	62.4	38	6	AX425220	AX425220
62.4	35	6	AR000139	AR000139 Sequence	479	10.6	62.4	38	6	AX425300	AX425300
62.4	35	6	I66253	I66253 Sequence 5	480	10.6	62.4	38	6	AX425321	AX425321
62.4	35	6	AR397919	AR397919 Sequence	481	10.6	62.4	38	6	AX425324	AX425324
62.4	35	11	C75907	C75907 Homo sapien	482	10.6	62.4	38	6	AX425376	AX425376
62.4	36	6	AR033955	AR033955 Sequence	483	10.6	62.4	38	6	AX425388	AX425388
62.4	36	6	AR175088	AR175088 Sequence	484	10.6	62.4	38	6	AX425429	AX425429
62.4	36	6	AR285904	AR285904 Sequence	485	10.6	62.4	38	6	AX425433	AX425433
62.4	36	6	AX032536	AX032536 Sequence	486	10.6	62.4	38	6	BD012178	BD012178
62.4	37	6	AR397894	AR397894 Sequence	487	10.6	62.4	40	6	AR3621	AR3621
62.4	37	6	AX581915	AX581915 Sequence	488	10.6	62.4	40	6	BD166453	BD166453
62.4	38	6	AR286592	AR286592 Sequence	489	10.6	62.4	41	6	AX514811	AX514811
62.4	38	6	AR286703	AR286703 Sequence	490	10.6	62.4	41	6	AX517169	AX517169
62.4	38	6	AR286723	AR286723 Sequence	491	10.6	62.4	44	6	I75987	I75987
62.4	38	6	AR286740	AR286740 Sequence	492	10.6	62.4	47	6	BD124134	BD124134
62.4	38	6	AR286816	AR286816 Sequence	493	10.6	62.4	48	6	AX391335	AX391335
62.4	38	6	AR286821	AR286821 Sequence	494	10.6	62.4	50	6	AX164969	AX164969
62.4	38	6	AR286832	AR286832 Sequence	495	10.6	62.4	50	6	AX277229	AX277229
62.4	38	6	AR286836	AR286836 Sequence	496	10.6	62.4	51	6	AX000112	AX000112
62.4	38	6	AR286884	AR286884 Sequence	497	10.6	62.4	51	6	AX000229	AX000229
62.4	38	6	AR286913	AR286913 Sequence	498	10.6	62.4	51	6	AX158452	AX158452
62.4	38	6	AR286919	AR286919 Sequence	499	10.6	62.4	51	6	AX159567	AX159567
62.4	38	6	AR286984	AR286984 Sequence	500	10.6	62.4	51	6	AX280272	AX280272
62.4	38	6	AR287034	AR287034 Sequence	501	10.6	62.4	51	6	BD271119	BD271119
62.4	38	6	AR287039	AR287039 Sequence	502	10.6	62.4	54	6	BD271125	BD271125
62.4	38	6	AR287055	AR287055 Sequence	503	10.6	62.4	54	6		

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62.4	54	6	AX000113	Sequence	577	10.4	61.2	24	6	AX444730
62.4	54	6	AX000230	Sequence	578	10.4	61.2	24	6	AX922624
62.4	54	9	AF305521	Homo sapi	579	10.4	61.2	24	6	BD017385
62.4	57	6	E30631	Antibody an	580	10.4	61.2	25	6	A97532
62.4	57	6	E31240	Device for	581	10.4	61.2	25	6	AR239182
62.4	59	6	AR031481	Sequence	582	10.4	61.2	25	6	AR350155
62.4	59	6	AR031481	Sequence	583	10.4	61.2	25	6	AR278984
62.4	59	6	AR374547	Sequence	584	10.4	61.2	25	6	AX281070
62.4	59	6	AR374547	Sequence	585	10.4	61.2	25	6	AX322634
62.4	60	6	AR031473	Sequence	586	10.4	61.2	25	6	AX609392
62.4	60	6	AR031473	Sequence	587	10.4	61.2	25	6	AX683285
62.4	60	6	AR374539	Sequence	588	10.4	61.2	26	6	BD170718
62.4	60	6	AR374539	Sequence	589	10.4	61.2	27	6	AR002481
61.2	12	6	AR121279	Sequence	590	10.4	61.2	27	6	AX455011
61.2	12	6	AR139766	Sequence	591	10.4	61.2	27	6	AX742862
61.2	12	6	AR165925	Sequence	592	10.4	61.2	28	9	S80742
61.2	12	6	BD231392	Isolated	593	10.4	61.2	29	6	AR135344
61.2	12	6	IL3332	Sequence 6	594	10.4	61.2	29	6	I46773
61.2	12	6	IL3332	Sequence 6	595	10.4	61.2	29	6	I95021
61.2	12	6	AR201396	Sequence	596	10.4	61.2	30	6	AR086689
61.2	12	6	AR208444	Sequence	597	10.4	61.2	30	6	AX766127
61.2	12	6	AR225779	Sequence	598	10.4	61.2	31	6	AX248154
61.2	12	6	AR230328	Sequence	599	10.4	61.2	31	6	AX248439
61.2	12	6	AR243310	Sequence	600	10.4	61.2	31	6	AX440501
61.2	12	6	AR264185	Sequence	601	10.4	61.2	31	6	BD016882
61.2	12	6	AR279228	Sequence	602	10.4	61.2	32	6	AR000590
61.2	12	6	AR310023	Sequence	603	10.4	61.2	32	6	AR174604
61.2	12	6	AR339823	Sequence	604	10.4	61.2	32	6	AR174613
61.2	12	6	AR350435	Sequence	605	10.4	61.2	32	6	AR174615
61.2	12	6	AX023542	Sequence	606	10.4	61.2	32	6	BD248997
61.2	12	6	AX301752	Sequence	607	10.4	61.2	32	6	BD249006
61.2	12	6	AX347896	Sequence	608	10.4	61.2	32	6	BD249008
61.2	12	6	AX348103	Sequence	609	10.4	61.2	32	6	AR208903
61.2	12	6	AX384672	Sequence	610	10.4	61.2	32	6	AR374096
61.2	12	6	AX459952	Sequence	611	10.4	61.2	32	6	AR374105
61.2	12	6	AX470044	Sequence,	612	10.4	61.2	32	6	AR374107
61.2	12	6	BD016444	Gene deri	613	10.4	61.2	33	6	A31501
61.2	12	6	BD080840	Asthma-re	614	10.4	61.2	33	6	AR004756
61.2	12	6	BD082008	Aslhma as	615	10.4	61.2	33	6	AR085171
61.2	12	6	BD086212	Transcrip	616	10.4	61.2	33	6	BD235483
61.2	12	6	BD106871	Isolated	617	10.4	61.2	33	6	E12453
61.2	12	6	BD195210	Method fo	618	10.4	61.2	33	6	AR256883
61.2	12	6	BD223679	Leptin-me	619	10.4	61.2	33	6	AX085550
61.2	17	6	I37629	Sequence 64	620	10.4	61.2	33	6	BD062058
61.2	17	6	I94479	Sequence 64	621	10.4	61.2	34	6	AR218090
61.2	17	6	AR192089	Sequence	622	10.4	61.2	35	6	AR016271
61.2	17	6	AR192089	Sequence	623	10.4	61.2	35	6	AR016273
61.2	17	6	AR325971	Sequence	624	10.4	61.2	35	6	AR084255
61.2	17	6	AR325972	Sequence	625	10.4	61.2	36	6	A65536
61.2	17	6	AR3217231	Sequence	626	10.4	61.2	36	6	AX047218
61.2	17	6	AX419971	Sequence	627	10.4	61.2	36	6	AX755153
61.2	17	6	AX736810	Sequence	628	10.4	61.2	36	6	AX755164
61.2	17	6	AX760374	Sequence	629	10.4	61.2	37	6	BD161877
61.2	17	6	BD197528	Method an	630	10.4	61.2	38	6	AR000588
61.2	18	6	AR110042	Sequence	631	10.4	61.2	38	6	AR208901
61.2	18	6	AX029247	Sequence	632	10.4	61.2	38	6	AX924434
61.2	18	6	BD008906	High leve	633	10.4	61.2	40	6	E37760
61.2	18	12	AB069423	Synthetic	634	10.4	61.2	41	6	AX514878
61.2	19	6	AX020423	Sequence	635	10.4	61.2	41	6	AX517020
61.2	20	6	I79517	Sequence 8	636	10.4	61.2	41	6	AX519531
61.2	20	6	AR313886	Sequence	637	10.4	61.2	41	6	AX520176
61.2	20	6	AX453690	Sequence	638	10.4	61.2	41	6	AX520177
61.2	20	6	BD128225	Primer fo	639	10.4	61.2	42	6	A76875
61.2	20	11	DOGDCN1B	L77441 Canis fami	640	10.4	61.2	44	3	CCA427066
61.2	22	6	AX106989	Sequence	641	10.4	61.2	44	3	CCA427078
61.2	23	6	I13182	Sequence 6	642	10.4	61.2	45	9	HSB1A1G1B
61.2	23	6	BD012531	Inhibitor	643	10.4	61.2	46	6	AX612098
61.2	23	6	BD017007	Detection	644	10.4	61.2	47	6	AR288486
61.2	24	6	AR070885	Sequence	645	10.4	61.2	47	6	AR289580
61.2	24	6	AR088622	Sequence	646	10.4	61.2	47	6	AR291043
61.2	24	6	AR122727	Sequence	647	10.4	61.2	48	6	A13267
61.2	24	6	E11770	Synthetic o	648	10.4	61.2	48	6	I09475
61.2	24	6	AR429447	Sequence	649	10.4	61.2	49	6	A13268

61.2	43	6	I09476	I09476 Sequence 2	723	10.2	60.0	24	6	AX443815
61.2	49	6	AR239838	AR239838 Sequence	724	10.2	60.0	25	6	AR069348
61.2	49	6	AX279640	AX279640 Sequence	725	10.2	60.0	25	6	I64565
61.2	50	6	A13269	A13269 oligonucleo	726	10.2	60.0	25	6	AX259784
61.2	50	6	I09477	I09477 Sequence 3	727	10.2	60.0	25	6	AX349981
61.2	51	6	AX165529	AX165529 Sequence	728	10.2	60.0	25	6	AX354438
61.2	51	6	AX165586	AX165586 Sequence	729	10.2	60.0	25	6	AX447739
61.2	51	9	HSDFCRV08	Z27186 H.sapiens r	730	10.2	60.0	25	6	AX447796
61.2	51	10	AF005611	AF005611 Mus muscu	731	10.2	60.0	25	6	AX650588
61.2	53	6	A14820	A14820 Nucleotide	732	10.2	60.0	25	6	AX650589
61.2	53	6	A14821	A14821 Nucleotide	733	10.2	60.0	25	6	AX650590
61.2	57	6	AR075442	AR075442 Sequence	734	10.2	60.0	25	6	AX650591
61.2	57	6	AR174607	AR174607 Sequence	735	10.2	60.0	25	6	AX650592
61.2	57	6	BD249000	BD249000 Novel cyt	736	10.2	60.0	25	6	AX650593
61.2	57	6	AR374039	AR374039 Sequence	737	10.2	60.0	25	6	AX650594
61.2	57	6	AX277164	AX277164 Sequence	738	10.2	60.0	25	6	AX650595
61.2	57	9	AF234185	AF234185 Homo sapi	739	10.2	60.0	25	6	AX650596
61.2	60	6	E22195	E22195 Yeast capab	740	10.2	60.0	25	6	AX650597
61.2	60	6	E35599	E35599 Novel DNAs	741	10.2	60.0	25	6	AX650598
60.0	17	6	I52069	I52069 Sequence 11	742	10.2	60.0	26	6	AR199674
60.0	17	6	AX215217	AX215217 Sequence	743	10.2	60.0	27	6	AX429675
60.0	17	6	AX649084	AX649084 Sequence	744	10.2	60.0	27	6	AX236776
60.0	17	6	AX649085	AX649085 Sequence	745	10.2	60.0	27	6	AX236778
60.0	17	6	AX649086	AX649086 Sequence	746	10.2	60.0	27	6	AX458033
60.0	17	6	AX710719	AX710719 Sequence	747	10.2	60.0	27	6	BD171716
60.0	18	6	BD104990	BD104990 Kit and m	748	10.2	60.0	28	6	AR060524
60.0	18	6	BD176748	BD176748 Novel pro	749	10.2	60.0	28	6	E30200
60.0	19	6	AR292703	AR292703 Sequence	750	10.2	60.0	28	6	AR262748
60.0	19	6	AX398090	AX398090 Sequence	751	10.2	60.0	28	6	AX015595
60.0	19	6	BD089801	BD089801 A method	752	10.2	60.0	28	6	AX592213
60.0	19	12	AB068728	AB068728 Synthetic	753	10.2	60.0	28	6	AX592216
60.0	20	6	E40117	E40117 Method for	754	10.2	60.0	28	6	AX592222
60.0	20	6	AR133841	AR133841 Sequence	755	10.2	60.0	28	6	AX592225
60.0	20	6	AR338211	AR338211 Sequence	756	10.2	60.0	28	6	BD097676
60.0	20	6	AR338212	AR338212 Sequence	757	10.2	60.0	28	6	BD141269
60.0	20	6	AX293302	AX293302 Sequence	758	10.2	60.0	28	6	BD194450
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60.0	20	6	AX323432	AX323432 Sequence	760	10.2	60.0	29	6	BD259963
60.0	20	6	AX662830	AX662830 Sequence	761	10.2	60.0	29	6	BD260976
60.0	20	6	AX805100	AX805100 Sequence	762	10.2	60.0	29	6	AX045390
60.0	21	6	A51697	A51697 Sequence 3	763	10.2	60.0	29	6	AX045449
60.0	21	6	A65479	A65479 Sequence 7	764	10.2	60.0	30	6	I50889
60.0	21	6	AR043373	AR043373 Sequence	765	10.2	60.0	30	6	AR183906
60.0	21	6	AR167576	AR167576 Sequence	766	10.2	60.0	30	6	AX028867
60.0	21	6	E13821	E13821 PCR primer	767	10.2	60.0	30	6	AX793181
60.0	21	6	AR217175	AR217175 Sequence	768	10.2	60.0	30	6	BD128601
60.0	21	6	AR298993	AR298993 Sequence	769	10.2	60.0	30	6	BD128602
60.0	21	6	AX016240	AX016240 Sequence	770	10.2	60.0	31	6	AR125078
60.0	21	6	AX027211	AX027211 Sequence	771	10.2	60.0	31	6	AX456450
60.0	21	6	AX138382	AX138382 Sequence	772	10.2	60.0	31	6	AX781260
60.0	21	6	AX686838	AX686838 Sequence	773	10.2	60.0	31	6	AX781276
60.0	21	6	BD011635	BD011635 Recombina	774	10.2	60.0	32	6	AX302473
60.0	21	6	BD135018	BD135018 Vector ha	775	10.2	60.0	33	6	AX698601
60.0	21	6	BD182303	BD182303 Stem cell	776	10.2	60.0	34	6	AR285863
60.0	22	6	A68011	A68011 Sequence 6	777	10.2	60.0	34	6	AR285870
60.0	22	6	A68013	A68013 Sequence 8	778	10.2	60.0	34	6	AR285880
60.0	22	6	A70793	A70793 Sequence 11	779	10.2	60.0	34	6	AR285912
60.0	22	6	A79277	A79277 Sequence 11	780	10.2	60.0	34	6	AR285921
60.0	22	6	AR067343	AR067343 Sequence	781	10.2	60.0	35	6	AR397853
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60.0	22	6	AR163114	AR163114 Sequence	783	10.2	60.0	35	6	AR397870
60.0	22	6	AR404467	AR404467 Sequence	784	10.2	60.0	35	6	AR397902
60.0	22	6	BD003507	BD003507 A gene re	785	10.2	60.0	35	6	AR397911
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60.0	24	6	AR033732	AR033732 Sequence	787	10.2	60.0	35	6	AX710496
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60.0	37	6	AR397903	Sequence	869	10.2	60.0	38	6	AX223129	AX223129
60.0	37	6	AR397912	Sequence	870	10.2	60.0	38	6	AX228749	AX228749
60.0	37	6	AX057241	Sequence	871	10.2	60.0	38	6	AX273927	AX273927
60.0	37	6	BD136678	Method of	872	10.2	60.0	38	6	AX273942	AX273942
60.0	37	6	BD205260	Crystall	873	10.2	60.0	38	6	AX273947	AX273947
60.0	38	6	AR286776	Sequence	874	10.2	60.0	38	6	AX273977	AX273977
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60.0	38	6	AR286779	Sequence	876	10.2	60.0	38	6	AX273992	AX273992
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60.0	38	6	AR286786	Sequence	878	10.2	60.0	38	6	AX274008	AX274008
60.0	38	6	AR286793	Sequence	879	10.2	60.0	38	6	AX425285	AX425285
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60.0	38	6	AR286899	Sequence	885	10.2	60.0	38	6	AX425446	AX425446
60.0	38	6	AR286904	Sequence	886	10.2	60.0	38	6	AX425452	AX425452
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## ALIGNMENTS

.5288 5825 from patent US 6559294.  
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Unclassified.  
1 (bases 1 to 20)  
Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J.,  
Sankaran,B. and Fletcher,L.D.  
Chlamydia pneumoniae polynucleotides and uses thereof  
Patent: US 6559294-A 5825 06-MAY-2003;  
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DEFINITION Method and reagent for treating diseases or conditions c  
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ACCESSION BD197525  
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KEYWORDS JP 2002509721-A/551.  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hom  
1 (bases 1 to 17)  
Payco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswi  
Method and reagent for treating diseases or conditions c  
molecule participating in vasculogenic response  
Patent: JP 2002509721-A 551 02-APR-2002;  
RIBOZYME PHARMACEUTICALS INC  
OS Homo sapiens (human)  
PN JP 2002509721-A/551  
PD 02-APR-2002  
PF 24-MAR-1999 JP 2000541291  
PR 27-MAR-1998 US 60/079678  
PI FAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIR  
PI JAMES A MCSWIGGEN  
PC  
C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61  
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**ORGANISM** Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom  
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**REFERENCE**  
**AUTHORS** Fuchs,S., Ilani,T. and Perl,O.  
**TITLE** Method for the diagnosis and follow up of schizophrenia  
mental and neurodegenerative disorders  
**JOURNAL** Patent: WO 0214547-A 1 21-FEB-2002;  
YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)  
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**ACCESSION** AR285893  
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**SOURCE** Unknown.  
**ORGANISM** Unknown.  
Unclassified.  
**REFERENCE** 1 (bases 1 to 36)  
**AUTHORS** Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,  
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.  
**TITLE** Synthetic ribonucleic acids with RNase activity  
**JOURNAL** Patent: US 6528640-A 265 04-MAR-2003;  
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**ORGANISM** Homo sapiens  
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**REFERENCE**  
**AUTHORS** Susilo,R., Korting,H.C., Gassen,H.G., Hils,M. and Paster  
**TITLE** Method for producing recombinant proteins in micro-orgar  
**JOURNAL** Patent: WO 03066842-A 25 14-AUG-2003;  
Trommsdorff GmbH & Co.KG Arzneimittel (DE)



(bases 1 to 38)  
gelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
Matic-Adamic,J., Sweedler,D. and Zinnen,S.  
thetic ribonucleic acids with RNase activity  
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(bases 1 to 38)  
gelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
Matic-Adamic,J., Sweedler,D. and Zinnen,S.  
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KEYWORDS  
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REFERENCE  
1 (bases 1 to 38)  
Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
Matic-Adamic,J., Sweedler,D. and Zinnen,S.  
Oligoribonucleotides with enzymatic activity  
Patent: US 6617438-A 1302 09-SEP-2003;  
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REFERENCE  
1 (bases 1 to 38)  
Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,  
Matic-Adamic,J., Sweedler,D. and Zinnen,S.  
Oligoribonucleotides with enzymatic activity  
Patent: US 6617438-A 1331 09-SEP-2003;  
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Sequence 5926 from Patent WO0159103.  
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VERSION

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t.L., Mcswiggen,J. and Chowrira,B.M.  
od and reagent for the modulation and diagnosis of cd20 and  
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nt: WO 0159103-A 5926 16-AUG-2001;  
ZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
iggen, James (US) ; Chowrira, Bharat M. (US)  
Location/Qualifiers

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8757 38 bp RNA linear PAT 10-SEP-2001  
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8757.1 GI:15557898

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aeY,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.  
od and reagent for the inhibition of checkpoint kinase-1 (chk  
nzyme

nt: WO 0157206-A 2129 09-AUG-2001;  
ZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)  
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3935 38 bp RNA linear PAT 29-OCT-2001  
ence 1504 from Patent WO0162911.

3935.1 GI:16546672

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is,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and  
S.J.H.

TITLE Method and reagent for the inhibition of grid  
JOURNAL Patent: WO 0162911-A 1504 30-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITE

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Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CGAGTGAAGATCCCTT 17  
|||||  
Db 18 CGAGTCAAGGTCCTT 34

RESULT 24  
AX425294

LOCUS AX425294 38 bp RNA linear PAT  
DEFINITION Sequence 3630 from Patent WO0188124.

ACCESSION AX425294  
VERSION AX425294.1 GI:21528676

KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1

AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,  
Randi,A.M.

TITLE Method and reagent for the inhibition of erg

JOURNAL Patent: WO 0188124-A 3630 22-NOV-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITE

FEATURES

Location/Qualifiers  
1. .38  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 38;  
Best Local Similarity 82.4%; Pred. NO. 1.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

Qy 1 CGAGTGAAGATCCCTT 17  
|||||  
Db 18 CGAGTCAAGGTCCTT 34

RESULT 25  
AX43628

LOCUS AX43628 38 bp DNA linear PAT  
DEFINITION Sequence 7 from Patent WO0250290.

ACCESSION AX43628  
VERSION AX43628.1 GI:21886388

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
Mammalia; Euthera; Primates; Catarrhini; Hom

REFERENCE 1

AUTHORS Nagai,N., Laroche,Y. and Collen,D.J.

TITLE A yeast expression vector and a method of making a recom  
protein by expression in a yeast cell  
JOURNAL Patent: WO 0250290-A 7 27-JUN-2002;  
THROMB X NV (BE)

FEATURES

Location/Qualifiers  
1. .38  
/organism="Homo sapiens"

/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

71.8%; Score 12.2; DB 6; Length 38;  
ilarity 82.4%; Pred. No. 1.4e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||||  
AGAAAAGAGCCCTT 28

35954 40 bp DNA linear PAT 25-NOV-2003  
ence 9 from Patent WO03060159.

35954  
35954.1 GI:38522865

thetic construct  
thetic construct  
ificial sequences.

i, K. and Holck, A.

ods of nucleic acid amplification  
nt: WO 03060159-A 9 24-JUL-2003;

ORSK, Norwegian Food Research Institute (NO)

Location/Qualifiers

1..40

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="primer"

71.8%; Score 12.2; DB 6; Length 40;  
ilarity 82.4%; Pred. No. 1.4e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||||  
AGCGAAGATCTCTT 36

6440 46 bp DNA linear PAT 16-MAY-2001  
ence 67 from patent US 6180341.

6440  
6440.1 GI:14113033

own.

assified.

'bases 1 to 46)

-son, B.L., Georgiou, G. and Burks, E.A.

itro scanning saturation mutagenesis of proteins

nt: US 6180341-A 67 30-JAN-2001;

Location/Qualifiers

1..46

/organism="unknown"

/mol\_type="unassigned DNA"

71.8%; Score 12.2; DB 6; Length 46;  
ilarity 82.4%; Pred. No. 1.3e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||||  
AGGTGATGATCCCAT 19

RESULT 28  
AX759214/c

LOCUS AX759214 17 bp DNA linear PAT  
DEFINITION Sequence 2535 from Patent WO03040369.

ACCESSION AX759214

VERSION AX759214.1 GI:32253830

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Ho

REFERENCE

AUTHORS

TITLE

1 Telerman, A., Amson, R. and Tuijinder, M.

Sequences involved in tumoral suppression, tumoral reve

apoptosis and/or viral resistance phenomena and their u

medicines

Patent: WO 03040369-A 2535 15-MAY-2003;

Molecular Engines Laboratories (FR)

Location/Qualifiers

1..17

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 70.6%; Score 12; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 1 CGAGTGAAGATC 12

|||||

Db 12 CGAGTGAAGATC 1

RESULT 29  
AX762760/c

LOCUS AX762760 17 bp DNA linear PAT  
DEFINITION Sequence 6081 from Patent WO03040369.

ACCESSION AX762760

VERSION AX762760.1 GI:32257376

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Ho

REFERENCE

AUTHORS

TITLE

1 Telerman, A., Amson, R. and Tuijinder, M.

Sequences involved in tumoral suppression, tumoral reve

apoptosis and/or viral resistance phenomena and their u

medicines

Patent: WO 03040369-A 6081 15-MAY-2003;

Molecular Engines Laboratories (FR)

Location/Qualifiers

1..17

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 70.6%; Score 12; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 1 CGAGTGAAGATC 12

|||||

Db 12 CGAGTGAAGATC 1

RESULT 30  
AX753432

LOCUS AX753432 26 bp DNA linear PAT  
DEFINITION Sequence 20 from Patent WO03037362.

3432  
3432.1 GI:32166193  
helic construct  
helic construct  
ficial sequences.  
ernagel,A., Eulenberger,K., Broenner,G., Ciossek,T., Rudolph,B.,  
lph,D., Belgore,F. and Jaekel,S.  
kinase homologous proteins involved in the regulation of energy  
etasis and organelle metabolism  
nt: WO 03037362-A 20 08-MAY-2003;  
logen Aktiengesellschaft fuer entwicklungsbiologische Forschung  
Location/Qualifiers  
1. .26  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Human Mnk2b forward primer"  
70.6%; Score 12; DB 6; Length 26;  
ilarity 100.0%; Pred. No. 1.9e+05;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
GTGAAGATCC 13  
|||||  
GTGAAGATCC 23  
36  
36.1 GI:18622672  
000312586-A/2.  
helic construct  
helic construct  
ficial sequences.  
ases 1 to 31)  
jima,H. and Nagasawa,A.  
od for imparting herbicide tolerance  
nt: JP 2000312586-A 2 14-NOV-2000;  
TOMO CHEM CO LTD  
Artificial Sequence  
JP 2000312586-A/2  
14-NOV-2000  
28-APR-1999 JP 1999121955  
HIROKI NAKAJIMA,AKITO NAGASAWA  
C12N15/09,A01H5/00,C12N5/10,C12N9/88//A01N63/00,C12N15/00, PC  
N5/00  
Key Location/Qualifiers  
source 1. .31  
/organism="Artificial Sequence".  
Location/Qualifiers  
1. .31  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
70.6%; Score 12; DB 6; Length 31;  
ilarity 100.0%; Pred. No. 1.9e+05;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
ACTGAAGATC 12  
|||||  
ACTGAAGATC 12

RESULT 32  
AR340181/c  
LOCUS AR340181 31 bp DNA linear PAT  
DEFINITION Sequence 2 from patent US 6570070.  
ACCESSION AR340181  
VERSION AR340181.1 GI:33731581  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Nakajima,H. and Nagasawa,A.  
TITLE Production of plants either transformed with the protopc  
IX binding subunit of a magnesium chelataase or a ferroch  
having increased herbicide resistance  
JOURNAL Patent: US 6570070-A 2 27-MAY-2003;  
FEATURES  
source Location/Qualifiers  
1. .31  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 70.6%; Score 12; DB 6; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
QY 1 CGAGTGAAGATC 12  
|||||  
Db 23 CGAGTGAAGATC 12  
RESULT 33  
AX135624/c  
LOCUS AX135624 38 bp DNA linear PAT  
DEFINITION Sequence 2 from Patent WO0132896.  
ACCESSION AX135624  
VERSION AX135624.1 GI:14271894  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Alexandrov,K. and Grun,M.  
TITLE Protein expression systems for non-pathogenic kinetoplas  
JOURNAL Patent: WO 0132896-A 2 10-MAY-2001;  
Jena Bioscience GmbH (DE)  
FEATURES Location/Qualifiers  
source 1. .38  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"  
ORIGIN  
Query Match 70.6%; Score 12; DB 6; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
QY 1 CGAGTGAAGATC 12  
|||||  
Db 25 CGAGTGAAGATC 14  
RESULT 34  
I71937  
LOCUS I71937 43 bp DNA linear PAT  
DEFINITION Sequence 3 from patent US 5683870.  
ACCESSION I71937  
VERSION I71937.1 GI:3008076  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

classified.  
(bases 1 to 43)  
mond,P. and Endozo,A.  
leic acid probes to Chlamydia pneumoniae  
nt: US 5683870-A 3 04-NOV-1997;  
Location/Qualifiers  
1. .43  
/organism="unknown"  
/mol\_type="unassigned DNA"

70.6%; Score 12; DB 6; Length 43;  
nilarity 100.0%; Pred. No. 1.8e+05;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGATCCCGCTT 17  
|||||  
AGATCCCGCTT 25

6871 17 bp RNA linear PAT 07-SEP-2001  
ence 2313 from Patent WO0159103.

6871.1 GI:15526932

thetic construct  
thetic construct  
ificial sequences.

t,L., Mcswiggen,J. and Chowrira,B.M.  
od and reagent for the modulation and diagnosis of cd20 and  
> gene expression  
nt: WO 0159103-A 2313 16-AUG-2001;  
ZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;  
wigen, James (US) ; Chowrira, Bharat M. (US)  
Location/Qualifiers  
1. .17

/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

69.4%; Score 11.8; DB 6; Length 17;  
nilarity 86.7%; Pred. No. 2.7e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAAGATCCCGCTT 17  
|||||  
ATGAATATCCCGCTT 3

36625 20 bp DNA linear PAT 21-NOV-2001  
ence 8387 from Patent WO0179548.

36625.1 GI:17058314

thetic construct  
thetic construct  
ificial sequences.

any,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.  
od of designing addressable array for detection of nucleic acid  
ence differences using ligase detection reaction  
nt: WO 0179548-A 8387 25-OCT-2001;  
WELL RESEARCH FOUNDATION, INC. (US)  
Location/Qualifiers  
1. .20  
/organism="synthetic construct"

/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Hypothetical Probe Sequence"

# ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 20;  
Best Local Similarity 86.7%; Pred. No. 2.6e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 2 GAGTGAAGATCCCGCTT 16  
|||||

Db 5 GAGTGAAGATCCCGCTT 19  
|||||

# RESULT 37

AX537893 20 bp DNA linear PAT  
LOCUS Sequence 44 from Patent WO02072822.  
DEFINITION AX537893  
ACCESSION AX537893  
VERSION AX537893.1 GI:25270001  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

# REFERENCE

1  
AUTHORS Hadano,S., Ikeda,J.E. and Hayden,M.R.  
TITLE Als2 gene and amyotrophic lateral sclerosis type 2  
JOURNAL Patent: WO 02072822-A 44 19-SEP-2002;  
The University of British Columbia (CA) ; Japan Science  
Technology Corporation (JP)

# FEATURES

Location/Qualifiers  
1. .20  
source  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
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/note="synthesized oligonucleotide"

# ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 20;  
Best Local Similarity 86.7%; Pred. No. 2.6e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 3 AGTGAAGATCCCGCTT 17  
|||||

Db 16 AATGAAGATCCCGCTT 2  
|||||

# RESULT 38

AX291992 24 bp DNA linear PAT  
LOCUS Sequence 3754 from Patent WO0179548.  
DEFINITION AX291992  
ACCESSION AX291992  
VERSION AX291992.1 GI:17053675  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

# REFERENCE

1  
AUTHORS Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.  
TITLE Method of designing addressable array for detection of  
sequence differences using ligase detection reaction  
JOURNAL Patent: WO 0179548-A 3754 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)

Location/Qualifiers  
1. .24  
source  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Hypothetical Probe Sequence"

# ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 24;  
Best Local Similarity 86.7%; Pred. No. 2.5e+05;

[illegible]



74382 33 bp DNA linear PAT 12-AUG-2002  
ence 6 from Patent EP1223220.  
74382  
74382.1 GI:22213988

thetic construct  
thetic construct  
ificial sequences.  
vab.H., Glieder,A., Kratky,C., Dreveny,I., Poehlauer,P.,  
anc.W., Mayrhofer,H., Wirth,I., Neuhofer,R. and Bona,R.  
as coding for hydroxynitrile lyase, recombinant proteins with  
oxynitrile lyase activity and their use  
nt: EP 1223220-A 6 17-JUL-2002;  
Fine Chemicals Austria Nfg GmbH & Co KG (AT)  
Location/Qualifiers  
1. .33  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

69.4%; Score 11.8; DB 6; Length 33;  
ilarity 86.7%; Pred.No.2.4e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
GTGAGATCCCTT 17  
|||||  
TAGAGATCCCTT 16

73213 33 bp DNA linear PAT 27-AUG-2002  
th hormone and related protein derivative.

73213.1 GI:22618816  
2001510033-A/2.  
thetic construct  
thetic construct  
ificial sequences.  
(bases 1 to 33)  
G.N.C.

th hormone and related protein derivative  
nt: JP 2001510033-A 2 31-JUL-2001;  
DER BIOTECHNOLOGY INC

Artificial Sequence  
JP 2001510033-A/2  
31-JUL-2001

13-JUL-1998 JP 2000503109  
14-JUL-1997 US 60/052516  
GEORGE N COX III

15/09,C07K14/475,C07K14/505,C07K14/52,C07K14/53,C07K14/535, PC  
K14/54,  
C07K14/55,C07K14/555,C07K14/56,C07K14/565,C07K14/57,C12N15/00  
Description of Artificial Sequence:PCR Primer FH Key  
Location/Qualifiers  
source  
1. .33  
/organism='Artificial Sequence'.  
Location/Qualifiers  
1. .33  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

69.4%; Score 11.8; DB 6; Length 33;  
ilarity 86.7%; Pred.No.2.4e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGAGTGAAGATCCCC 15  
| | | | | | | | | |  
Db 16 CTAGTGAGATCCCC 2

## RESULT 45

BD181899/c

LOCUS

DEFINITION

Novel gene containing DNA sequence encoding hydroxynitr  
recombinant protein originating in the gene and having  
hydroxynitrile lyase activity and utilization thereof.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PD 19-NOV-2002

PF 11-JAN-2002

PR 16-JAN-2001

HELMUT SCHWAB,ANTON GREEDER,CHRISTOPH KRATKY,INGREET DRI

RUDOLPH BONA,

MILFOEFAR,ILMA VIRUTO,

PC C12N15/09,C07K19/00,C12N9/04,C12N9/88,C12P13/00,CL:

Description of the artificial sequence: primer FH Key

Location/Qualifiers

FT source

FT

source

FEATURES

ORIGIN

Query Match

Best Local Similarity

Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 3 AGTGAAGATCCCTT 17

Db 30 AGAGAAGATCCTCTT 16

Search completed: February 29, 2004, 09:43:40

Job time : 542.753 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

February 29, 2004, 07:46:14 ; Search time 145.052 Seconds  
(without alignments)  
497.986 Million cell updates/sec

US-10-090-326-17

1 cgagtgagatccctt 17

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

3373863 seqs, 2124099041 residues

hits satisfying chosen parameters: 3308108

length: 0

length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

N Geneseq\_29Jan04.\*

1: geneseqn1980s.\*

2: geneseqn1990s.\*

3: geneseqn2000s.\*

4: geneseqn2001as.\*

5: geneseqn2001bs.\*

6: geneseqn2002as.\*

7: geneseqn2003as.\*

8: geneseqn2003bs.\*

9: geneseqn2003cs.\*

10: geneseqn2004s.\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

# SUMMARIES

Query Match	Length	DB	ID	Description
100.0	17	6	ABQ82551	Abq82551 Glucuroni
100.0	22	6	ABQ82538	Abq82538 Beta-gluc
100.0	22	9	ADD68259	Add68259 PCR prime
90.6	50	2	AAQ12740	Aaq12740 UidA-2 pr
78.8	20	2	AXX96499	Aax96499 PCR prime
78.8	25	8	ACK21696	Ack21696 Human mic
78.8	32	6	ABA05396	Aba05396 Human IL-
78.8	33	6	AAI45621	Aal45621 T lymphoc
78.8	41	6	ABA94071	Aba94071 Human oes
78.8	41	6	AAI45624	Aal45624 T lymphoc
78.8	41	6	AAI45623	Aal45623 T lymphoc
78.8	41	6	ABA94074	Aba94074 Human oes
78.8	41	6	ABA94073	Aba94073 Human oes
75.3	25	8	ACI66631	Act66631 Human mic
75.3	25	8	ACT114844	Act114844 Human mic
75.3	25	8	ACT160413	Act160413 Human mic
75.3	25	8	ACT130900	Act130900 Human mic
75.3	25	8	ACK09897	Ack09897 Human mic
75.3	29	4	AAI65129	Aai65129 PCR prime
75.3	50	6	ABZ00943	Abz00943 Human leu
75.3	60	6	ABN59114	Abn59114 Human spl
72.9	17	2	AAAI7325	Aaal7325 Aryl hydr
72.9	17	2	AAAI7326	Aaal7326 Aryl hydr

C 24	12.4	72.9	29	3	AAA99103	Aaa99103
C 25	12.4	72.9	32	2	AAQ41588	Aaq41588
C 26	12.4	72.9	32	3	AAZ88659	Aaz88659
C 27	12.4	72.9	32	3	AAC60150	Aac60150
C 28	12.4	72.9	32	3	AAA07479	Aaa07479
C 29	12.4	72.9	32	3	AAA12286	Aaa12286
C 30	12.4	72.9	41	6	ABZ47913	Abz47913
C 31	12.4	72.9	41	6	ABL54116	AbL54116
C 32	12.4	72.9	17	4	ABK00658	AbK00658
C 33	12.2	71.8	24	2	AAZ30691	Aaz30691
C 34	12.2	71.8	24	6	ABQ00239	Abq00239
C 35	12.2	71.8	24	6	ABQ04478	AbQ04478
C 36	12.2	71.8	24	6	ABQ10765	AbQ10765
C 37	12.2	71.8	24	6	ABQ10806	Abq10806
C 38	12.2	71.8	24	6	ABQ04519	AbQ04519
C 39	12.2	71.8	25	6	AAD27955	Aad27955
C 40	12.2	71.8	25	6	ABQ12342	AbQ12342
C 41	12.2	71.8	25	6	ABQ12301	AbQ12301
C 42	12.2	71.8	25	8	ACI15438	Act115438
C 43	12.2	71.8	25	8	ACK09806	Ack09806
C 44	12.2	71.8	38	4	AAH96915	Aah96915
C 45	12.2	71.8	38	4	ABK05926	AbK05926
C 46	12.2	71.8	38	4	ABL47871	AbL47871
C 47	12.2	71.8	38	6	ABN89462	Abn89462
C 48	12.2	71.8	38	6	ABK20983	AbK20983
C 49	12.2	71.8	46	4	AAF73142	Aaf73142
C 50	12.2	71.8	50	6	ABA97764	AbA97764
C 51	12	70.6	17	9	ADB42212	Adb42212
C 52	12	70.6	17	9	ADB45758	Adb45758
C 53	12	70.6	25	8	ACI13905	Act113905
C 54	12	70.6	25	8	ACK22725	Ack22725
C 55	12	70.6	26	7	ACC57605	Acc57605
C 56	12	70.6	30	3	AAZ92403	Aaz92403
C 57	12	70.6	31	3	AAZ45268	Aaz45268
C 58	12	70.6	38	5	AAH24333	Aah24333
C 59	12	70.6	43	2	AAQ44465	Aaq44465
C 60	11.8	69.4	17	4	ABK02313	AbK02313
C 61	11.8	69.4	20	6	ABI96667	Abi96667
C 62	11.8	69.4	20	6	ABQ82286	AbQ82286
C 63	11.8	69.4	20	9	ADE71382	Ade71382
C 64	11.8	69.4	20	9	ADE71377	Ade71377
C 65	11.8	69.4	23	2	AAQ34295	Aaq34295
C 66	11.8	69.4	24	6	ABI89905	Abi89905
C 67	11.8	69.4	24	6	ABI89904	Abi89904
C 68	11.8	69.4	25	8	ACI52164	Act52164
C 69	11.8	69.4	25	8	ACI68983	Act68983
C 70	11.8	69.4	25	8	ACK21697	Ack21697
C 71	11.8	69.4	25	8	ACI52792	Act52792
C 72	11.8	69.4	25	8	ACH61998	Ach61998
C 73	11.8	69.4	27	2	AAT48267	Aat48267
C 74	11.8	69.4	28	5	AAH73870	Aah73870
C 75	11.8	69.4	31	2	AAH38717	Aah38717
C 76	11.8	69.4	33	2	AAZ21961	Aaz21961
C 77	11.8	69.4	33	3	AAZ47773	Aaz47773
C 78	11.8	69.4	33	6	AAF88765	Aaf88765
C 79	11.8	69.4	50	2	AAZ76532	Aaz76532
C 80	11.8	69.4	50	4	AAI27796	Aai27796
C 81	11.8	69.4	50	6	ABZ05688	Abz05688
C 82	11.8	69.4	50	8	ADB17673	Adb17673
C 83	11.8	69.4	51	4	AAI27149	Aai27149
C 84	11.8	69.4	51	4	AAI27387	Aai27387
C 85	11.8	69.4	52	2	AAV76576	Aav76576
C 86	11.8	69.4	53	3	AAA47183	Aaa47183
C 87	11.8	69.4	57	2	AAZ27832	Aaz27832
C 88	11.8	69.4	60	6	ABN35808	Abn35808
C 89	11.8	69.4	60	6	ABN42825	Abn42825
C 90	11.4	67.1	17	2	AAZ64009	Aaz64009
C 91	11.4	67.1	17	2	AAAI7327	Aaai7327
C 92	11.4	67.1	17	4	ABK02675	AbK02675
C 93	11.4	67.1	17	4	ABK02674	AbK02674
C 94	11.4	67.1	20	2	AAZ05109	Aaz05109
C 95	11.4	67.1	20	2	AAZ97026	Aaz97026
C 96	11.4	67.1	20	2	AAZ94029	Aaz94029

67.1	20	2	AAx95372	AAx95372 PCR prime	170	11.2	65.9	20	6	AAI69369	AAI69369
67.1	21	3	AAA30533	AAA30533 C. tropic	171	11.2	65.9	20	6	ABI97463	ABI97463
67.1	21	6	ABK31852	ABK31852 Candida t	172	11.2	65.9	20	7	ABZ69288	ABZ69288
67.1	21	8	ADA73994	ADA73994 PCR prime	173	11.2	65.9	20	7	AGC70535	AGC70535
67.1	21	9	ADC45047	ADC45047 Yeast CYP	c 174	11.2	65.9	22	2	AAQ25485	AAQ25485
67.1	21	9	ADC45617	ADC45617 Yeast CYP	c 175	11.2	65.9	22	2	AAQ47482	AAQ47482
67.1	21	9	ADE52128	ADE52128 C. tropic	c 176	11.2	65.9	22	2	AAQ47481	AAQ47481
67.1	21	10	ADE64292	ADE64292 C. tropic	c 177	11.2	65.9	22	2	AAQ47478	AAQ47478
67.1	22	6	ABK33518	ABK33518 Human nov	c 178	11.2	65.9	22	2	AAT59005	AAT59005
67.1	23	2	AAV51668	AAV51668 Zea mays	c 179	11.2	65.9	22	9	ADC42663	ADC42663
67.1	23	4	AAH26387	AAH26387 Arabidops	180	11.2	65.9	24	1	AAZ48745	AAZ48745
67.1	25	7	ABZ84293	ABZ84293 Toxicology	181	11.2	65.9	24	2	AAQ03988	AAQ03988
67.1	25	8	ACI08297	ACI08297 Human mic	182	11.2	65.9	24	6	ABI91496	ABI91496
67.1	25	8	ACI24037	ACI24037 Human mic	c 183	11.2	65.9	24	6	ABI91497	ABI91497
67.1	25	8	ACI96759	ACI96759 Human mic	184	11.2	65.9	25	8	ACI60412	ACI60412
67.1	25	8	ACK06719	ACK06719 Human mic	185	11.2	65.9	25	8	ACI52542	ACI52542
67.1	25	8	ACI84796	ACI84796 Human mic	186	11.2	65.9	25	8	ACI14845	ACI14845
67.1	25	8	ACT72482	ACT72482 Human mic	187	11.2	65.9	25	8	ACK27387	ACK27387
67.1	25	8	ACK02959	ACK02959 Human mic	188	11.2	65.9	25	8	ACI60528	ACI60528
67.1	25	8	ACI81958	ACI81958 Human mic	189	11.2	65.9	25	8	ACI60529	ACI60529
67.1	25	8	ACH64513	ACH64513 DNA tagge	c 190	11.2	65.9	25	8	ACI86997	ACI86997
67.1	26	2	AAV41896	AAV41896 Nucleotid	191	11.2	65.9	25	8	ACK27386	ACK27386
67.1	28	3	AA9A90486	AA9A90486 Human GM-	192	11.2	65.9	25	8	ACI30901	ACI30901
67.1	29	3	AA9A7475	AA9A7475 Human cyt	c 193	11.2	65.9	25	8	ACK09896	ACK09896
67.1	29	3	AA66470	AA66470 Chlmaeric	194	11.2	65.9	25	8	ACI66630	ACI66630
67.1	29	3	AA62388	AA62388 PCR prime	c 195	11.2	65.9	25	8	ACH56625	ACH56625
67.1	29	4	AA65402	AA65402 Oligonucl	196	11.2	65.9	26	2	AAQ35448	AAQ35448
67.1	29	6	ABA92587	ABA92587 His-tagge	c 197	11.2	65.9	28	5	AAZ89563	AAZ89563
67.1	30	7	ABQ82808	ABQ82808 Human Akt	198	11.2	65.9	28	5	AAI71525	AAI71525
67.1	30	7	ABV76894	ABV76894 PCR prime	199	11.2	65.9	29	2	AAZ28381	AAZ28381
67.1	30	7	ABQ82821	ABQ82821 Human Akt	c 200	11.2	65.9	29	5	AAH79354	AAH79354
67.1	30	7	ABA00527	ABA00527 Human Akt	201	11.2	65.9	30	2	AAQ31229	AAQ31229
67.1	30	7	ABA00725	ABA00725 IL-1 anti	202	11.2	65.9	30	2	AAT58617	AAT58617
67.1	30	9	ADD96166	ADD96166 Human Akt	203	11.2	65.9	30	5	AA773600	AA773600
67.1	30	9	ADD96162	ADD96162 Human Akt	204	11.2	65.9	30	6	ABX69090	ABX69090
67.1	30	9	ADE06650	ADE06650 Primer #1	205	11.2	65.9	33	2	AAQ63125	AAQ63125
67.1	30	9	ADE15864	ADE15864 Primer #1	206	11.2	65.9	33	3	AAZ92394	AAZ92394
67.1	33	2	AAV49532	AAV49532 Human DR4	207	11.2	65.9	34	3	AAZ92392	AAZ92392
67.1	33	3	AA02220	AA02220 Human Dea	208	11.2	65.9	34	7	ACD66090	ACD66090
67.1	33	6	ABL54272	ABL54272 Human kid	209	11.2	65.9	36	7	ACD66014	ACD66014
67.1	35	3	AA770370	AA770370 3' oligon	210	11.2	65.9	36	7	AAZ55016	AAZ55016
67.1	36	2	AA717651	AA717651 ATP kinas	211	11.2	65.9	37	2	AAQ79551	AAQ79551
67.1	37	6	ABQ74340	ABQ74340 Truncated	212	11.2	65.9	37	2	AAT42364	AAT42364
67.1	40	2	AA778196	AA778196 Micro gen	213	11.2	65.9	37	6	AAZ42543	AAZ42543
67.1	41	2	AAV51139	AAV51139 Maize pol	214	11.2	65.9	37	8	ACH00385	ACH00385
67.1	41	4	AAH46990	AAH46990 Primer MP	215	11.2	65.9	38	4	ABK05930	ABK05930
67.1	41	4	AAV47887	AAV47887 PCR mutag	216	11.2	65.9	38	4	ABK08615	ABK08615
67.1	42	2	AAV03899	AAV03899 Primer MP	217	11.2	65.9	38	4	ABK05963	ABK05963
67.1	42	3	AA30545	AA30545 C. tropic	218	11.2	65.9	38	4	ABL47952	ABL47952
67.1	42	4	AAH46989	AAH46989 PCR mutag	219	11.2	65.9	38	4	ABL47877	ABL47877
67.1	42	6	ABK31864	ABK31864 Candida t	220	11.2	65.9	38	4	ABL47923	ABL47923
67.1	42	9	ADC45059	ADC45059 Yeast CYP	221	11.2	65.9	38	6	ABK21136	ABK21136
67.1	42	9	ADC45629	ADC45629 Yeast CYP	222	11.2	65.9	38	6	ABK21007	ABK21007
67.1	42	9	ADE52140	ADE52140 C. tropic	223	11.2	65.9	38	6	ABK21127	ABK21127
67.1	42	10	ADE64304	ADE64304 C. tropic	224	11.2	65.9	38	7	ACD54078	ACD54078
67.1	45	2	AAT77766	AAT77766 Human Fce	225	11.2	65.9	38	7	ACD53781	ACD53781
67.1	47	3	AAZ66237	AAZ66237 Human map	226	11.2	65.9	38	7	ACD53867	ACD53867
67.1	47	3	AAZ69386	AAZ69386 Human map	227	11.2	65.9	38	7	ACD54081	ACD54081
67.1	47	7	ACA61137	ACA61137 VEE virus	228	11.2	65.9	41	6	ABZ48126	ABZ48126
67.1	50	6	ABZ02370	ABZ02370 Human leu	229	11.2	65.9	41	6	AA519996	AA519996
67.1	50	7	AC61138	AC61138 Vector en	c 230	11.2	65.9	42	6	ABK50960	ABK50960
67.1	51	4	AAL26839	AAL26839 Human SNP	231	11.2	65.9	43	2	AAT03423	AAT03423
67.1	51	6	AAZ30141	AAZ30141 Human pit	232	11.2	65.9	43	2	AAT03419	AAT03419
67.1	51	8	AAZ30535	AAZ30535 Human PTT	233	11.2	65.9	44	2	AAT31178	AAT31178
67.1	51	8	ABV12543	ABV12543 Human pro	c 234	11.2	65.9	45	2	AAV04792	AAV04792
67.1	60	6	ABN48834	ABN48834 Human spl	c 235	11.2	65.9	45	2	AAV31047	AAV31047
67.1	60	6	ABN38174	ABN38174 Human spl	c 236	11.2	65.9	45	3	AAV71611	AAV71611
67.1	60	6	ABN35972	ABN35972 Human spl	237	11.2	65.9	45	3	AAV71610	AAV71610
67.1	60	6	ABN59571	ABN59571 Human spl	238	11.2	65.9	46	7	AAZ48234	AAZ48234
67.1	60	6	ABN43569	ABN43569 Human spl	c 239	11.2	65.9	47	2	AAV04796	AAV04796
65.9	20	2	AAZ93660	AAZ93660 PCR prime	c 240	11.2	65.9	47	2	AAV31051	AAV31051
65.9	20	3	AAZ74612	AAZ74612 Human bia	241	11.2	65.9	47	2	AAZ05441	AAZ05441
					242	11.2	65.9	50	4	AAZ29316	AAZ29316

65.9	4	AAI75313	Aai75313 Human sil	C 316	11	64.7	50	10	ADB80169	Ade80169
65.9	51	AD43510	Aad43510 Human cal	C 317	11	64.7	52	6	ABN196178	Abn196178
65.9	52	AAA47181	Aaa47181 Primer fo	318	11	64.7	52	6	ABN50524	Abn50524
65.9	53	AAA47179	Aaa47179 Primer fo	319	11	64.7	60	6	ABN41748	Abn41748
65.9	54	ACC85158	Aac85158 Murine CI	320	11	64.7	60	6	ABN42087	Abn42087
65.9	55	AB228983	Ab228983 Candida g	321	11	64.7	60	6	ABN42966	Abn42966
65.9	60	AA219589	Aaa19589 Complem	C 322	10.8	63.5	15	4	AAF53294	Aaf53294
65.9	60	AA655301	Aaa65301 Vimentin	C 322	10.8	63.5	15	4	AAF53294	Aaf53294
65.9	60	ABN49856	Abn49856 Human spl	C 323	10.8	63.5	15	4	AAF53293	Aaf53293
65.9	60	ABN37258	Abn37258 Human spl	C 324	10.8	63.5	17	2	AA176748	Aat176748
65.9	60	ABN44256	Abn44256 Human spl	C 325	10.8	63.5	17	2	AA174598	Aax74598
65.9	60	AB272671	Ab272671 Detection	C 326	10.8	63.5	18	2	AA27882	Aax7882
64.7	15	AA315104	Aax31504 Tag sequ	C 327	10.8	63.5	18	2	AA27882	Aax7882
64.7	15	ABK32458	Abk32458 Human pan	C 328	10.8	63.5	18	8	ACC85188	Acc85188
64.7	17	ABU96154	Abi96154 Nucleic a	C 329	10.8	63.5	19	9	ADE29661	Ade29661
64.7	17	ACC67120	Acc67120 Murine ol	C 330	10.8	63.5	19	9	ADE29445	Ade29445
64.7	17	ACC65573	Acc65573 Murine ol	C 331	10.8	63.5	19	9	ADE29608	Ade29608
64.7	17	ADC04876	Adc04876 Human Na/	C 332	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04873	Adc04873 Human Na/	C 333	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04877	Adc04877 Human Na/	C 334	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04871	Adc04871 Human Na/	C 335	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04872	Adc04872 Human Na/	C 336	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04875	Adc04875 Human Na/	C 337	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04876	Adc04876 Human Na/	C 338	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04877	Adc04877 Human Na/	C 339	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04878	Adc04878 Human Na/	C 340	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04879	Adc04879 Human Na/	C 341	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04880	Adc04880 Human Na/	C 342	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04881	Adc04881 Human Na/	C 343	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04882	Adc04882 Human Na/	C 344	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04883	Adc04883 Human Na/	C 345	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04884	Adc04884 Human Na/	C 346	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04885	Adc04885 Human Na/	C 347	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04886	Adc04886 Human Na/	C 348	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04887	Adc04887 Human Na/	C 349	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04888	Adc04888 Human Na/	C 350	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04889	Adc04889 Human Na/	C 351	10.8	63.5	20	2	AAV03707	Aav03707
64.7	17	ADC04890	Adc04890 Human Na/	C 352	10.8	63.5	20	2	AAV037	

63.5	25	8	ACH65721	Ach65721 DNA seque	462	10.8	63.5	47	3	AAZ65874	Aaz65874
63.5	25	8	ACH55596	Ach55596 DNA targe	C 463	10.8	63.5	47	4	AHH88577	Aah88577
63.5	25	8	ACH53411	Ach53411 DNA targe	C 464	10.8	63.5	47	6	AAD23733	Aad23733
63.5	25	8	ACH61594	Ach61594 DNA targe	C 465	10.8	63.5	48	2	AAQ12494	Aaq12494
63.5	26	6	ABQ96692	Abq96692 KIAA 0858	466	10.8	63.5	48	2	AAV29088	Aav29088
63.5	27	2	AAx80874	Aax80874 Oligonuc1	467	10.8	63.5	50	3	AAA37167	Aaa37167
63.5	27	6	ABA92330	Aba92330 Human neu	468	10.8	63.5	50	4	AAF54365	Aaf54365
63.5	28	2	AAQ34762	Aaq34762 PCR prime	469	10.8	63.5	50	4	AHH89715	Aah89715
63.5	28	2	AAQ41583	Aaq41583 XYZ const	470	10.8	63.5	50	6	ABZ28951	Abz28951
63.5	29	3	AAV26135	Aav26135 IBRV gD g	471	10.8	63.5	50	6	ABX03302	Abx03302
63.5	29	3	AZZ88654	Aaz88654 Human TRF	472	10.8	63.5	50	6	ABZ05971	Abz05971
63.5	29	3	AAQ60145	Aaq60145 cDNA #3.	473	10.8	63.5	50	6	ACD68402	Acd68402
63.5	29	3	AAQ07474	Aaq07474 Oligonuc1	474	10.8	63.5	50	8	ACH04504	Ach04504
63.5	29	3	AAQ12281	Aaq12281 Primer us	475	10.8	63.5	50	8	ACD68048	Acd68048
63.5	29	4	AAF73430	Aaf73430 Grand fir	476	10.8	63.5	50	9	ADCL18099	Adcl18099
63.5	29	6	ABA05907	Aba05907 Human RTN	477	10.8	63.5	50	9	ADD70745	Add70745
63.5	29	6	ABA01904	Aba01904 Human Cha	478	10.8	63.5	50	9	ADD39822	Add39822
63.5	29	9	ADD41419	Add41419 Murine G+	479	10.8	63.5	50	9	ADD70268	Add70268
63.5	30	1	AAV91929	Aav91929 Variable	480	10.8	63.5	50	9	ADD38389	Add38389
63.5	30	2	AAQ2380	Aaq2380 Alpha-car	481	10.8	63.5	50	9	ADD39345	Add39345
63.5	30	3	AAQ88016	Aaq88016 Human CLA	482	10.8	63.5	50	9	ADD38868	Add38868
63.5	30	3	AAQ55309	Aaq55309 Activatio	483	10.8	63.5	50	9	ADD39345	Add39345
63.5	30	3	AAA49125	Aaa49125 P4M1AS pr	484	10.8	63.5	50	9	ADD40299	Add40299
63.5	30	4	AAQ17808	Aaq17808 Zea maye	485	10.8	63.5	50	9	ADE50520	Ade50520
63.5	30	6	ABX67997	Abx67997 Novel Hel	486	10.8	63.5	50	9	ADE20132	Ade20132
63.5	30	6	ABX69283	Abx69283 Novel Hel	487	10.8	63.5	50	9	ADD93362	Add93362
63.5	30	6	ABK89309	Abk89309 N-acetyl	488	10.8	63.5	50	9	ADD21601	Add21601
63.5	30	6	ABK84938	Abk84938 Cadherin-	489	10.8	63.5	51	2	AAQ24985	Aaq24985
63.5	30	6	ABK84958	Abk84958 Cadherin-	490	10.8	63.5	51	2	AAV19306	Aav19306
63.5	30	7	ABX77184	Abx77184 Mouse ser	491	10.8	63.5	51	4	AAI73420	Aai73420
63.5	30	9	ADE25894	Ade25894 GalNac-tr	492	10.8	63.5	51	4	AAI73418	Aai73418
63.5	31	2	AAQ90543	Aaq90543 Human SII	493	10.8	63.5	51	4	AAH73419	Aah73419
63.5	31	2	AAQ60010	Aaq60010 RNA polym	494	10.8	63.5	51	4	AAH89233	Aah89233
63.5	31	7	ABZ75115	Abz75115 Cole1 ori	495	10.8	63.5	51	4	AAH89714	Aah89714
63.5	33	2	AAZ06811	Aaz06811 Maize met	496	10.8	63.5	51	4	AAH89714	Aah89714
63.5	33	5	AAQ63968	Aaq63968 Human TRF	497	10.8	63.5	51	4	AAH79568	Aah79568
63.5	34	6	ABA01513	Aba01513 TyLM2 PCR	498	10.8	63.5	53	7	ACC80814	Acc80814
63.5	36	2	AAQ47524	Aaq47524 Human hep	499	10.8	63.5	54	1	AAV11173	Aav11173
63.5	36	8	ACA61590	Acac61590 Human hep	500	10.8	63.5	55	6	ABK70409	Abk70409
63.5	38	2	AAQ28045	Aaq28045 Primer CA	501	10.8	63.5	60	2	AAZ19575	Aaz19575
63.5	39	6	ABG61136	Abg61136 Human pol	502	10.8	63.5	60	2	AAZ25695	Aaz25695
63.5	40	2	AAV69456	Aav69456 Plasmid p	503	10.8	63.5	60	3	AAZ34765	Aaz34765
63.5	40	2	AAH88880	Aah88880 Circular	504	10.8	63.5	60	6	ABN37568	Abn37568
63.5	41	2	AAQ36338	Aaq36338 Primer ML	505	10.8	63.5	60	6	ABN41483	Abn41483
63.5	41	4	AAH75954	Aah75954 Arrestin	506	10.8	63.5	60	6	ABN46458	Abn46458
63.5	41	6	ABK50367	Abk50367 Embryonic	507	10.8	63.5	60	7	ADA89026	Ada89026
63.5	41	6	ABL54117	Ab154117 Lithium s	508	10.8	63.5	60	8	ABT43554	Abt43554
63.5	41	6	ABV73446	Abv73446 Novel pol	509	10.8	63.5	60	8	ABT43554	Abt43554
63.5	42	3	AAZ64640	Aaz64640 Hairpin r	510	10.6	62.4	13	5	ABC05503	Abc05503
63.5	43	2	AAQ20830	Aaq20830 Primer PC	511	10.6	62.4	13	5	ABC05502	Abc05502
63.5	43	2	AAQ20831	Aaq20831 Primer PC	512	10.6	62.4	18	2	AAV01067	Aav01067
63.5	43	2	AAQ55335	Aaq55335 ICAM-1 pr	513	10.6	62.4	18	2	AAV12357	Aav12357
63.5	43	2	AAQ55334	Aaq55334 ICAM-1 pr	514	10.6	62.4	19	3	AAZ75693	Aaz75693
63.5	43	2	AAV03175	Aav03175 PCR prime	515	10.6	62.4	20	7	AAZ75693	Aaz75693
63.5	43	2	AAV03176	Aav03176 PCR prime	516	10.6	62.4	20	7	AAZ75693	Aaz75693
63.5	43	2	AAV40177	Aav40177 DNA seque	517	10.6	62.4	21	3	AAA35394	Aaa35394
63.5	43	2	AAQ04202	Aaq04202 Truncated	518	10.6	62.4	21	3	AAZ62117	Aaz62117
63.5	43	3	AAQ04203	Aaq04203 Truncated	519	10.6	62.4	22	5	AAH49299	Aah49299
63.5	43	3	AAA07188	Aaa07188 PCR prime	520	10.6	62.4	23	4	AAI70050	Aai70050
63.5	43	3	AAZ89946	Aaz89946 PCR prime	521	10.6	62.4	23	6	ABL99937	Ab199937
63.5	43	3	AAZ89945	Aaz89945 PCR prime	522	10.6	62.4	24	2	AAI16974	Aai16974
63.5	43	3	AAZ06983	Aaz06983 GABA B re	523	10.6	62.4	24	4	AAZ06829	Aaz06829
63.5	43	3	AAZ46393	Aaz46393 IL-6 rece	524	10.6	62.4	25	3	AAA35478	Aaa35478
63.5	45	2	AAQ74805	Aaq74805 Cannabino	525	10.6	62.4	25	6	ABZ29888	Abz29888
63.5	45	2	AAV71056	Aav71056 Primer Rh	526	10.6	62.4	25	6	ABZ29888	Abz29888
63.5	45	3	AAZ06983	Aaz06983 GABA B re	527	10.6	62.4	25	8	ACI09567	Act09567
63.5	45	3	AAZ46393	Aaz46393 IL-6 rece	528	10.6	62.4	25	8	ACI09567	Act09567
63.5	45	4	AAQ04061	Aaq04061 R. sphaer	529	10.6	62.4	25	8	ACK30923	Ack30923
63.5	46	2	AAZ59756	Aaz59756 Primer P1	530	10.6	62.4	25	8	ACK09807	Ack09807
63.5	46	3	AAZ64262	Aaz64262 PCR prime	531	10.6	62.4	25	8	ACI171492	Act171492
63.5	46	6	ABL41019	Ab141019 Human fib	532	10.6	62.4	25	8	ACI39340	Act39340
63.5	47	3	AAZ66170	Aaz66170 Human map	533	10.6	62.4	25	8	ACI15439	Act15439
					534	10.6	62.4	25	8	ACI11362	Act11362

62.4	25	8	ACI070801	Human mic	608	10.6	62.4	38	6	ABK21077	ABk21077
62.4	25	8	ACI30817	Human mic	609	10.6	62.4	38	6	ABK30890	ABk30890
62.4	25	8	ACI45908	Human mic	610	10.6	62.4	38	7	ACD54053	ACd54053
62.4	25	8	ACK15855	Human mic	611	10.6	62.4	38	7	ACD53974	ACd53974
62.4	25	8	ACI09566	Human mic	612	10.6	62.4	38	7	ACD54069	ACd54069
62.4	25	8	ACI06917	Human mic	613	10.6	62.4	38	7	ACD53888	ACd53888
62.4	25	8	ACK14137	Human mic	614	10.6	62.4	38	7	ACD53707	ACd53707
62.4	25	8	ACK02617	Human mic	615	10.6	62.4	38	7	ACD54002	ACd54002
62.4	25	8	ACI08930	Human mic	616	10.6	62.4	39	6	ABS61164	ABs61164
62.4	25	8	ACI181976	Human mic	617	10.6	62.4	40	6	ABS53840	ABs53840
62.4	25	8	ACI06156	Human mic	618	10.6	62.4	47	2	AZ066997	Az066997
62.4	25	8	ACI69675	Human mic	619	10.6	62.4	47	3	AZ066944	Az066944
62.4	25	8	ACK6328	Human mic	620	10.6	62.4	48	4	AAC93125	AAC93125
62.4	25	8	ACH62969	DNA targe	621	10.6	62.4	50	1	AAN91670	AAN91670
62.4	25	8	ACH64693	DNA targe	622	10.6	62.4	50	4	AAL33780	AAL33780
62.4	27	2	AAX60980	HIV-1 gag	623	10.6	62.4	50	4	AAL20738	AAL20738
62.4	28	6	ABQ82519	Pyrolidol	624	10.6	62.4	50	5	ABL00173	ABl00173
62.4	29	3	AA99345	PCR prime	625	10.6	62.4	50	6	ABZ03886	ABz03886
62.4	30	2	AAV64585	Tobacco C	626	10.6	62.4	50	6	ABZ02293	ABz02293
62.4	30	4	AAI69870	Bovine la	627	10.6	62.4	50	7	ABX79093	ABx79093
62.4	31	2	AAQ90108	VCAM-1 ex	628	10.6	62.4	51	4	AAL28634	AAL28634
62.4	33	2	AAV58706	Nucleotid	629	10.6	62.4	51	4	AAL33431	AAL33431
62.4	34	2	AAZ32615	Tetr (tet	630	10.6	62.4	51	4	AAI74839	AAI74839
62.4	34	3	AA63507	PCR prime	631	10.6	62.4	51	4	AAI75954	AAI75954
62.4	34	6	AD26378	Left SOR	632	10.6	62.4	51	4	AAS59923	AAS59923
62.4	34	7	ACD65956	Anti-HCV	633	10.6	62.4	51	4	AAS59924	AAS59924
62.4	34	7	ACD66088	Anti-HCV	634	10.6	62.4	54	2	AZ06429	Az06429
62.4	35	2	AAQ79589	Primer to	635	10.6	62.4	54	2	AZ06423	Az06423
62.4	35	9	ADC08969	PCR prime	636	10.6	62.4	57	3	AZ44220	Az44220
62.4	36	2	AAQ22009	Subtilisi	637	10.6	62.4	57	3	AZ58678	Az58678
62.4	36	2	AAI34758	PCR prime	638	10.6	62.4	59	2	AAI16859	AAI16859
62.4	36	2	AAI86982	Primer us	639	10.6	62.4	59	2	AAI16859	AAI16859
62.4	36	7	ACA60735	Mouse MHC	640	10.6	62.4	60	2	AQ34076	Aq34076
62.4	36	7	ACD65957	Anti-HCV	641	10.6	62.4	60	2	AAI16851	AAI16851
62.4	36	7	ACD66079	Anti-HCV	642	10.6	62.4	60	2	AAI16851	AAI16851
62.4	37	6	ABQ83137	Human HGP	643	10.6	62.4	60	6	ABN39843	ABn39843
62.4	37	6	ACK59382	Human CLC	644	10.6	62.4	60	6	ABN48722	ABn48722
62.4	37	7	ACA08168	Necrosis	645	10.6	62.4	60	6	ABN36428	ABn36428
62.4	38	4	AAH96871	Human Chk	646	10.6	62.4	60	6	ABN47773	ABn47773
62.4	38	4	AAH96936	Human Chk	647	10.6	62.4	60	8	ACC83844	ACC83844
62.4	38	4	AAH96831	Human Chk	648	10.4	61.2	12	2	AAQ65643	AAq65643
62.4	38	4	AAH96870	Human Chk	649	10.4	61.2	12	2	AAI00035	AAI00035
62.4	38	4	AAH96812	Human Chk	650	10.4	61.2	12	2	AAI13200	AAI13200
62.4	38	4	ABK05862	Human NOG	651	10.4	61.2	12	2	AAV27829	AAv27829
62.4	38	4	ABK05954	Human NOG	652	10.4	61.2	12	2	AAV58766	AAv58766
62.4	38	4	ABK05608	Human NOG	653	10.4	61.2	12	2	AAI13385	AAI13385
62.4	38	4	ABK05667	Human NOG	654	10.4	61.2	12	2	AAI37659	AAI37659
62.4	38	4	ABK05837	Human NOG	655	10.4	61.2	12	2	AAZ24706	AAZ24706
62.4	38	4	ABK05898	Human CD2	656	10.4	61.2	12	3	AAZ36288	AAZ36288
62.4	38	4	ABK05897	Human NOG	657	10.4	61.2	12	3	AAZ95371	AAZ95371
62.4	38	4	ABK05828	Human CD2	658	10.4	61.2	12	3	AAZ89526	AAZ89526
62.4	38	4	ABK05744	Human NOG	659	10.4	61.2	12	3	AAZ52273	AAZ52273
62.4	38	4	ABK05837	Human NOG	660	10.4	61.2	12	3	AAZ36632	AAZ36632
62.4	38	4	ABK05949	Human NOG	661	10.4	61.2	12	3	AAZ28824	AAZ28824
62.4	38	4	ABK05821	Human NOG	662	10.4	61.2	12	4	AAF24050	AAF24050
62.4	38	4	ABK05856	Human NOG	663	10.4	61.2	12	4	AAO6786	AAO6786
62.4	38	4	ABK08517	Human CD2	664	10.4	61.2	12	5	AAI68209	AAI68209
62.4	38	4	ABK08543	Human CD2	665	10.4	61.2	12	6	AAI17930	AAI17930
62.4	38	4	ABK05777	Human NOG	666	10.4	61.2	12	6	AAI30626	AAI30626
62.4	38	4	ABK05896	Human NOG	667	10.4	61.2	12	6	ABK47769	ABk47769
62.4	38	4	ABL47909	Human GRI	668	10.4	61.2	12	6	AAI47924	AAI47924
62.4	38	4	ABL47860	Human GRI	669	10.4	61.2	12	6	AAI17618	AAI17618
62.4	38	4	ABL47857	Human GRI	670	10.4	61.2	12	6	AAI23999	AAI23999
62.4	38	4	ABL47953	Human GRI	671	10.4	61.2	12	6	AAI72945	AAI72945
62.4	38	6	ABL41275	Staphyloc	672	10.4	61.2	12	6	ABX04212	ABx04212
62.4	38	6	ABK21118	Human ERG	673	10.4	61.2	12	6	ABX29770	ABx29770
62.4	38	6	ABK21122	Human ERG	674	10.4	61.2	12	6	AAI27132	AAI27132
62.4	38	6	ABK20902	Human ERG	675	10.4	61.2	12	7	AAI41517	AAI41517
62.4	38	6	ABK21010	Human ERG	676	10.4	61.2	12	7	ABX93693	ABx93693
62.4	38	6	ABK21065	Human ERG	677	10.4	61.2	13	5	ABH15160	ABh15160
62.4	38	6	ABK20909	Human ERG	678	10.4	61.2	13	5	ABH15161	ABh15161
62.4	38	6	ABK20989	Human ERG	679	10.4	61.2	15	2	AAQ52355	AAq52355
62.4	38	6	ABK21013	Human ERG	680	10.4	61.2	15	4	AAF50246	AAf50246

61.2	15	4	AAFS3291	Aaf53291	IGF-I oli	c 754	10.4	61.2	25	8	ACK18351
61.2	15	4	AAFS0245	Aaf50245	IGF-I oli	755	10.4	61.2	25	8	ACK12740
61.2	15	4	AAFS0244	Aaf50244	IGF-I oli	c 756	10.4	61.2	25	8	ACK13786
61.2	15	4	AAFS3292	Aaf53292	IGF-I oli	757	10.4	61.2	25	8	ACK130879
61.2	15	4	AAFS0247	Aaf50247	IGF-I oli	758	10.4	61.2	25	8	ACK13904
61.2	15	6	AAD43414	Aaf43414	Human CYP	c 759	10.4	61.2	25	8	ACK13904
61.2	17	2	AAX64010	Aax64010	Rabbit sc	c 760	10.4	61.2	25	8	ACK22724
61.2	17	2	AAX74827	Aax74827	Mouse flt	761	10.4	61.2	25	8	ACK22724
61.2	17	2	AAX74828	Aax74828	Mouse flt	762	10.4	61.2	25	8	ACK22724
61.2	17	2	AAV96611	Aav96611	Potato ci	c 763	10.4	61.2	25	8	ACK162900
61.2	17	2	AAV17328	Aav17328	Aryl hydr	c 764	10.4	61.2	25	8	ACK162900
61.2	17	2	AAV9674	Aav9674	Human IKB	c 765	10.4	61.2	25	8	ACK162900
61.2	17	6	ABL46341	Abi46341	Human NOG	c 766	10.4	61.2	25	8	ACK162900
61.2	17	9	ADB43372	Abd43372	Tumour su	c 767	10.4	61.2	25	8	ACK14189
61.2	18	2	AAV64144	Aav64144	Rat activ	c 768	10.4	61.2	25	8	ACK14189
61.2	18	2	AAV23330	Aav23330	Synthetic	769	10.4	61.2	25	8	ACK14189
61.2	19	3	AAA35433	Aaa35433	Myrtaceae	770	10.4	61.2	25	8	ACK14189
61.2	19	3	AAA40309	Aaa40309	Human GMR	c 771	10.4	61.2	25	8	ACK14189
61.2	19	4	ADL11604	Adl11604	RT-PCR pr	c 772	10.4	61.2	25	8	ACK14189
61.2	20	2	AAV01242	Aav01242	Decorin p	773	10.4	61.2	25	8	ACK14189
61.2	20	2	AAV06462	Aav06462	Avian sex	775	10.4	61.2	25	8	ACK14189
61.2	20	2	AAV95097	Aav95097	PCR prime	776	10.4	61.2	25	8	ACK14189
61.2	20	3	AAA74731	Aaa74731	Zebrafish	c 777	10.4	61.2	25	8	ACK14189
61.2	20	4	AAK95196	Aak95196	Human CDN	c 778	10.4	61.2	25	8	ACK14189
61.2	20	5	AAH41513	Aah41513	Rat1 rela	c 779	10.4	61.2	25	8	ACK14189
61.2	20	6	ADJ36944	Adj36944	Human MCP	c 780	10.4	61.2	25	8	ACK14189
61.2	20	7	ABZ86188	Abz86188	Human pho	c 781	10.4	61.2	25	8	ACK14189
61.2	20	7	ABZ98122	Abz98122	Human MCP	782	10.4	61.2	25	8	ACK14189
61.2	20	7	ABZ98041	Abz98041	Human MCP	783	10.4	61.2	25	8	ACK14189
61.2	20	7	ABZ98074	Abz98074	Human MCP	c 784	10.4	61.2	25	8	ACK14189
61.2	20	8	ADJ38140	Adj38140	Anticense	c 785	10.4	61.2	25	8	ACK14189
61.2	21	3	AAO09916	Aao09916	Mouse Gry	c 786	10.4	61.2	25	8	ACK14189
61.2	21	4	AAF95404	Aaf95404	Human Gen	c 787	10.4	61.2	25	8	ACK14189
61.2	21	5	ABAI10008	Abai10008	Tail prim	c 788	10.4	61.2	25	8	ACK14189
61.2	21	6	AAI72417	Aai72417	Chloropia	789	10.4	61.2	25	8	ACK14189
61.2	22	3	AACT2135	Aac2135	Single nu	790	10.4	61.2	25	8	ACK14189
61.2	22	3	AACT2132	Aac2132	Single nu	791	10.4	61.2	25	8	ACK14189
61.2	22	4	AAO23375	Aao23375	Brassica	792	10.4	61.2	25	8	ACK14189
61.2	22	5	AAO22289	Aao22289	Human COL	793	10.4	61.2	25	8	ACK14189
61.2	22	5	AAV99518	Aav99518	Human NOV	794	10.4	61.2	25	8	ACK14189
61.2	22	6	ABV99521	Abv99521	Human NOV	c 795	10.4	61.2	25	8	ACK14189
61.2	23	2	AAO74633	Aao74633	Bacillus	c 796	10.4	61.2	25	8	ACK14189
61.2	23	5	AAH41633	Aah41633	Rat coupl	c 797	10.4	61.2	25	8	ACK14189
61.2	23	6	ABAO1710	Abao1710	Apple chl	798	10.4	61.2	25	8	ACK14189
61.2	23	8	ABH84016	Abh84016	Human NUR	c 799	10.4	61.2	25	8	ACK14189
61.2	24	2	AAQ23022	Aaq23022	PCR prime	c 800	10.4	61.2	25	8	ACK14189
61.2	24	2	AAQ40636	Aaq40636	Ribonucle	c 801	10.4	61.2	25	8	ACK14189
61.2	24	2	AAQ96269	Aaq96269	E.coli va	c 802	10.4	61.2	25	8	ACK14189
61.2	24	2	AAW43673	Aaw43673	Primer-1	c 803	10.4	61.2	25	8	ACK14189
61.2	24	2	AAW87899	Aaw87899	Upper pri	c 804	10.4	61.2	25	8	ACK14189
61.2	24	2	AAV41335	Aav41335	Nucleotid	c 805	10.4	61.2	25	8	ACK14189
61.2	24	2	AAV81574	Aav81574	Interleuk	c 806	10.4	61.2	25	8	ACK14189
61.2	24	6	ABQ06259	Abq06259	Oligonuel	c 807	10.4	61.2	25	8	ACK14189
61.2	24	6	ABQ06340	Abq06340	Oligonuel	c 808	10.4	61.2	25	8	ACK14189
61.2	24	6	ABQ11178	Abq11178	Oligonuel	c 809	10.4	61.2	25	8	ACK14189
61.2	25	2	AAT28179	Aat28179	Oligonuel	c 810	10.4	61.2	25	8	ACK14189
61.2	25	2	AAQ25308	Aaq25308	B-cell he	c 811	10.4	61.2	25	8	ACK14189
61.2	25	6	ABA98321	Abag8321	Primer 1	c 812	10.4	61.2	25	8	ACK14189
61.2	25	6	ABA91146	Abag1146	Physomit	c 813	10.4	61.2	25	8	ACK14189
61.2	25	7	ACA92544	Act92544	Human bre	c 814	10.4	61.2	25	8	ACK14189
61.2	25	7	ACK24553	Act24553	Pseudomon	c 815	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK190146	Act190146	Human mic	c 816	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK188015	Act188015	Human mic	c 817	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK140257	Act140257	Human mic	c 818	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK19444	Act19444	Human mic	c 819	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK180194	Act180194	Human mic	c 820	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK14881	Act14881	Human mic	c 821	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK197651	Act197651	Human mic	c 822	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK181959	Act181959	Human mic	c 823	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK181959	Act181959	Human mic	c 824	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK181959	Act181959	Human mic	c 825	10.4	61.2	25	8	ACK14189
61.2	25	8	ACK181959	Act181959	Human mic	c 826	10.4	61.2	25	8	ACK14189

61.2	33	4	AAH74189	Aah74189 s1 RNA bi	C 900	10.4	61.2	60	6	ABN37235	Abn37235
61.2	33	4	AAH49782	Aah49782 Human gam	901	10.4	61.2	60	6	ABN38490	Abn38490
61.2	33	6	ABK12617	Abk12617 NRD inver	C 902	10.4	61.2	60	6	ABN42436	Abn42436
61.2	33	6	ABA96887	Aba96887 Retinal b	C 903	10.4	61.2	60	6	ABN41914	Abn41914
61.2	33	6	AAAL54040	Aal54040 Human Ef-	904	10.4	61.2	60	6	ABNS8871	Abns8871
61.2	33	6	ABK88397	Abk88397 Human clu	C 905	10.4	61.2	60	6	ABN37537	Abn37537
61.2	33	6	ABZ20665	Abz20665 Human G p	906	10.4	61.2	60	6	ABN38700	Abn38700
61.2	33	6	ABQ76776	Abq76776 Human bin	907	10.4	61.2	60	6	ABN38450	Abn38450
61.2	33	6	ACC47533	Acc47533 Human L-a	908	10.4	61.2	60	6	ABN49945	Abn49945
61.2	33	6	ABA93682	Aba93682 Human zin	C 909	10.4	61.2	60	6	ABN41445	Abn41445
61.2	33	6	ABV77388	Abv77388 DNA bindi	910	10.4	61.2	60	6	ABNS0405	Abns0405
61.2	33	6	AAAL42073	Aal42073 Human apo	911	10.4	61.2	60	6	ABN49956	Abn49956
61.2	33	6	ABL56255	AbL56255 Ribosomal	912	10.4	61.2	60	6	ABN36109	Abn36109
61.2	33	6	AAI99781	Aai99781 Human nuc	913	10.4	61.2	60	6	ABN38242	Abn38242
61.2	33	6	ABA96635	Aba96635 Human adh	C 914	10.4	61.2	60	6	ABN41094	Abn41094
61.2	33	7	ABX12246	Abx12246 Human lys	915	10.4	61.2	60	6	ABN49600	Abn49600
61.2	34	2	AAZ23458	Aaz23458 Plant Dre	916	10.2	60.0	15	4	AAFS2071	Aafs2071
61.2	34	4	AAI65144	Aai65144 Neurogene	C 917	10.2	60.0	17	4	ABK00659	Abk00659
61.2	34	5	AAH75521	Aah75521 Human hun	918	10.2	60.0	17	6	ABN10489	Abn10489
61.2	35	2	AAV31138	Aav31138 C-Jun ami	919	10.2	60.0	17	6	ABN10490	Abn10490
61.2	35	2	AAV31140	Aav31140 Fos amino	920	10.2	60.0	17	6	ABN10491	Abn10491
61.2	35	4	RAF74463	Raf74463 Human PRO	C 921	10.2	60.0	17	7	ACDS0674	Acds0674
61.2	36	2	AAQ74213	Aaq74213 Influenza	922	10.2	60.0	17	7	ACD61500	Acd61500
61.2	36	2	AAQ74230	Aaq74230 Influenza	C 923	10.2	60.0	17	7	ACD54536	Acd54536
61.2	36	2	AAT90211	Aat90211 DP-1 PCR	C 924	10.2	60.0	17	7	ACD64416	Acd64416
61.2	36	6	AAAD35820	Aad35820 Human MIS	C 925	10.2	60.0	17	8	ACF05206	Acf05206
61.2	36	7	ACC69897	Acc69897 HIV-1 pla	C 926	10.2	60.0	17	9	ADC04439	Adc04439
61.2	36	7	ACC69886	Acc69886 HIV-1 pla	C 927	10.2	60.0	17	9	ADC04437	Adc04437
61.2	37	6	ABK87815	Abk87815 Human Kai	C 928	10.2	60.0	17	9	ADC04438	Adc04438
61.2	38	2	AAI29811	Aai29811 Sense pri	929	10.2	60.0	18	6	ABV72903	Abv72903
61.2	38	2	AAI45848	Aai45848 Hepatitis	930	10.2	60.0	18	6	ABL31605	AbL31605
61.2	38	4	AAF82375	Aaf82375 Rabies vi	931	10.2	60.0	19	3	AAZ70082	Aaz70082
61.2	38	4	AAF82383	Aaf82383 Rabies vi	C 932	10.2	60.0	19	6	ABL45001	AbL45001
61.2	40	3	AAC61030	Aac61030 Protease	933	10.2	60.0	19	6	ADJ32689	Adj32689
61.2	40	7	ABX76598	Abx76598 M. avium	C 934	10.2	60.0	19	9	ADD00605	Add00605
61.2	41	6	ABA05171	Aba05171 Human gam	C 935	10.2	60.0	19	9	ADD00606	Add00606
61.2	41	6	ABA05170	Aba05170 Human gam	936	10.2	60.0	20	2	AAQ56797	Aaq56797
61.2	41	6	ABZ46434	Abz46434 Human ald	937	10.2	60.0	20	2	AAT93918	Aat93918
61.2	41	6	ABZ44292	Abz44292 Human ATP	C 938	10.2	60.0	20	2	AAT93919	Aat93919
61.2	41	6	ABZ46504	Abz46504 Human ALD	939	10.2	60.0	20	2	AAT93919	Aat93919
61.2	41	6	ABZ49034	Abz49034 Human ALD	C 940	10.2	60.0	20	2	AAT93919	Aat93919
61.2	41	6	ABZ48946	Abz48946 Human ald	C 941	10.2	60.0	20	2	AAZ04976	Aaz04976
61.2	41	8	ACC42076	Acc42076 Human SCN	C 942	10.2	60.0	20	3	AAQ95052	Aaq95052
61.2	47	3	AAZ67299	Aaz67299 Human map	943	10.2	60.0	20	3	AAQ80853	Aaq80853
61.2	47	3	AAZ66968	Aaz66968 Human map	944	10.2	60.0	20	4	AAH25872	Aah25872
61.2	47	3	AAZ668431	Aaz668431 Human map	945	10.2	60.0	20	6	ADJ34331	Adj34331
61.2	48	1	AAH82108	Aah82108 Part of r	C 946	10.2	60.0	20	6	ABQ74671	Abq74671
61.2	48	1	AAH91668	Aah91668 Cloning s	C 947	10.2	60.0	20	6	ABQ74671	Abq74671
61.2	48	2	AAH91668	Aah91668 Cloning s	947	10.2	60.0	20	6	ABQ74671	Abq74671
61.2	48	2	AAH91668	Aah91668 Cloning s	948	10.2	60.0	20	6	ABQ74671	Abq74671
61.2	49	1	AAH82109	Aah82109 Part of r	C 949	10.2	60.0	20	6	ABQ74671	Abq74671
61.2	49	1	AAH82109	Aah82109 Part of r	C 950	10.2	60.0	20	6	ABQ74671	Abq74671
61.2	49	5	ABA10683	Aba10683 Cloning s	C 951	10.2	60.0	20	7	ABZ89261	Abz89261
61.2	50	1	AAH82110	Aah82110 Part of r	C 952	10.2	60.0	20	7	ABZ89261	Abz89261
61.2	50	4	AAAL33543	Aal33543 Human SNP	C 953	10.2	60.0	20	9	ADC36977	Adc36977
61.2	50	4	AAAF86408	Aaf86408 Human pro	C 954	10.2	60.0	20	9	ADC36977	Adc36977
61.2	50	6	ABZ01340	Abz01340 Human SNP	C 955	10.2	60.0	20	9	ADC36977	Adc36977
61.2	50	6	ABZ04848	Abz04848 Human leu	C 956	10.2	60.0	21	2	AAQ66899	Aaq66899
61.2	50	6	ABZ06154	Abz06154 Human leu	C 957	10.2	60.0	21	2	AAQ66899	Aaq66899
61.2	50	6	ABZ02443	Abz02443 Human leu	C 958	10.2	60.0	21	2	AAQ66899	Aaq66899
61.2	51	4	AAAL31922	Aal31922 Human SNP	C 959	10.2	60.0	21	2	AAQ66899	Aaq66899
61.2	51	4	AAAL33266	Aal33266 Human SNP	C 960	10.2	60.0	21	2	AAQ66899	Aaq66899
61.2	51	4	AAAL33400	Aal33400 Human SNP	C 961	10.2	60.0	21	2	AAQ66899	Aaq66899
61.2	51	4	AAAL33441	Aal33441 Human SNP	C 962	10.2	60.0	21	2	AAQ66899	Aaq66899
61.2	51	5	ABL00733	AbL00733 Human ami	C 963	10.2	60.0	21	3	AAZ76372	Aaz76372
61.2	51	5	ABL00790	AbL00790 Human ami	964	10.2	60.0	21	3	AAZ76372	Aaz76372
61.2	51	6	AAD400790	Aad400790 Human ami	C 965	10.2	60.0	21	3	AAZ76372	Aaz76372
61.2	51	6	AAAL41422	Aal41422 FMDV DNA	C 966	10.2	60.0	21	5	AAZ76372	Aaz76372
61.2	53	1	AAH97169	Aah97169 Clar-BamH	966	10.2	60.0	21	5	AAZ76372	Aaz76372
61.2	57	3	AAH75586	Aah75586 PCR prime	C 967	10.2	60.0	21	9	ABZ21588	Abz21588
61.2	57	4	AAH32991	Aah32991 DNA encod	C 968	10.2	60.0	21	9	ABZ21588	Abz21588
61.2	57	6	AAH20697	Aah20697 Human zal	969	10.2	60.0	22	2	AAQ82691	Aaq82691
61.2	58	9	AAH59860	Aah59860 Bacillus	970	10.2	60.0	22	2	AAQ82691	Aaq82691
61.2	60	2	AAH15730	Aah15730 PCR prime	971	10.2	60.0	22	2	AAQ82691	Aaq82691
61.2	60	3	AAH29382	Aah29382 Holliday	972	10.2	60.0	22	2	AAQ82691	Aaq82691



60.0 22 3 AAZ43166  
 60.0 24 2 AAT91333  
 60.0 24 3 AAZ54548  
 60.0 24 3 AAZ54540  
 60.0 24 4 AAT32563  
 60.0 24 4 AAS09674  
 60.0 24 6 ABK33443  
 60.0 24 6 ABQ04543  
 60.0 24 6 ABQ10691  
 60.0 24 6 ABQ10830  
 60.0 24 6 ABQ00206  
 60.0 24 6 ABQ04445  
 60.0 24 6 ABQ10732  
 60.0 24 6 ABQ10871  
 60.0 24 6 ABQ04502  
 60.0 24 6 ABQ00263  
 60.0 24 6 ABQ04404  
 60.0 24 6 ABK13817  
 60.0 24 6 AB185885  
 60.0 24 6 AB183258  
 60.0 24 6 AB183259  
 60.0 24 6 AB184968  
 60.0 24 6 AB192525  
 60.0 24 6 AB184959  
 60.0 24 6 AB192524  
 60.0 24 9 ADC71555  
 60.0 25 4 AAI65599

Aaz43166 PCR prime  
 Aat91333 Bacillus  
 Aaz54548 Neisseria  
 Aaz54540 Neisseria  
 Aat32563 Energy tr  
 Aas09674 Oat Beta  
 Abk33443 Human TNF  
 Abq04543 Oligonuc  
 Abq10691 Oligonuc  
 Abq10830 Oligonuc  
 Abq00206 Oligonuc  
 Abq04445 Oligonuc  
 Abq10732 Oligonuc  
 Abq10871 Oligonuc  
 Abq04502 Oligonuc  
 Abq00263 Oligonuc  
 Abq04404 Oligonuc  
 Abk13817 RT-PCR pr  
 Ab185885 Capture o  
 Ab183258 Capture o  
 Ab183259 Capture o  
 Ab184968 Capture o  
 Ab192525 Capture o  
 Ab184959 Capture o  
 Ab192524 Capture o  
 Adc71555 Human NOV  
 Aai65599 Primer fo

## ALIGNMENTS

andard; DNA; 17 BP.

; (first entry)

use PCR primer SEQ ID NO:17.

oma; oesophagus; malignancy; PCR primer; ss.

S.

-Al.

; 2002WO-US006504.

; 2001US-0273277P.

V PITTSBURGH.

Luketich JD, Raja S, Kelly LA, Finkelstein SD;

32795/79.

CR method for detecting malignancies, e.g. adenocarcinoma of  
 us comprises conducting a PCR amplification on a DNA sample in  
 ion mixture.

ge 40; 141pp; English.

invention describes a multiplex polymerase chain reaction  
 comprising conducting PCR on a DNA sample in a reaction  
 ducted in first and second amplification stages, each with one  
 cycles comprising denaturing, annealing and elongating steps  
 longating step may be conducted at the same temperature as the  
 tep. The second amplification stage of (M1) is conducted under

CC different reaction conditions from that of the first amplifica  
 CC to modulate the relative rate of production of the first ampli  
 CC first primer set and a second amplicon by a second primer set  
 CC first and second amplification stages. Also described: (1) an  
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) int  
 CC PCR diagnostic; (3) rapid detection of a malignancy or of met  
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use in  
 CC automated PCR system. (M1) is useful for detecting malignancie  
 CC adenocarcinoma of the oesophagus. (M1) eliminates contaminatio  
 CC decreases the time it takes to carry out a PCR reaction. The p  
 CC sequence represents a glucuronidase (gus) PCR primer, which is  
 CC example from the present invention  
 XX  
 SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 17; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
 |||||  
 Db 1 CGAGTGAAGATCCCTT 17

## RESULT 2

ABQ82538  
 ID ABQ82538 standard; DNA; 22 BP.

AC ABQ82538;

XX  
 DT 18-DEC-2002 (first entry)

DE Beta-glucuronidase PCR primer SEQ ID NO:4.

XX Adenocarcinoma; oesophagus; malignancy; PCR primer; ss.

XX Homo sapiens.

XX WO200270751-Al.

XX 12-SEP-2002.

XX 04-MAR-2002; 2002WO-US006504.

XX 02-MAR-2001; 2001US-0273277P.

XX (UYPI-) UNIV PITTSBURGH.

XX Godfrey TE, Luketich JD, Raja S, Kelly LA, Finkelstein SD;

XX WPI; #2002-732795/79.

XX Multiplex PCR method for detecting malignancies, e.g. adenocarc  
 PT the oesophagus comprises conducting a PCR amplification on a DNA  
 PT a PCR reaction mixture.

XX Claim 4; Page 30; 141pp; English.

CC The present invention describes a multiplex polymerase chain re  
 CC (PCR) (M1) comprising conducting PCR on a DNA sample in a react  
 CC mixture conducted in first and second amplification stages, eac  
 CC or more PCR cycles comprising denaturing, annealing and elongat  
 CC where the elongating step may be conducted at the same temperat  
 CC annealing step. The second amplification stage of (M1) is condu  
 CC different reaction conditions from that of the first amplificat  
 CC to modulate the relative rate of production of the first ampli  
 CC first primer set and a second amplicon by a second primer set  
 CC first and second amplification stages. Also described: (1) an  
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) intr  
 CC PCR diagnostic; (3) rapid detection of a malignancy or of met  
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use in  
 CC automated PCR system. (M1) is useful for detecting malignancies  
 CC adenocarcinoma of the oesophagus. (M1) eliminates contamination

09:38:23 2004

us-10-090-326-17.max.rng

he time it takes to carry out a PCR reaction. The present presents a beta-glucuronidase (beta-gus) PCR primer, which is example from the present invention

BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

ilarity 100.0%; Score 17; DB 6; Length 22;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ACTGAAGATCCCTT 17  
|||||  
ACTGAAGATCCCTT 18

andard; DNA; 22 BP.

(first entry)

relating to the invention ZC40,575 SEQ ID NO.129.

imer; zcytor17; antiinflammatory; dermatological;  
essive; antimicrobial; vaccine; inflammatory disease;  
y bowel disease; ulcerative colitis; Crohn's disease;  
atitis; eczema; psoriasis; endotoxaemia; septicemia;  
syndrome; infectious disease.

D-A2.

; 2003WO-US0001984.

; 2002US-0350325P.

; 2002US-0375323P.

; 2002US-0435315P.

GENETICS INC.

; Kuijper JL, Dasovich MM, Grant FJ, Hammond AK;  
Gross JA, Dillon SR;

18179/58.

7 ligand polypeptides, useful for treating inflammatory  
ach as inflammatory bowel disease, ulcerative colitis, Crohn's  
pic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.

SEQ ID NO 129; 372pp; English.

on relates to a novel isolated zcytor17 ligand polypeptide. A  
of the invention has antiinflammatory, dermatological,  
assive, and antimicrobial activity, and may have a use in a  
a polypeptide is useful for treating inflammatory diseases,  
lammatory bowel disease, ulcerative colitis, Crohn's disease,  
atitis, eczema, psoriasis, endotoxaemia, septicemia, toxic  
me or infectious diseases. The present sequence is used in  
fication of the invention.

BP; 5 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

ilarity 100.0%; Score 17; DB 9; Length 22;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||||

Db 2 CGAGTGAAGATCCCTT 18

RESULT 4

AAQ12740/c

ID AAQ12740 standard; DNA; 50 BP.

XX

AC AAQ12740;

XX

DT 25-MAR-2003 (revised)

DT 09-JAN-2003 (revised)

DT 26-SEP-1991 (first entry)

XX

DE Uida-2 probe for E. coli, S. sonnei and S. flexneri detection.

XX

KW Detection; probe; Uida; pathogens; PCR; Shigella.

XX

OS Synthetic.

XX EP438115-A.

XX

XX

XX

XX 15-JAN-1991; 91EP-00100408.

XX

XX 19-JAN-1990; 90US-00467813.

XX

XX (PEKE ) PERKIN-ELMER CORP.

XX

PI Atlas RM, Bej AK, Mahbubani MH, Miller R, Steffan RJ;

XX

DR WPI; 1991-216812/30.

XX

PT Detection of microbial pathogens and faecal contamination indic  
recovery cells, lysing, recovering DNA, amplifying by polymer  
reaction, and detection of amplified sequence.

XX

PS Claim 22; Page 22; 14pp; English.

XX

CC A 166 bp region of the E. coli Uida gene, based upon the sequen  
reported by Jefferson et al., FNAS 83:8447-8451 (1986), was amp  
using the primers 1939E-1 (AAQ12728) and 2085R-1 (AAQ12729). Th  
is located between 1998 bp and 2047 bp. The primers and this pr  
used in the detection of E. coli, S. sonnei and S. flexneri de  
CC (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 2  
to correct PA field.)

XX

XX Sequence 50 BP; 11 A; 15 C; 13 G; 11 T; 0 U; 0 Other;

Query Match 90.6%; Score 15.4; DB 2; Length 50;

Best Local Similarity 94.1%; Pred. No. 1.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17

|||||

Db 17 CGAGTGAAGATCCCTT 1

RESULT 5

AAK96499/c

ID AAK96499 standard; DNA; 20 BP.

XX

AC AAK96499;

XX

DT 13-SEP-1999 (first entry)

XX

DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX

KW Respiratory disease; pneumonia; bronchitis; heart disease; sarc  
sinusitis; purulent otitis media; erythema nodosum; pharyngitis;  
KW neutralising epitope; PCR primer; ss.

XX

OS Synthetic.

la pneumoniae.

2.

; 98WO-IB001890.

; 97FR-00014673.

; 98US-0107078P.

SET.

57842/30.

ence of Chlamydia pneumoniae.

Disclosure; 1912pp; English.

7517 represent PCR primers used to amplify open reading frames nucleic acid sequences from the genome of Chlamydia pneumoniae 90). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in se, sarcoidosis, sinusitis, purulent otitis media, erythema pharyngitis. The polypeptides encoded by the open reading he C. pneumoniae genome (see AAY34584-AAY35879) can be used nic compositions as vaccines. Vectors containing C. pneumoniae sequences can also be used as immunogenic compositions, where the vector directs the expression of a neutralising C. pneumoniae

BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

ilarity 78.8%; Score 13.4; DB 2; Length 20;

Conservative 93.3%; Pred. NO. 1.6e+03;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AGTGAAGATCCCC 15

|||||

AATGAAGATCCCC 3

andard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 121677.

obe; expressed sequence tag; microarray; gene expression; iation; biallelic marker; polymorphism; human; es comparison.

IS.

.0-A1.

1.

; 2002US-00098263.

; 2001US-0276759P.

YMETRIX INC.

2;

;67953/53.

XX New array of nucleic acid probes, useful for in situ hybridizat  
PT Southern, Northern or dot-blot hybridization to identify or det  
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 121677; 9pp; English.

XX The invention discloses a microarray comprising a plurality of  
CC acid probes including one of 2,018,500 fully defined sequences,  
CC perfect match, perfect mismatch, antisense match or antisense m  
CC Also disclosed is a method of gene expression analysis. The arr  
CC in monitoring gene expression levels by hybridisation to a DNA  
CC in analysis of genetic variation or in hybridisation of tag-lab  
CC compounds. The nucleic acid probes are specifically designed fo  
CC of at least one target sequence. The method of analysis compris  
CC hybridising at least one or more nucleic acids to at least two  
CC nucleic acid probes and detecting the hybridisation. The nuclei  
CC probes are attached to a solid support. The analysis comprises  
CC gene expression levels, identifying biallelic markers or polymo  
CC or family members of a gene and a cross-species comparison. Eac  
CC nucleic acids further comprises a tag sequence. The array of nu  
CC probes is useful in situ hybridisation, in Southern, Northern  
CC blot hybridisation to identify or detect the sequence or specif  
CC mutations of any gene, in mapping the 5' termini of mRNA molecu  
CC primer extensions or in screening cDNA or genomic libraries or  
CC for additional subclones containing segments of DNA that have b  
CC isolated and previously sequenced. The sequence presented is on  
CC nucleic acid probes incorporated in the microarray. Note: The s  
CC data for this patent can also be obtained in electronic format  
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BF; 10 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 78.8%; Score 13.4; DB 8; Length 25;

Best Local Similarity 93.3%; Pred. NO. 1.6e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0;

Qy 1 CGAGTGAAGATCCCC 15

|||||

Db 9 CGAGTGAAGATCCCC 23

RESULT 7

ABA05396/c

ID ABA05396 standard; DNA; 32 BP.

XX ABA05396;

XX 26-FEB-2002 (first entry)

XX Human IL-1beta PCR primer R1.

XX Human; IL-1 beta gene; IL-1M; IL-1beta; PCR primer; ss.

XX Homo sapiens.

XX CN1307138-A.

XX 08-AUG-2001.

XX 28-JAN-2000; 2000CN-00100695.

XX 28-JAN-2000; 2000CN-00100695.

XX (PREC-) PRECLINICAL MEDICINE INST MILITARY ACAD.

XX Ling S, Song X;

XX WPI; 2002-026898/04.

XX Expression vector pBVIL1 comprising modified human IL-1 beta ge  
PT and endoenzyme sites, useful for antigen expression.

XX

|||||  
3TGAGATCCCAT 26

Page 21(Disclosure); 35pp; Chinese.

Db 2 GAGTGAAGATCCCAT 16

ndard; DNA; 41 BP.

(first entry)

gen receptor related protein 9.13 probe 1 SEQ ID NO:8.

ogen receptor related protein 9.13; cytostatic; haemostatic; immunomodulatory; antiinflammatory; gene therapy; haemopathy; tumour; human immunodeficiency virus infection; HIV infection; disease; inflammation; probe; ss.

1.

-A1.

2001WO-CN000891.

2000CN-00116318.

IGHAI BLOWINDOW GENE DEV INC.

Y;

'5586/10.

receptor related protein 9.13 and encoding polynucleotide, used for treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and

Page 20; 36pp; Chinese.

invention describes human oestrogen-receptor related protein (I) has cytostatic, haemostatic, virucide, immunomodulatory and antitumor activities. The polynucleotide (II) encoding (I) can be used in the diagnosis and therapy. (I) and (II) can be used in the diagnosis and therapy of malignant tumor, haemopathy, human immunodeficiency virus infection, immunological diseases and various inflammations. The invention represents a probe for human oestrogen receptor related protein, which is used in an example from the present invention

BP; 12 A; 11 C; 7 G; 11 T; 0 U; 0 Other;

Similarity 78.8%; Score 13.4; DB 6; Length 41;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TTGAAGATCCCT 16

TTGAAGATCCCT 16

andard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 66622.

obe; expressed sequence tag; microarray; gene expression; variation; biallelic marker; polymorphism; human; es comparison.

XX Homo sapiens.  
OS  
XX US2003104410-A1.  
PN  
XX 05-JUN-2003.  
PD  
XX 15-MAR-2002; 2002US-00098263.  
PF  
XX 16-MAR-2001; 2001US-0276759P.  
PR  
XX (AFFY-) AFFYMETRIX INC.  
PA  
XX Mittmann MP;  
PI  
XX WPI; 2003-567953/53.  
DR  
XX New array of nucleic acid probes, useful for in situ hybridization; Southern, Northern or dot-blot hybridization to identify or detect sequence or specific mutations of any gene.  
PT  
XX Claim 1; SEQ ID NO 66622; 9pp; English.  
PS

CC The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA probe in analysis of genetic variation or in hybridisation of tag-labeled compounds. The nucleic acid probes are specifically designed for hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises one or family members of a gene and a cross-species comparison. Each nucleic acid further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules, primer extensions or in screening cDNA or genomic libraries or for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one nucleic acid probe incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format (data) from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 3 A; 6 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 8; Length 25;  
Best Local Similarity 87.5%; Pred. No. 3.5e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCT 16

Db 8 CGAGTGAAGATCCCT 23

RESULT 15

AC114844

ID AC114844 standard; DNA; 25 BP.

XX AC114844;

XX 13-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 14835.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.

XX Homo sapiens.

OS

0-A1.

2002US-00098263.  
2001US-0276759P.  
YMETRIX INC.

67953/53.

f nucleic acid probes, useful for in situ hybridization, in  
orthern or dot-blot hybridization to identify or detect the  
specific mutations of any gene.

Q ID NO 14835; 9pp; English.

on discloses a microarray comprising a plurality of nucleic  
including one of 2,018,500 fully defined sequences, or its  
ch, perfect mismatch, antisense match or antisense mismatch.  
sed is a method of gene expression analysis. The array is used  
ng gene expression levels by hybridization to a DNA library,  
of genetic variation or in hybridization of tag-labelled  
The nucleic acid probes are specifically designed for analysis  
one target sequence. The method of analysis comprises  
at least one or more nucleic acids to at least two or more  
d probes and detecting the hybridization. The nucleic acid  
attached to a solid support. The analysis comprises monitoring  
sion levels, identifying biallelic markers or polymorphisms,  
embers of a gene and a cross-species comparison. Each of the  
ds further comprises a tag sequence. The array of nucleic acid  
sful in situ hybridization, in Southern, Northern or dot-  
ization to identify or detect the sequence or specific  
f any gene, in mapping the 5' termini of mRNA molecules by  
nations or in screening cDNA or genomic libraries or subclones  
nal subclones containing segments of DNA that have been  
d previously sequenced. The sequence presented is one of the  
d probes incorporated in the microarray. Note: The sequence  
is patent can also be obtained in electronic format directly  
at seqdata.uspto.gov/sequence.html

BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;

75.3%; Score 12.8; DB 8; Length 25;

ilarity 87.5%; Pred. No. 3.5e+03;

Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCCT 16

|||||

AGTGAAGACCTCT 23

andard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 60404.

robe; expressed sequence tag; microarray; gene expression;  
iation; biallelic marker; polymorphism; human;  
es comparison.

US.

0-A1.

XX PD 05-JUN-2003.

XX XX

XX PF 15-MAR-2002; 2002US-00098263.

XX XX

XX PR 16-MAR-2001; 2001US-0276759P.

XX XX

XX PA (AFFY-) AFFYMETRIX INC.

XX XX

XX PI Mittmann MP;

XX XX

XX DR WPI; 2003-567953/53.

XX XX

PT New array of nucleic acid probes, useful for in situ hybridizat  
Southern, Northern or dot-blot hybridization to identify or det  
sequence or specific mutations of any gene.

PT  
XX  
PS Claim 1; SEQ ID NO 60404; 9pp; English.  
XX

CC The invention discloses a microarray comprising a plurality of  
CC acid probes including one of 2,018,500 fully defined sequences,  
CC perfect match, perfect mismatch, antisense match or antisense m  
CC Also disclosed is a method of gene expression analysis. The arr  
CC in monitoring gene expression levels by hybridization to a DNA  
CC in analysis of genetic variation or in hybridization of tag-lab  
CC compounds. The nucleic acid probes are specifically designed fo  
CC of at least one target sequence. The method of analysis compris  
CC hybridizing at least one or more nucleic acids to at least two  
CC nucleic acid probes and detecting the hybridization. The nuclei  
CC probes are attached to a solid support. The analysis comprises  
CC gene expression levels, identifying biallelic markers or polymo  
CC or family members of a gene and a cross-species comparison. Eac  
CC nucleic acids further comprises a tag sequence. The array of nu  
CC probes is useful in situ hybridization, in Southern, Northern  
CC blot hybridization to identify or detect the sequence or specifi  
CC mutations of any gene, in mapping the 5' termini of mRNA molecu  
CC primer extensions or in screening cDNA or genomic libraries or  
CC for additional subclones containing segments of DNA that have b  
CC isolated and previously sequenced. The sequence presented is o  
CC nucleic acid probes incorporated in the microarray. Note: The s  
CC data for this patent can also be obtained in electronic format  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX

SQ Sequence 25 BP; 5 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 8; Length 25;

Best Local Similarity 87.5%; Pred. No. 3.5e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 1 CGAGTGAAGATCCCT 16

|||||

Db 8 CGAGTGAAGATCCCT 23

RESULT 17

ACI30900

ID ACI30900 standard; DNA; 25 BP.

XX XX

XX AC ACI30900;

XX XX

DT 13-OCT-2003 (first entry)

XX XX

DE Human microarray DNA oligonucleotide SEQ ID NO 30891.

XX XX

KW EST; ss; probe; expressed sequence tag; microarray; gene expres  
genetic variation; biallelic marker; polymorphism; human;  
cross-species comparison.

XX OS Homo sapiens.  
XX OS

XX PN US2003104410-A1.

XX XX

XX PD 05-JUN-2003.

2002US-00098263.

2001US-0276759P.

METRIX INC.

7953/53.

nucleic acid probes, useful for in situ hybridization, in Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

ID NO 30891; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, each perfect match, antisense match or antisense mismatch. The array is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises gene expression levels, identifying biallelic markers or polymorphisms or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one nucleic acid probe incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

BP; 9 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 8; Length 25;

Best Local Similarity 87.5%; Pred. NO. 3.5e+03;

Matches 0; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAAGATCCCT 16

|||||

GTGAGAGACCTCT 16

undard; DNA; 25 BP.

(first entry)

array DNA oligonucleotide SEQ ID NO 109878.

be; expressed sequence tag; microarray; gene expression; .ation; biallelic marker; polymorphism; human; is comparison.

;

-A1.

2002US-00098263.

XX

16-MAR-2001; 2001US-0276759P.

XX

(AFFY-) AFFYMETRIX INC.

XX

Mittmann MP;

XX

WPI; 2003-567953/53.

XX

New array of nucleic acid probes, useful for in situ hybridization Southern, Northern or dot-blot hybridization to identify or detect sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 109878; 9pp; English.

XX

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, each perfect match, antisense match or antisense mismatch. The array is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises gene expression levels, identifying biallelic markers or polymorphisms or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one nucleic acid probe incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Sequence 25 BP; 6 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 8; Length 25;

Best Local Similarity 87.5%; Pred. NO. 3.5e+03;

Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCT 16

|||||

16 CGAGTGAAGATCCCT 1

RESULT 19

AAI65129/c

ID AAI65129 standard; DNA; 29 BP.

XX

AAI65129;

XX

29-NOV-2001 (first entry)

XX

PCR primer #6.

XX

PCR primer; Charcot-Leyden Crystal 2; CLL2; ss.

XX

Unidentified.

OS

CN1303940-A.

XX

18-JUL-2001.

XX

27-OCT-1999; 99CN-00119870.

XX

27-OCT-1999; 99CN-00119870.

XX

(UYFU-) UNIV FUDAN.

PA



, Zhao Y;  
 58363/63.  
 ot-leyden crystal 2, its code sequence and preparation method  
 tion.  
 Page 15 (Disclosure); 26pp; Chinese.  
 invention relates to coding sequences for human Charcot-  
 tal 2 (CUL2; see A165125 and A165132). The present sequence  
 iner which was used in an example of the present invention  
 BP; 8 A; 7 C; 7 G; 7 T; 0 U; 0 Other;  
 75.3%; Score 12.8; DB 4; Length 29;  
 ilarity 87.5%; Pred. No. 3.5e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 AGTGAAGATCCCT 16  
 |||||  
 ATTGAGATCCCT 2  
 andard; DNA; 50 BP.  
 (first entry)  
 cyte gene expression profiling probe SEQ ID NO 934.  
 te; gene expression profiling; allograft rejection;  
 osis; congestive heart failure; systemic lupus erythematosus;  
 arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
 us.  
 -A2.  
 .  
 .; 2001WO-US047856.  
 ; 2000US-0241994P.  
 .; 2001US-0296764P.  
 )CARDIA INC.  
 J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;  
 ward R, Queternous T, Johnson F;  
 36525/68.  
 for leukocyte expression profiling, diagnosing a disease, or  
 (the rate of) progression of a disease, e.g. atherosclerosis  
 ve heart failure, comprises diagnostic oligonucleotides.  
 age 354; Opp; English.  
 ion relates to a system for detecting gene expression, which  
 one or two isolated DNA molecules that detect expression of a  
 the gene corresponds to any of 8143 oligonucleotides  
 ABZ08152) each having 50 base pairs (bp). The system is useful  
 te expression profiling. It is particularly useful for  
 a disease, monitoring (rate of) progression of a disease,  
 therapeutic outcome, determining prognosis for a patient,  
 disease complications in an individual or monitoring response  
 in an individual. The diseases include cardiac allograft

CC rejection, kidney allograft rejection, liver allograft rejectio  
 CC atherosclerosis, congestive heart failure, systemic lupus eryth  
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infecti  
 XX  
 SQ Sequence 50 BP; 11 A; 11 C; 12 G; 16 T; 0 U; 0 Other;  
 Query Match 75.3%; Score 12.8; DB 6; Length 50;  
 Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0;  
 QY 1 CGAGTGAAGATCCCT 16  
 |||||  
 Db 32 CTATGAGATCCCT 47  
 RESULT 21  
 ABNS9114/c  
 ID ABNS9114 standard; DNA; 60 BP.  
 XX  
 AC ABNS9114;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:31  
 XX  
 KW Human; mouse; rat; splice transcript; detection; RNA transcript  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200210449-A2.  
 XX  
 PD 07-FEB-2002.  
 XX  
 PF 20-JUL-2001; 2001WO-IB001903.  
 XX  
 PR 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX  
 PA (COMP-) COMPUGEN INC.  
 XX  
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX  
 DR WPI; 2002-257383/30.  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcrip  
 PT genome, useful for detecting tissue-, pathology-, and developme  
 PT specific genes.  
 XX  
 PS Example 1; SEQ ID NO 31862; 47pp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for c  
 CC messenger RNAs that populate a (sub-)transcriptome, where the  
 CC )transcriptome comprises messenger RNAs transcribed from mult  
 CC transcription units that populate a genome. The library compr  
 CC oligonucleotides, each capable of hybridising selectively to a  
 CC messenger RNAs transcribed from a given transcription unit of t  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitat  
 CC quantitatively characterising the corresponding transcriptome,  
 CC detecting RNA transcripts and splice variants of human or anim  
 CC transcriptomes. The libraries may also be used as specialised n  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC biological or pathological state, and so allowing the detectio  
 CC - and pathology-specific genes such as those genes only express  
 CC specific tissue under a specific pathological condition; to det  
 CC developmental specific genes; and to detect RNA transcripts and  
 CC variants of a transcriptome of a patient suffering from a parti  
 CC disorder. ABN27253 to ABNS9589 represent oligonucleotide sequ  
 CC rats, humans and mice, which are used in the exemplification of  
 CC present invention. N.B. The sequence data for this patent did

09:38:23 2004

us-10-090-326-17.max.rng

printed specification, but was obtained in electronic format  
m WIPO at ftp.wipo.int/pub/published\_pct\_sequences

BP; 12 A; 16 C; 18 G; 14 T; 0 U; 0 Other;  
75.3%; Score 12.8; DB 6; Length 60;  
larity 87.5%; Pred. No. 3.8e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TGAAGATCCGCTT 17  
|||||  
TCAAGATCGCTT 12

ndard; RNA; 17 BP.

(first entry)

arbon nuclear transport substrate sequence SEQ ID NO:551.

hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
ha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
ibozyme; angiogenic factor; cytosolic; antidiabetic;  
ic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;  
al; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
macular degeneration; inflammation; neovascular glaucoma;  
eration; psoriasis; verruca vulgaris; angiofibroma;  
erosis; pot-wine stain; Sturge Weber syndrome;  
unay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

99WO-US006507.

98US-0079678P.

RYME PHARM INC.

oberts E, Jarvis T, Coeshott C, Mcswiggen JA;

1315/50.

mes for modulating the synthesis, expression and/or stability  
ncoding an angiogenic factors.

age 72; 305pp; English.

invention describes enzymatic nucleic acid molecules with RNA  
ivity, which specifically cleave RNA encoded by an aryl  
nuclear transporter (ARNT) gene, an integrin subunit beta 3  
egin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
i AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
3 to AAA17560 and AAA17623 to AAA17684 represent their  
ng target sequences; AAA17685 to AAA18385 and AAA19087 to  
present ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
5 to AAA19222 represent their corresponding target sequences;  
AAA20361 and AAA21501 to AAA21595 represent ribozyme  
or integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
AAA21688 represent their corresponding target sequences;  
AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
a subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
present their corresponding target sequences. The ribozymes of  
n are used for modulating the synthesis, expression and/or  
f an mRNA encoding angiogenic factor, especially ARNT,  
unit beta-3, integrin subunit alpha-6, or Tie-2. They are

CC especially used to treat cancer, diabetic retinopathy, age relat  
CC macular degeneration (ARMD), inflammation, and arthritis, as well  
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca v  
CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Webe  
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syn  
CC and other syndromes and diseases related to the levels of ARNT,  
CC integrin subunit alpha-6, or integrin subunit beta-3

SQ Sequence 17 BP; 3 A; 3 C; 4 G; 0 T; 7 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 2; Length 17;  
Best Local Similarity 92.9%; Pred. No. 5.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 3 ACTGAAGATCCCT 16  
|||||  
Db 17 AGTGAAGATACCT 4

RESULT 23  
AAA17326/c  
ID AAA17326 standard; RNA; 17 BP.

XX AC AAA17326;

XX 19-JUN-2000 (first entry)

XX Aryl hydrocarbon nuclear transport substrate sequence SEQ ID NO:  
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogen  
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin riboz  
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic  
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic;  
XX dermatological; RNA cleavage; cancer; diabetic retinopathy; art  
XX age related macular degeneration; inflammation; neovascular glau  
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;  
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

OS Homo sapiens.

XX WO9950403-A2.

XX 07-OCT-1999.

XX 24-MAR-1999; 99WO-US006507.

XX 27-MAR-1998; 98US-0079678P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

XX WPI; 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or  
PT of an mRNA encoding an angiogenic factors.

XX Claim 53; Page 72; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules  
CC cleaving activity, which specifically cleave RNA encoded by an  
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit  
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA167  
CC AAA17617 and AAA17561 to AAA17622 represent ribozyme sequences  
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent the  
CC corresponding target sequences; AAA17685 to AAA18385 and AAA1901  
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to  
CC and AAA19155 to AAA19222 represent their corresponding target s  
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozym  
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA2150  
CC AAA21596 to AAA21688 represent their corresponding target sequen  
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozym

a subunit beta 3, and AAA22476 to AAA23262, AAA23343 to present their corresponding target sequences. The ribozymes of on are used for modulating the synthesis, expression and/or f an mRNA encoding angiogenic factor, especially ARNT, bunit beta-3, integrin subunit alpha-6, or Tie-2. They are used to treat cancer, diabetic retinopathy, age related generation (ARMD), inflammation, and arthritis, as well as glaucoma, myopic degeneration, psoriasis, verruca vulgaris, a of tuberous sclerosis, pot-wine stains, Sturge Weber ipel-Treanunay-Weber syndrome, Osler-Weber-Rendu syndrome, yndromes and diseases related to the levels of ARNT, Tie-2, bunit alpha-6, or integrin subunit beta-3

BP; 3 A; 3 C; 4 G; 0 T; 7 U; 0 Other;

72.9%; Score 12.4; DB 2; Length 17;

ilarity 92.9%; Pred. No. 5.5e+03;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGAAGATCCCTT 16

|||||  
TGAAGATCCCTT 2

andard; DNA; 29 BP.

(first entry)

PCR primer SEQ ID NO:9.

4; PCR primer; ss.

s.

; 98CN-00126050.

; 98CN-00126050.

V FUDAN.

Y, Tu Q;

44299/50.

in Rab24, its coding sequence, preparation and usage.

Page 13; 22pp; Chinese.

invention describes human Rab24. The human Rab24 protein is to mouse Rab24. The present sequence represents a PCR primer ab24 which is used in an example from the present invention

BP; 8 A; 9 C; 9 G; 3 T; 0 U; 0 Other;

72.9%; Score 12.4; DB 3; Length 29;

ilarity 92.9%; Pred. No. 5.8e+03;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TGAAGATCCCTT 17

|||||  
'GAGGATCCCTT 1

ID AAQ41588 standard; DNA; 32 BP.  
XX  
AC AAQ41588;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-AUG-1993 (first entry)  
XX  
DE ZXY construct primer Y BAW.  
XX  
KW Human T cell reactive feline protein; TRFP; epitope; recombitop  
XX  
OS Synthetic.  
XX  
FN WO9308280-A1.  
XX  
PD 29-APR-1993.  
XX  
PF 16-OCT-1992; 92WO-US008694.  
XX  
PR 16-OCT-1991; 91US-00777859.  
PR 13-DEC-1991; 91US-00807529.  
XX  
PA (IMMU-) IMMULOGIC PHARM CORP.  
XX  
FI Rogers BL, Mergenstern JP, Bond JF, Garman RD, Kuo M, Morv  
XX  
DR WPI; 1993-152473/18.  
XX  
PT Recombitope peptide having T-cell stimulating activity - for th  
PT diagnosis and treatment of sensitivity to protein allergens,  
PT auto:antigens and protein antigens.  
XX  
PS Disclosure; Fig 10; 73pp; English.  
XX  
CC The primer is used in the construction of recombitope peptides  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 32 BF; 4 A; 11 C; 5 G; 12 T; 0 U; 0 Other;  
  
Query Match 72.9%; Score 12.4; DB 2; Length 32;  
Best Local Similarity 92.9%; Pred. No. 5.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;  
  
Oy 2 GAGTGAAGATCCCC 15  
Db 14 GAGTGAAGATCCCC 1  
  
RESULT 26  
AAZ88659/c  
ID AAZ88659 standard; DNA; 32 BP.  
XX  
AC AAZ88659;  
XX  
DT 22-MAY-2000 (first entry)  
XX  
DE Human TRFP derived primer #8.  
XX  
KW T-cell reactive feline protein; TRFP; T cell epitope; T cell re  
KW down regulation; immune response; allergen; immunoglobulin E;  
KW sensitivity; cat protein allergen; human; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6019972-A.  
XX  
PD 01-FEB-2000.  
XX  
PF 02-SEP-1994; 94US-00300928.  
XX  
PR 03-NOV-1989; 89US-00431565.  
PR 28-FEB-1991; 91US-00662276.  
PR 13-DEC-1991; 91US-00807529.

; 92US-00857311.  
; 92US-00884718.  
; 93US-00006116.

JLOGIC PHARM CORP.

Greenstein JL, Kuo M, Briner TJ, Morville M;

16862/13.

human T cell reactive feline protein for treating sensitivity  
in allergens comprise at least one T cell epitope recognized  
receptor specific for the human T cell reactive feline

Col 123-124; 105pp; English.

ion describes a novel peptide (I) of human T cell reactive  
sin (hTRFP) having at least one T cell epitope recognized by a  
prior specific for the human T cell reactive feline protein,  
consisting of at least 7-30 amino acids, and having an amino  
ce derived from an amino acid sequence comprising 94, 96, 97,  
residues, given in the specification. The peptides down,  
a immune response to the allergen. The peptides have reduced  
lin E binding and reduce T cell responsiveness. The peptide  
all in compositions for treating sensitivity to a cat protein  
a subject. This sequence represents a primer used to  
aptides comprising of two or more regions of human TRFP

BP; 4 A; 11 C; 5 G; 12 T; 0 U; 0 Other;

72.9%; Score 12.4; DB 3; Length 32;  
ilarity 92.9%; Pred. No. 5.9e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAGATCCCC 15  
|||||  
GTGAGGATCCCC 1

undard; CDNA; 32 BP.

(first entry)

; human T cell reactive feline protein; hTRFP; immunotherapy;

1.

; 95US-00431184.  
; 89US-00431565.  
; 91US-00662276.  
; 91US-00807529.  
; 92US-00857311.  
; 92US-00884718.  
; 93US-00006116.  
; 94US-00300928.

JLOGIC PHARM CORP.

Garman RD, Greenstein JL, Bond JF;

XX WPI; 2000-601477/57.  
XX

PT Detecting, preventing and treating sensitivity to cat protein a  
PT comprises combining a biological sample with a human T cell rea  
PT feline protein and determining the extent of binding that occur  
XX Disclosure; Col 123; 106pp; English.

XX The present invention relates to the detection of sensitivity t  
CC protein allergen by combining a blood sample from a subject wit  
CC peptide of human T cell reactive feline protein (hTRFP). This m  
CC the hTRFP peptides are useful for diagnosing, preventing and tr  
CC allergies by reducing or abolishing an individual's allergic re  
CC a cat allergen. DNA encoding the TRFP may be used as probes to  
CC equivalent sequences present in other species. These may furthe  
CC to study the mechanism of immunotherapy of cat allergy, and to  
CC modified derivatives, analogues or functional equivalents usefu  
CC immunotherapy. The present sequence was used in the invention  
XX Sequence 32 BP; 4 A; 11 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 3; Length 32;  
Best Local Similarity 92.9%; Pred. No. 5.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCCC 15  
|||||  
Db 14 GAGTGAGGATCCCC 1

RESULT 28  
AAAA07479/c  
ID AAA07479 standard; DNA; 32 BP.

XX AAA07479;

XX 13-JUL-2000 (first entry)

XX Oligonucleotide used in isolation of TRFP coding sequence.

XX Cat; TRFP; human T-cell reactive feline protein; cat protein al  
XX house dust; Fel d I; cat allergy; Felis domesticus sensitivity;  
XX diagnosis; goat; sheep; horse; rabbit; dog; ss.

XX Synthetic.

XX US6025162-A.

XX 15-FEB-2000.

XX 28-APR-1995; 95US-00430944.

XX 03-NOV-1989; 89US-00431565.

XX 28-FEB-1991; 91US-00662276.

XX 13-DEC-1991; 91US-00807529.

XX 25-MAR-1992; 92US-00857311.

XX 15-MAY-1992; 92US-00884718.

XX 15-JAN-1993; 93US-00006116.

XX 02-SEP-1994; 94US-00300928.

XX (IMMU-) IMMULOGIC PHARM CORP.

XX Morgenstern JP, Griffith IJ, Rogers BL;

XX WPI; 2000-181812/16.

XX New human T cell reactive feline protein, useful for desensitizi  
PT allergic individuals to cat allergens.

XX Disclosure; Col 123-124; 108pp; English.

XX This sequence is an oligonucleotide used to isolate TRFP. The ir

1 09:38:23 2004

us-10-090-326-17.max.rng

a human T cell reactive feline protein (TRFP). The protein is an allergen, and was isolated from a vacuum bag extract of house dust collected from several cats. TRFP is composed of two covalently linked peptide chains. TRFP is also referred to as Fel d 1. TRFP and its peptides are reducing or preventing the adverse effects that exposure to allergens has on cat allergic individuals (i.e. to individuals to cat allergens or block the effect of the TRFP is also used in methods of diagnosing sensitivity to allergens in an individual. DNA sequences encoding TRFP can be used to locate equivalent sequences present in other species, sheep, horse, rabbit and dog, that may be useful in diagnostic and therapeutic applications

BP; 4 A; 11 C; 5 G; 12 T; 0 U; 0 Other;  
Query Match 72.9%; Score 12.4; DB 3; Length 32;  
Best Local Similarity 92.9%; Pred. No. 5.9e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAGATCCCC 15  
|||||  
GTGAGATCCCC 1

standard; DNA; 32 BP.

(first entry)

in construction of TRFP derived peptides ZXY.

active feline protein; TRFP; Fel d 1; cat allergen; primer;  
c; T cell stimulator; diagnostic; immunotherapy; ss.

95US-00430014.

89US-00431565.  
91US-00662276.  
91US-00807529.  
92US-00857311.  
92US-00884718.  
93US-00006116.  
94US-00300928.

ULOGIC PHARM CORP.

ers BL, Gefter ML, Morgenstern JP, Brauer AW;  
JL, Griffith IJ, Garman RD;

16905/27.

cell reactive feline protein useful for reducing or individual's allergic response to cat allergen comprising two covalently linked peptide chains.

Col 123-124; 106pp; English.

ion describes a novel naturally occurring cat protein allergen T cell reactive feline protein (TRFP), comprising two covalently linked peptide chains with a molecular weight of 20 or 130 kD under non-reducing conditions and 5 kD or 10-18 kD under reducing conditions. The products of the invention have c activity and act as human T cell stimulators. TRFP is useful

for reducing or preventing the adverse effects of cat allergens on allergic individuals and in ex vivo diagnostic tests to determine cat sensitivity so as to selectively use them to desensitize individual. Purified TRFP is also useful for study of mechanism of immunotherapy of cat allergy and to design modified derivatives, analogs or functional equivalents that are more useful in immunotherapy against cat allergy. DNA sequences encoding TRFP as probes to locate equivalent sequences present in other species, sheep, dogs, rabbits or horses) that may be useful in diagnostic therapeutics. Fully defined and characterized TRFP provides a very simple desensitization therapy. This sequence represents used in the construction of TRFP derived peptides ZXY, YXZ and XX are used in the method of the invention

Sequence 32 BP; 4 A; 11 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 72.9%; Score 12.4; DB 3; Length 32;  
Best Local Similarity 92.9%; Pred. No. 5.9e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAGATCCCC 15  
|||||  
Db 14 GAGTGAGATCCCC 1

RESULT 30

ABZ47913/c

ID ABZ47913 standard; DNA; 41 BP.

AC ABZ47913;

DT 26-JUN-2003 (first entry)

Human ATP-binding cassette ABOG1 gene polymorphic site, #4697.

Human; drug metabolising enzyme; gene; drug metabolism; chromosomal polymorphic site; drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism;

Homo sapiens.

Key Location/Qualifiers

variation replace(21,A)

/\*tag= a

/standard\_name= "Single nucleotide polymorphism

WO200252044-A2.

04-JUL-2002.

27-DEC-2001; 2001WO-JP011592.

27-DEC-2000; 2000JP-00399443.

02-MAY-2001; 2001JP-00135256.

27-AUG-2001; 2001JP-00256862.

(RIKE ) RIKEN KK.

Nakamura Y, Sekine A, Iida A, Saito S;

WPI; 2002-583571/62.

Identifying individuals having a polymorphism, useful for determining effectiveness or side effect of a drug or treatment protocol, c detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.

Claim 23; Page 153; 2785pp; English.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within encoding enzymes associated with drug metabolism. The invention to methods and compositions for identifying individuals who have

phism in such drug metabolising enzyme-encoding genes. The ns may be identified in a nucleic acid sample using probes or a specific for a sequence selected from ABZ43217-ABZ50887 using a detection assays, including hybridisation assays, nucleic acid PCR-based methods. The invention also encompasses methods of and screening drugs using genetic polymorphism data. Genetic a data, particularly that relating to single nucleotide ns (SNPs), may be used in studying the relationship between a variations and human diseases, conditions, and responses to are also useful as polymorphism markers for discovering genes or exacerbate certain diseases. SNPs are particularly useful a respects as they are stable in populations, occur and have lower mutation rates than other genome variations ating sequences. The detection and analysis of polymorphisms coding drug metabolising enzymes allows the customisation of les based upon the genetic profile of individual patients. not only take the guesswork out of selecting the drug with the arapeutic effect for a particular patient, but would also likelihood of adverse reactions, thereby increasing safety. he invention are also useful in the drug discovery and cesses. For example, individuals could be selected for als only if their genetic profiles indicate that they are responding to a particular drug or drug class, and previously candidates could be revived if they were matched with more patient populations. The methods, data and compositions of n may therefore lead to an increase in the range of g targets and decreases in the number of adverse drug ailed drug trials, the time taken for a drug to be approved, f time patients are on medication and the number of different a patient needs to take before finding an effective therapy

BP; 9 A; 9 C; 17 G; 6 T; 0 U; 0 Other;

72.9%; Score 12.4; DB 6; Length 41;

ilarity 92.9%; Pred. No. 6e+03;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GTGAAGATCCCC 15

|||||

GTGAAGATCCCC 26

indard; DNA; 41 BP.

(first entry)

itive 3' diphosphate nucleotidase 11.99 probe #1.

ite nucleotidase 11.99; enzyme; human; acidosis; gene therapy;

3.

; 2000CN-00116599.

; 2000CN-00116599.

GHAI BIODOOR GENE DEV CO LTD.

Y;

05422/35.

peptide-human lithium sensitive 3' diphosphate nucleotidase  
ly nucleotide for coding this polypeptide.

XX Example 6; Page 22 (Disclosure); 35pp; Chinese.  
XX The present invention relates to novel human lithium sensitive  
CC diphosphate nucleotidase 11.99 (see AB875982). The enzyme and i  
CC sequence are useful for treating several diseases, such as horm  
CC related dysfunction disease and metabolic acid-base disequilib  
CC (acidosis). The present sequence is a probe, which was used in  
CC from the invention  
XX  
SQ Sequence 41 BP; 9 A; 9 C; 8 G; 15 T; 0 U; 0 Other;  
  
Query Match 72.9%; Score 12.4; DB 6; Length 41;  
Best Local Similarity 92.9%; Pred. No. 6e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;  
  
QY 4 GTGAAGATCCCCCT 17  
|||||  
Db 16 GTGATGATCCCCCT 29  
  
RESULT 32  
ABK0658/c  
ID ABK0658 standard; RNA; 17 BP.  
XX  
AC ABK0658;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human NOGO Hammerhead Ribozyme #658.  
XX  
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; hae  
KW cerebrotective; nootropic; neuroprotective; antiparkinsonian  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead  
KW DNase; inozyme; G-cleaver; amperzyme; zinzyme; lymphoma; leuk  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leuk  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell l  
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; demen  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sc  
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerativ  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200159103-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001WO-US004273.  
XX  
PR 11-FEB-2000; 2000US-0181797P.  
PR 28-FEB-2000; 2000US-0185516P.  
PR 06-MAR-2000; 2000US-0187128P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGGEN J.  
PA (CHOW/) CHOWRIKA B M.  
XX  
PI Blatt L, Mcswiggen J, Chowrika BM;  
XX WPI; 2001-607195/69.  
XX  
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antise  
PT constructs, which down regulate expression of a CD20 gene or ne  
PT growth inhibitor gene useful for treating, e.g., lymphoma, leuk  
PT central nervous system injury.  
XX  
PS Claim 88; Page 76; 200pp; English.  
XX

on relates to a nucleic acid molecule which down regulates of a CD20 gene and a nucleic acid molecule which down expression of a neurite growth inhibitor gene (NOCO). The 3s may be enzymatic nucleic acids (e.g. a ribozyme or a inozyme (an endolytic nucleic acid cleaving an RNA molecule an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr e (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA motif). The CD20-targeting nucleic acid is used to cleave RNA the presence of a divalent cation that is preferably Mg<sup>2+</sup>. it may be contacted with a cell to reduce CD20 activity of e treat a patient having a condition associated with the level e treatment may further comprise the use of one or more In particular, the CD20 targeting nucleic acid may be used to oma, leukaemia, B-cell lymphoma, low-grade or follicular non- ymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic HIV (human immunodeficiency virus) associated NHL, mantle-cell (CLL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, mbocytopenia, and inflammatory arthropathy. The NOGO- nucleic acid is used to cleave RNA of the NOGO gene in the a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the d may be contacted with a cell to reduce NOGO activity of the eat a patient having a condition associated with the level of e treatment may further comprise the use of one or more In particular, the NOGO-targeting nucleic acid may be used to al nervous system (CNS) injury and cerebrovascular accident e), Alzheimer's disease, dementia, multiple sclerosis (MS), y-induced neuropathy, amyotrophic lateral sclerosis (ALS), y-disease, ataxia, Huntington's disease, Creutzfeldt-Jakob uscular dystrophy, and/or other neurodegenerative disease h respond to the modulation of NOGO expression. The present ; a hammerhead ribozyme of the invention

1 BP; 5 A; 1 C; 5 G; 0 T; 6 U; 0 Other;

71.8%; Score 12.2; DB 4; Length 17;

ilarity 82.4%; Pred. No. 7.1e+03; Length 17;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3AGTGAAGATCCCTT 17  
| | | | |  
AATGATATCCCTT 1

Standard; DNA; 24 BP.

1 (first entry)

alcohol dehydrogenase promoter primer 3.

alcohol dehydrogenase; genetic engineering; PCR; amplification;  
us protein; gene expression; primer; ss.

s oryzae.

-A.

9.

8; 98JP-00105712.

8; 98JP-00105712.

ANO PHARM KK.  
ENCY OF IND SCI & TECHNOLOGY.

626935/54.

oter derived from an Aspergillus genus microbe - useful for

PT producing exotic proteins.  
XX  
PS Example 2; Page 4; 11pp; Japanese.  
XX  
CC Primers AAZ30689-Z30691 were used to PCR amplify the promoter s  
CC from the alcohol dehydrogenase gene (AAZ30680) from Aspergillus  
CC The invention relates to novel gene promoters (AAZ30680-Z30685)  
CC from Aspergillus oryzae which can be used in genetic engineering  
CC express heterologous proteins in Aspergillus  
XX  
SQ Sequence 24 BP; 5 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 2; Length 24;  
Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
| | | | |  
Db 20 CCAGTGAAGATCCCTT 4

RESULT 34  
ABQ00239

ID ABQ00239 standard; DNA; 24 BP.

XX ABQ00239;

XX 11-JUN-2002 (first entry)

DE Oligonucleotide adapter/capture probe 230.

XX Oligonucleotide array; adapter sequence; probe; ss.

XX Synthetic.

XX WO200216649-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US026519.

XX 25-AUG-2000; 2000US-0227948P.

XX 29-AUG-2000; 2000US-0228854P.

XX (ILLU-) ILLUMINA INC.

XX Gunderson K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or  
PT target nucleic acid sequence, has different addresses compris  
PT different specific capture probes.

XX Claim 1; Page 49; 261pp; English.

XX The invention relates to an oligonucleotide array (I) compris  
CC 25 different addresses (adapter sequences) with each compris  
CC different capture probe selected from a group consisting of th  
CC given in ABQ0010-ABQ13409. (I) is useful for immobilising a t  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ  
CC ABQ13409) to a target nucleic acid to form a modified target n  
CC and contacting the modified target nucleic acid with (I). The  
CC above method is useful for detecting a target nucleic acid, wh  
CC comprises detecting the presence of the modified target nuclei

XX Sequence 24 BP; 5 A; 9 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 6; Length 24;  
Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17

||||| ||| ||  
GTGAGACCCCAT 17

ndard; DNA; 24 BP.

(first entry)

ide adapter/capture probe 4469.

ide array; adapter sequence; probe; ss.

A2.

2001WO-US026519.

2000US-0227948P.

2000US-0228854P.

MINA INC.

12068/33.

ing adapter sequences useful for immobilizing or detecting a  
ic acid sequence, has different addresses comprising  
pecific capture probes.

ie 145; 261pp; English.

on relates to an oligonucleotide array (I) comprising at least  
; addresses (adapter sequences) with each comprising a  
pture probe selected from a group consisting of the sequences  
00010-ABQ13409. (I) is useful for immobilizing a target  
l sequence by attaching a adapter nucleic acid (ABQ00010-  
; a target nucleic acid to form a modified target nucleic acid  
ng the modified target nucleic acid with (I). The steps of  
l is useful for detecting a target nucleic acid, which further  
etecting the presence of the modified target nucleic acid

BP; 5 A; 9 C; 6 G; 4 T; 0 U; 0 Other;

larity 71.8%; Score 12.2; DB 6; Length 24;

Conservative 82.4%; Pred. No. 7.4e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17

||||| ||| ||

GTGAGACCCCAT 17

andard; DNA; 24 BP.

(first entry)

ide adapter/capture probe 10756.

ide array; adapter sequence; probe; ss.

XX WO200216649-A2.  
XX  
XX PD 28-FEB-2002.  
XX PF 27-AUG-2001; 2001WO-US026519.  
XX PR 25-AUG-2000; 2000US-0227948P.  
XX PR 29-AUG-2000; 2000US-0228854P.  
XX PA (ILLU-) ILLUMINA INC.  
XX PI Gunderson K;  
XX DR WPI; 2002-292068/33.  
XX  
XX PT Array comprising adapter sequences useful for immobilizing or de  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.  
XX PS Claim 1; Page 222; 261pp; English.  
XX  
XX CC The invention relates to an oligonucleotide array (I) comprising  
CC 25 different addresses (adapter sequences) with each comprising  
CC different capture probe selected from a group consisting of the  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a ta  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00  
CC ABQ13409) to a target nucleic acid to form a modified target nu  
CC and contacting the modified target nucleic acid with (I). The st  
CC above method is useful for detecting a target nucleic acid, whic  
CC comprises detecting the presence of the modified target nucleic  
XX  
XX SQ Sequence 24 BP; 5 A; 9 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 71.8%; Score 12.2; DB 6; Length 24;  
Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;  
OY 1 CGAGTGAAGATCCCTT 17  
Db 1 CGCGTGAGACCCCAT 17  
RESULT 37  
ABQ10806/c  
ID ABQ10806 standard; DNA; 24 BP.  
XX AC ABQ10806;  
XX  
DT 11-JUN-2002 (first entry)  
XX  
DE Oligonucleotide adapter/capture probe 10797.  
XX  
KW Oligonucleotide array; adapter sequence; probe; ss.  
XX  
OS Synthetic.  
XX  
PN WO200216649-A2.  
XX  
XX PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US026519.  
XX  
XX PR 25-AUG-2000; 2000US-0227948P.  
XX PR 29-AUG-2000; 2000US-0228854P.  
XX  
XX PA (ILLU-) ILLUMINA INC.  
XX PI Gunderson K;  
XX DR WPI; 2002-292068/33.  
XX  
XX PT Array comprising adapter sequences useful for immobilizing or d



elic acid sequence, has different addresses comprising specific capture probes.

ge 222; 261pp; English.

on relates to an oligonucleotide array (I) comprising at least t addresses (adapter sequences) with each comprising a capture probe selected from a group consisting of the sequences Q00010-ABQ13409. (I) is useful for immobilising a target d sequence by attaching a adapter nucleic acid (ABQ00010- o a target nucleic acid to form a modified target nucleic acid ing the modified target nucleic acid with (I). The steps of d is useful for detecting a target nucleic acid, which further detecting the presence of the modified target nucleic acid

BP; 4 A; 6 C; 9 G; 5 T; 0 U; 0 Other;

ilarity 71.8%; Score 12.2; DB 6; Length 24;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||||  
CGTGAAGATCCCTT 8

andard; DNA; 24 BP.

2 (first entry)

ptide adapter/capture probe 4510.

ptide array; adapter sequence; probe; ss.

3-A2.

2.

1; 2001WO-US026519.

0; 2000US-0227948P.

0; 2000US-0228654P.

LUMINA INC.

K;

292068/33.

rising adapter sequences useful for immobilizing or detecting a leic acid sequence, has different addresses comprising specific capture probes.

age 145; 261pp; English.

ion relates to an oligonucleotide array (I) comprising at least nt addresses (adapter sequences) with each comprising a capture probe selected from a group consisting of the sequences BQ00010-ABQ13409. (I) is useful for immobilising a target id sequence by attaching a adapter nucleic acid (ABQ00010- to a target nucleic acid to form a modified target nucleic acid ing the modified target nucleic acid with (I). The steps of od is useful for detecting a target nucleic acid, which further detecting the presence of the modified target nucleic acid

4 BP; 4 A; 6 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 6; Length 24;  
Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
|||  
DB 24 CGCGTGAAGATCCCTT 8

RESULT 39

AAD27956/c

ID AAD27956 standard; DNA; 25 BP.

XX AAD27956;

XX 16-JUL-2002 (first entry)

XX Human D3 dopamine receptor nucleic acid amplifying primer #1.

XX Mental disorder; neurodegenerative disorder; schizophrenia;

KW manic depression; Tourette's syndrome; Parkinson's disease;

KW Alzheimer's disease; Huntington's disease; PCR primer; human;

KW D3 dopamine receptor; ss.

XX Homo sapiens.

XX WO200214547-A2.

XX 21-FEB-2002.

XX 15-AUG-2001; 2001WO-IL000761.

XX 15-AUG-2000; 2000IL-00137865.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX Fuchs S, Ilani T, Perl O;

XX WPI; 2002-315412/35.

DR Diagnosing neurodegenerative disorder in an individual by eval  
PT ratio of D3 dopamine receptor mRNA and/or alpha7 nicotinic ace  
PT receptor mRNA of test individual, to control gene mRNA of heal  
PT individual.

PS Example 1; Page 8; 33pp; English.

XX The invention relates to a method of diagnosing a mental disor  
CC neurodegenerative disorder that involves measuring mRNA of D3  
CC receptor and/or alpha7 nicotinic acetylcholine receptor (alpha  
CC and of a control gene in peripheral blood lymphocytes (PBLs) o  
CC individual and of at least one healthy control individual, cal  
CC the ratio between D3 dopamine receptor mRNA and the control ge  
CC and/or the ratio between alpha7 ACHR mRNA and the control gene  
CC each individual, evaluating the ratios obtained for the tested  
CC and the healthy control individual. An increase in D3 dopamine  
CC mRNA and/or decrease in alpha7 ACHR mRNA in the tested individ  
CC comparison to the control individual indicates that the tested  
CC has a highly likelihood of having the disorder. The method is  
CC diagnosis and follow up of a mental disorder e.g. schizophrenia  
CC depression, Tourette's syndrome and a neurodegenerative disor  
CC Parkinson's disease, Alzheimer's disease or Huntington's disea  
CC individual. The present sequence is a PCR primer for amplifica  
CC human D3 dopamine receptor nucleic acid

SQ Sequence 25 BP; 8 A; 6 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 6; Length 25;  
Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17  
|||||

AGTGAAGATCCCTTT 9

andard; DNA; 25 BP.

(first entry)

tide adapter/capture probe 12333.

tide array; adapter sequence; probe; ss.

-A2.

; 2001WO-US026519.

; 2000US-0227948P.

; 2000US-0228854P.

UMINA INC.

;

92068/33.

using adapter sequences useful for immobilizing or detecting a nucleic acid sequence, has different addresses comprising specific capture probes.

ge 241; 261pp; English.

on relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of the above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid

BP; 4 A; 6 C; 9 G; 6 T; 0 U; 0 Other;

71.8%; Score 12.2; DB 6; Length 25;

ilarity 82.4%; Pred. No. 7.4e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTTT 17

CGTGAAGATCCCTTT 9

andard; DNA; 25 BP.

;(first entry)

tide adapter/capture probe 12292.

tide array; adapter sequence; probe; ss.

PN WO200216649-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US026519.  
XX  
PR 25-AUG-2000; 2000US-0227948P.  
PR 29-AUG-2000; 2000US-0228854P.  
XX  
PA (ILLU-) ILLUMINA INC.  
XX  
PI Gunderson K;  
PI  
XX  
DR WPI; 2002-292068/33.  
XX  
PT Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising different specific capture probes.  
PT  
XX  
PS Claim 1; Page 241; 261pp; English.  
XX  
CC The invention relates to an oligonucleotide array (I) comprising 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). The steps of the above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid  
XX  
SQ Sequence 25 BP; 5 A; 9 C; 6 G; 5 T; 0 U; 0 Other;  
Query Match 71.8%; Score 12.2; DB 6; Length 25;  
Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;  
Qy 1 CGAGTGAAGATCCCTTT 17  
Db 2 CGCGTGAAGATCCCTTT 18  
RESULT 42  
ACI15438/c  
ID ACI15438 standard; DNA; 25 BP.  
XX  
AC ACI15438;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 15429.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (APFY-) AFFYMETRIX INC.  
XX  
PI Mitmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization

northern or dot-blot hybridization to identify or detect the  
specific mutations of any gene.

3Q ID NO 15429; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences including one of 2,018,500 fully defined sequences, or its perfect match, antisense match or antisense mismatch. The array is used as a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises members of a gene and a cross-species comparison. The array of nucleic acids further comprises a tag sequence. The array of nucleic acids is useful in situ hybridisation, in Southern, Northern, Northern blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules or in screening cDNA or genomic libraries or subclones containing segments of DNA that have been previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

5 BP; 8 A; 4 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 8; Length 25;  
Best Local Similarity 82.4%; Pred. No. 7.4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0;

CGAGTGAAGTCCCTT 17  
|||||  
CGTCTGAGGTCCCTT 1

standard; DNA; 25 BP.

3 (first entry)

array DNA oligonucleotide SEQ ID NO 109787.

robe; expressed sequence tag; microarray; gene expression;  
hybridization; biallelic marker; polymorphism; human;  
comparison.

10-A1.

3.

2; 2002US-00098263.

1; 2001US-0276759P.

FYMETRIX INC.

P;

567953/53.

of nucleic acid probes, useful for in situ hybridization, in  
Northern or dot-blot hybridization to identify or detect the  
specific mutations of any gene.

XX

PS Claim 1; SEQ ID NO 109787; 9pp; English.

XX

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences including one of 2,018,500 fully defined sequences, or its perfect match, antisense match or antisense mismatch. The array is used as a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises members of a gene and a cross-species comparison. The array of nucleic acids further comprises a tag sequence. The array of nucleic acids is useful in situ hybridisation, in Southern, Northern blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules or in screening cDNA or genomic libraries or subclones containing segments of DNA that have been previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX Sequence 25 BP; 6 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 8; Length 25;

Best Local Similarity 82.4%; Pred. No. 7.4e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGTCCCTT 17

Db 23 CGTCTGAGGTCCCTT 7

RESULT 44

AAH96915

ID AAH96915 standard; RNA; 38 BP.

XX AAH96915;

XX 09-OCT-2001 (first entry)

XX Human Chk1 ribozyme SEQ ID NO: 2340.

DE Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene th

KW RNA cleavage; cancer; ss.

XX Homo sapiens.

OS WO200157206-A2.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US003504.

XX 03-FEB-2000; 2000US-0179983P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (FATT/) FATTAEY A R.

XX Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;

XX WPI; 2001-496922/54.

XX Novel nucleic acid molecule e.g., ribozymes or antisense nucle

PT molecules, which downregulates expression of a checkpoint kina

PT useful for treating colorectal, lung, breast or prostate cance

XX Claim 5; Page 72; 115pp; English.

PS

invention provides nucleic acid molecules capable of  
ing the expression of the human checkpoint kinase-1 (Chk1)  
may be antisense or ribozyme sequences, and are useful in the  
f diseases associated with conditions affected by Chk1 levels,  
ancer. The present sequence is an oligonucleotide described in  
fication of the invention

BP; 12 A; 10 C; 9 G; 0 T; 7 U; 0 Other;

71.8%; Score 12.2; DB 4; Length 38;

ilarity 58.8%; Pred. No. 7.7e+03; Indels 0; Gaps 0;

Conservative 4; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17

||: ||| : |||:

AGUCAAGGUCUCCU 34

andard; RNA; 38 BP.

(first entry)

Zinzyne substrate sequence #355.

antisense therapy; cytostatic; antiinflammatory; haemostatic;  
ective; nootropic; neuroprotective; antiparkinsonian;  
D20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
ozyme; G-cleaver; amberzyme; zinzyne; lymphoma; leukaemia;  
homa; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
odeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
cytoma; IMC; immune thrombocytopenia; stroke; dementia;  
Y arthropathy; central nervous system injury;  
ular accident; CVA; Alzheimer's disease; multiple sclerosis;  
Y-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
disease; ataxia; Huntington's disease; substrate sequence;  
-Jakob disease; muscular dystrophy; neurodegenerative disease.

S.

-A2.

; 2001WO-US004273.

; 2000US-0181797P.

; 2000US-0185516P.

; 2000US-0187128P.

OZYME PHARM INC.

TT L.

WIGGEN J.

WRIRA B M.

Icswiggen J, Chowrira BM;

07195/69.

d molecules, e.g., enzymatic nucleic acids and antisense  
which down regulate expression of a CD20 gene or neurite  
bitor gene useful for treating, e.g., lymphoma, leukemia, and  
vous system injury.

age 101; 200pp; English.

on relates to a nucleic acid molecule which down regulates  
of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO).  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme c  
CC DNzyme) an Inzyme (an endolytic nucleic acid cleaving a an RN  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN  
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyne (cle  
CC with a YGY motif). The CD20-targetting nucleic acid is used to  
CC of CD20 in the presence of a divalent cation that is preferably  
CC Furthermore, it may be contacted with a cell to reduce CD20 act  
CC the cell and treat a patient having a condition associated with  
CC of CD20. The treatment may further comprise the use of one or n  
CC therapies. In particular, the CD20 targetting nucleic acid may  
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follic  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, n  
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, n  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic ly  
CC immune thrombocytopenia, and inflammatory arthropathy. The NOG  
CC targetting nucleic acid is used to cleave RNA of the NOGO gene  
CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthe  
CC nucleic acid may be contacted with a cell to reduce NOGO activi  
CC cell and treat a patient having a condition associated with the  
CC NOGO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOGO-targetting nucleic acid may  
CC treat central nervous system (CNS) injury and cerebrovascular a  
CC (CVA, stroke). Alzheimer's disease, dementia, multiple sclerosis  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-  
CC disease, muscular dystrophy, and/or other neurodegenerative dis  
CC states which respond to the modulation of NOGO expression. The  
CC sequence is a substrate sequence for a nucleic acid of the inve  
CC based on the human NOGO sequence

XX Sequence 38 BP; 10 A; 9 C; 11 G; 0 T; 8 U; 0 Other;

Query Match 71.8%; Score 12.2; DB 4; Length 38;

Best Local Similarity 58.8%; Pred. No. 7.7e+03;

Matches 10; Conservative 4; Mismatches 3; Indels 0;

Qy 1 CGAGTGAAGATCCCTT 17

||||: ||| : |||:

Db 18 CGAGUCAAGGUCUCCU 34

Search completed: February 29, 2004, 09:03:59

Job time : 170.052 secs

GenCore version 5.1.6  
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leic search, using sw model

February 29, 2004, 08:44:24 ; Search time 32.013 Seconds

(without alignments)

294.698 Million cell updates/sec

US-10-090-326-17

1 cgagtgagatccccctt 17

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

682709 seqs, 277475446 residues

hits satisfying chosen parameters: 874574

length: 0

length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Issued Patents NA.\*

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5: /cgn2\_6/ptodata/2/ina/PTCUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
lived by analysis of the total score distribution.

# SUMMARIES

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72.9	32	1	US-07-807-529A-70	Sequence 70, Appl
72.9	32	3	US-08-300-928C-101	Sequence 101, App
72.9	32	3	US-08-430-944D-101	Sequence 101, App
72.9	32	3	US-08-430-014-101	Sequence 101, App
72.9	32	3	US-08-431-184-101	Sequence 101, App
71.8	36	4	US-09-474-432B-265	Sequence 265, App
71.8	37	4	US-09-476-387-264	Sequence 264, App
71.8	38	4	US-09-474-432B-1199	Sequence 1199, Ap
71.8	38	4	US-09-474-432B-1257	Sequence 1257, Ap
71.8	38	4	US-09-474-432B-1303	Sequence 1303, Ap
71.8	38	4	US-09-474-432B-1332	Sequence 1332, Ap
71.8	38	4	US-09-476-387-1198	Sequence 1198, Ap
71.8	38	4	US-09-476-387-1256	Sequence 1256, Ap
71.8	38	4	US-09-476-387-1302	Sequence 1302, Ap
71.8	38	4	US-09-476-387-1331	Sequence 1331, Ap
70.6	46	3	US-09-070-408-67	Sequence 67, Appl
70.6	31	4	US-09-302-357-2	Sequence 2, Appli
70.6	43	1	US-07-936-533A-3	Sequence 3, Appli
70.6	43	1	US-07-936-533A-32	Sequence 32, Appl
70.6	43	1	US-08-344-257A-3	Sequence 3, Appli
69.4	27	3	US-08-638-931-17	Sequence 17, Appl
69.4	33	4	US-09-462-941-25	Sequence 25, Appl
69.4	50	4	US-09-182-145-114	Sequence 114, App
69.4	52	4	US-08-956-171E-2265	Sequence 2265, Ap
69.4	57	3	US-08-908-643C-56	Sequence 56, Appl
67.1	17	1	US-08-390-850-641	Sequence 641, App

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c 38	11.4	67.1	36	1	US-08-299-498A-29	Sequence
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c 40	11.4	67.1	41	1	US-08-681-935-15	Sequence
c 41	11.4	67.1	41	3	US-08-939-323-15	Sequence
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63.5	29	3	US-08-686-968C-18	Sequence 18, Appl	c 228	10.6	62.4	38	4	US-09-474-432B-1188	Sequence
63.5	29	3	US-09-360-545-87	Sequence 87, Appl	c 229	10.6	62.4	38	4	US-09-474-432B-1193	Sequence
63.5	30	1	US-09-818-132-1	Sequence 1, Appli	c 230	10.6	62.4	38	4	US-09-474-432B-1204	Sequence
63.5	30	1	US-08-153-664-1	Sequence 1, Appli	c 231	10.6	62.4	38	4	US-09-474-432B-1208	Sequence
63.5	30	1	US-08-477-783A-1	Sequence 1, Appli	c 232	10.6	62.4	38	4	US-09-474-432B-1256	Sequence
63.5	30	3	US-08-976-278-1	Sequence 1, Appli	c 233	10.6	62.4	38	4	US-09-474-432B-1285	Sequence
63.5	30	3	US-09-441-315-1	Sequence 1, Appli	c 234	10.6	62.4	38	4	US-09-474-432B-1291	Sequence
63.5	31	4	US-09-536-977-103	Sequence 103, App	c 235	10.6	62.4	38	4	US-09-474-432B-1356	Sequence
63.5	31	1	US-08-524-757-34	Sequence 34, Appl	c 236	10.6	62.4	38	4	US-09-474-432B-1406	Sequence
63.5	33	3	US-09-257-584-28	Sequence 28, Appl	c 237	10.6	62.4	38	4	US-09-474-432B-1411	Sequence
63.5	38	1	US-08-111-080-38	Sequence 38, Appl	c 238	10.6	62.4	38	4	US-09-474-432B-1427	Sequence
63.5	38	1	US-08-104-072B-34	Sequence 34, Appl	c 239	10.6	62.4	38	4	US-09-474-432B-1456	Sequence
63.5	38	1	US-08-211-980-38	Sequence 38, Appl	c 240	10.6	62.4	38	4	US-09-474-432B-1477	Sequence
63.5	38	3	US-08-379-452-13	Sequence 13, Appl	c 241	10.6	62.4	38	4	US-09-476-387-963	Sequence
63.5	38	3	US-09-409-670-13	Sequence 13, Appl	c 242	10.6	62.4	38	4	US-09-476-387-1074	Sequence
63.5	38	5	PCT-US93-07967-38	Sequence 38, Appl	c 243	10.6	62.4	38	4	US-09-476-387-1094	Sequence
63.5	40	2	US-08-425-684-58	Sequence 58, Appl	c 244	10.6	62.4	38	4	US-09-476-387-1111	Sequence
63.5	40	2	US-08-675-502-58	Sequence 58, Appl	c 245	10.6	62.4	38	4	US-09-476-387-1187	Sequence
63.5	40	4	US-09-245-802-58	Sequence 58, Appl	c 246	10.6	62.4	38	4	US-09-476-387-1192	Sequence

62.4	38	4	US-09-476-387-1203	Sequence 1203, Ap	C 320	10.4	61.2	32	4	US-09-923-246-71	Sequence
62.4	38	4	US-09-476-387-1207	Sequence 1207, Ap	C 321	10.4	61.2	32	4	US-09-923-246-75	Sequence
62.4	38	4	US-09-476-387-1255	Sequence 1255, Ap	C 322	10.4	61.2	32	4	US-10-295-723-62	Sequence
62.4	38	4	US-09-476-387-1284	Sequence 1284, Ap	C 323	10.4	61.2	32	4	US-10-295-723-71	Sequence
62.4	38	4	US-09-476-387-1290	Sequence 1290, Ap	C 324	10.4	61.2	32	4	US-10-295-723-75	Sequence
62.4	38	4	US-09-476-387-1355	Sequence 1355, Ap	C 325	10.4	61.2	33	1	US-08-207-900B-7	Sequence
62.4	38	4	US-09-476-387-1405	Sequence 1405, Ap	C 326	10.4	61.2	33	2	US-08-930-605-12	Sequence
62.4	38	4	US-09-476-387-1410	Sequence 1410, Ap	C 327	10.4	61.2	33	3	US-09-073-569-14	Sequence
62.4	38	4	US-09-476-387-1416	Sequence 1416, Ap	C 328	10.4	61.2	33	4	US-09-169-205D-13	Sequence
62.4	38	4	US-09-476-387-1455	Sequence 1455, Ap	C 329	10.4	61.2	34	4	US-09-198-119C-20	Sequence
62.4	38	4	US-09-476-387-1476	Sequence 1476, Ap	C 330	10.4	61.2	35	1	US-08-683-877-7	Sequence
62.4	39	2	US-08-249-687C-12	Sequence 12, Appl	C 331	10.4	61.2	35	1	US-08-683-877-9	Sequence
62.4	44	1	US-07-662-388-11	Sequence 11, Appl	C 332	10.4	61.2	38	1	US-08-338-992B-20	Sequence
62.4	59	2	US-07-662-764D-42	Sequence 42, Appl	C 333	10.4	61.2	38	4	US-09-010-733-20	Sequence
62.4	59	2	US-07-662-764D-42	Sequence 42, Appl	C 334	10.4	61.2	47	4	US-09-422-978-221	Sequence
62.4	59	4	US-09-193-390A-42	Sequence 42, Appl	C 335	10.4	61.2	47	4	US-09-422-978-1315	Sequence
62.4	59	4	US-09-193-390A-42	Sequence 42, Appl	C 336	10.4	61.2	49	4	US-09-422-978-2778	Sequence
62.4	59	4	US-09-193-390A-42	Sequence 42, Appl	C 337	10.4	61.2	49	4	US-09-538-709-973	Sequence
62.4	60	2	US-07-662-764D-26	Sequence 26, Appl	C 338	10.4	61.2	57	2	US-08-612-858-34	Sequence
62.4	60	2	US-07-662-764D-26	Sequence 26, Appl	C 339	10.4	61.2	57	4	US-09-522-217-65	Sequence
62.4	60	4	US-09-193-390A-26	Sequence 26, Appl	C 340	10.4	61.2	57	4	US-09-523-246-65	Sequence
62.4	60	4	US-09-193-390A-26	Sequence 26, Appl	C 341	10.4	61.2	57	4	US-10-295-723-65	Sequence
61.2	12	1	US-07-974-447-6	Sequence 6, Appli	C 342	10.4	61.2	60	3	US-09-448-280-13	Sequence
61.2	12	1	US-08-149-199-6	Sequence 4, Appli	C 343	10.2	60.0	17	1	US-08-166-664-11	Sequence
61.2	12	2	US-08-993-118-4	Sequence 4, Appli	C 344	10.2	60.0	17	4	US-09-866-108A-10481	Sequence
61.2	12	3	US-08-748-130-26	Sequence 4, Appli	C 345	10.2	60.0	17	4	US-09-866-108A-10482	Sequence
61.2	12	3	US-08-845-528C-4	Sequence 4, Appli	C 346	10.2	60.0	17	4	US-09-866-108A-10483	Sequence
61.2	12	3	US-09-115-061-6	Sequence 11, Appl	C 347	10.2	60.0	19	4	US-09-422-978-4438	Sequence
61.2	12	3	US-08-969-815-11	Sequence 11, Appl	C 348	10.2	60.0	20	1	US-08-065-078-2	Sequence
61.2	12	3	US-09-120-025-11	Sequence 11, Appl	C 349	10.2	60.0	20	3	US-08-932-445-2	Sequence
61.2	12	3	US-09-178-573B-6	Sequence 6, Appli	C 350	10.2	60.0	20	4	US-09-198-452A-4378	Sequence
61.2	12	3	US-09-261-079-6	Sequence 6, Appli	C 351	10.2	60.0	20	4	US-09-068-506-32	Sequence
61.2	12	4	US-09-419-568F-6	Sequence 6, Appli	C 352	10.2	60.0	20	4	US-09-068-506-33	Sequence
61.2	12	4	US-09-354-243B-6	Sequence 11, Appl	C 353	10.2	60.0	21	1	US-08-644-271-19	Sequence
61.2	12	4	US-09-710-481-11	Sequence 12, Appl	C 354	10.2	60.0	21	3	US-08-860-038-3	Sequence
61.2	12	4	US-09-656-952-12	Sequence 4, Appli	C 355	10.2	60.0	21	4	US-09-422-978-10728	Sequence
61.2	12	4	US-08-493-260A-4	Sequence 4, Appli	C 356	10.2	60.0	22	2	US-08-117-952-691	Sequence
61.2	12	4	US-09-066-281B-4	Sequence 1, Appl	C 357	10.2	60.0	22	2	US-09-189-060B-6	Sequence
61.2	12	4	US-09-553-875-11	Sequence 4, Appli	C 358	10.2	60.0	22	3	US-09-189-060B-8	Sequence
61.2	12	4	US-08-488-446-4	Sequence 11, Appl	C 359	10.2	60.0	22	3	US-09-084-303B-109	Sequence
61.2	12	4	US-09-768-670-11	Sequence 4, Appli	C 360	10.2	60.0	24	2	US-08-790-813-1	Sequence
61.2	12	4	US-08-467-344A-4	Sequence 4, Appli	C 361	10.2	60.0	24	2	US-08-646-861-23	Sequence
61.2	12	4	US-09-468-433C-4	Sequence 4, Appli	C 362	10.2	60.0	24	3	US-09-501-078-1	Sequence
61.2	17	1	US-08-390-850-642	Sequence 642, App	C 363	10.2	60.0	25	1	US-08-387-315A-13	Sequence
61.2	17	1	US-08-435-634-642	Sequence 642, App	C 364	10.2	60.0	25	1	US-08-754-559-13	Sequence
61.2	17	4	US-08-584-040-7577	Sequence 7577, Ap	C 365	10.2	60.0	25	4	US-09-866-108A-15373	Sequence
61.2	17	4	US-08-584-040-7578	Sequence 7578, Ap	C 366	10.2	60.0	25	4	US-09-866-108A-15375	Sequence
61.2	17	4	US-09-371-772B-3373	Sequence 3373, Ap	C 367	10.2	60.0	25	4	US-09-866-108A-15376	Sequence
61.2	17	4	US-09-371-772B-3374	Sequence 3374, Ap	C 368	10.2	60.0	25	4	US-09-866-108A-15377	Sequence
61.2	17	4	US-08-717-294-43	Sequence 43, Appl	C 369	10.2	60.0	25	4	US-09-866-108A-15378	Sequence
61.2	18	3	US-08-634-331-8	Sequence 8, Appli	C 370	10.2	60.0	25	4	US-09-866-108A-15379	Sequence
61.2	20	1	US-09-198-452A-4423	Sequence 4423, Ap	C 371	10.2	60.0	26	4	US-09-866-108A-15380	Sequence
61.2	20	3	US-08-943-731-521	Sequence 521, App	C 372	10.2	60.0	27	4	US-09-866-108A-15381	Sequence
61.2	22	3	US-08-017-664-6	Sequence 6, Appli	C 373	10.2	60.0	28	2	US-09-866-108A-15382	Sequence
61.2	23	1	US-08-702-105A-36	Sequence 36, Appl	C 374	10.2	60.0	28	4	US-09-866-108A-15383	Sequence
61.2	24	2	US-09-075-395-8	Sequence 8, Appli	C 375	10.2	60.0	28	4	US-09-194-285-16	Sequence
61.2	24	2	US-08-702-110A-36	Sequence 36, Appl	C 376	10.2	60.0	28	4	US-09-741-171-2	Sequence
61.2	24	3	US-08-789-329C-17	Sequence 17, Appl	C 377	10.2	60.0	28	4	US-08-215-749A-1	Sequence
61.2	24	3	US-09-325-571-36	Sequence 36, Appl	C 378	10.2	60.0	30	1	US-08-814-052-38	Sequence
61.2	24	3	US-09-848-585-36	Sequence 36, Appl	C 379	10.2	60.0	30	3	US-08-812-829-30	Sequence
61.2	24	4	US-09-538-709-317	Sequence 317, App	C 380	10.2	60.0	30	3	US-09-230-180-11	Sequence
61.2	25	4	US-09-585-174-95	Sequence 95, Appl	C 381	10.2	60.0	30	3	US-09-230-180-12	Sequence
61.2	25	4	US-08-185-424B-4	Sequence 4, Appli	C 382	10.2	60.0	30	3	US-09-284-878-8	Sequence
61.2	27	1	US-08-342-411A-11	Sequence 11, Appl	C 383	10.2	60.0	31	3	US-08-485-355B-19	Sequence
61.2	29	1	US-08-106-981-7	Sequence 7, Appli	C 384	10.2	60.0	31	5	PCT-US92-06045-6	Sequence
61.2	29	3	US-09-338-671-7	Sequence 11, Appl	C 385	10.2	60.0	34	3	US-09-110-517-10	Sequence
61.2	29	5	PCT-US94-12883-11	Sequence 16, Appl	C 386	10.2	60.0				
61.2	30	2	US-08-962-284-16	Sequence 22, Appl	C 387	10.2	60.0				
61.2	32	1	US-08-338-992B-22	Sequence 22, Appl	C 388	10.2	60.0				
61.2	32	4	US-09-522-217-62	Sequence 71, Appl	C 389	10.2	60.0				
61.2	32	4	US-09-522-217-75	Sequence 22, Appl	C 390	10.2	60.0				
61.2	32	4	US-09-010-733-22	Sequence 62, Appl	C 391	10.2	60.0				
61.2	32	4	US-09-923-246-62		C 392	10.2	60.0				

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60.0	34	4	US-09-474-432B-242	Sequence 242, App	467	10.2	60.0	38	4	US-09-476-387-1427	Sequence
60.0	34	4	US-09-474-432B-252	Sequence 252, App	468	10.2	60.0	38	4	US-09-476-387-1430	Sequence
60.0	34	4	US-09-474-432B-284	Sequence 284, App	469	10.2	60.0	38	4	US-09-476-387-1438	Sequence
60.0	34	4	US-09-474-432B-293	Sequence 293, App	470	10.2	60.0	38	4	US-09-476-387-1442	Sequence
60.0	35	3	US-08-920-413-4	Sequence 4, Appl	471	10.2	60.0	38	4	US-09-476-387-1466	Sequence
60.0	35	4	US-09-476-387-234	Sequence 234, App	c 472	10.2	60.0	39	3	US-09-105-678A-10	Sequence
60.0	35	4	US-09-476-387-241	Sequence 241, App	c 473	10.2	60.0	39	3	US-09-105-678A-16	Sequence
60.0	35	4	US-09-476-387-251	Sequence 251, App	c 474	10.2	60.0	39	3	US-09-105-678A-22	Sequence
60.0	35	4	US-09-476-387-283	Sequence 283, App	c 475	10.2	60.0	39	3	US-09-421-208-10	Sequence
60.0	35	4	US-09-476-387-292	Sequence 292, App	c 476	10.2	60.0	39	3	US-09-421-208-16	Sequence
60.0	36	4	US-09-474-432B-253	Sequence 253, App	c 477	10.2	60.0	40	1	US-08-440-548-54	Sequence
60.0	36	4	US-09-474-432B-285	Sequence 285, App	c 478	10.2	60.0	40	1	US-08-466-344-54	Sequence
60.0	36	4	US-09-474-432B-294	Sequence 294, App	c 479	10.2	60.0	40	2	US-08-896-116-7	Sequence
60.0	37	2	US-09-028-361A-17	Sequence 17, Appl	c 480	10.2	60.0	40	3	US-08-896-122-7	Sequence
60.0	37	4	US-09-025-580-19	Sequence 19, Appl	c 481	10.2	60.0	40	3	PCT-US95-08487-7	Sequence
60.0	37	4	US-09-476-387-252	Sequence 252, App	c 482	10.2	60.0	40	5	US-09-189-060B-9	Sequence
60.0	37	4	US-09-476-387-293	Sequence 293, App	c 483	10.2	60.0	42	3	US-08-711-458B-58	Sequence
60.0	37	4	US-09-476-387-293	Sequence 293, App	c 484	10.2	60.0	43	3	US-07-744-282C-95	Sequence
60.0	38	4	US-09-474-432B-1148	Sequence 1148, App	c 485	10.2	60.0	45	1	US-08-944-982-1	Sequence
60.0	38	4	US-09-474-432B-1149	Sequence 1149, App	486	10.2	60.0	45	2	US-09-105-678A-13	Sequence
60.0	38	4	US-09-474-432B-1151	Sequence 1151, App	487	10.2	60.0	45	3	US-09-105-678A-19	Sequence
60.0	38	4	US-09-474-432B-1155	Sequence 1155, App	488	10.2	60.0	45	3	US-03-105-678A-25	Sequence
60.0	38	4	US-09-474-432B-1158	Sequence 1158, App	489	10.2	60.0	45	3	US-03-421-208-13	Sequence
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60.0	38	4	US-09-474-432B-1233	Sequence 1233, App	c 492	10.2	60.0	45	5	US-09-421-208-25	Sequence
60.0	38	4	US-09-474-432B-1258	Sequence 1258, App	493	10.2	60.0	47	4	US-09-422-978-1291	Sequence
60.0	38	4	US-09-474-432B-1261	Sequence 1261, App	494	10.2	60.0	47	4	US-09-422-978-1413	Sequence
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60.0	38	4	US-09-474-432B-1276	Sequence 1276, App	c 497	10.2	60.0	50	4	PCT-US95-06726-38	Sequence
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60.0	38	4	US-09-474-432B-1342	Sequence 1342, App	c 501	10.2	60.0	51	3	US-09-076-761-3	Sequence
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60.0	38	4	US-09-474-432B-1372	Sequence 1372, App	c 504	10.2	60.0	51	4	US-08-956-171E-2064	Sequence
60.0	38	4	US-09-474-432B-1373	Sequence 1373, App	c 505	10.2	60.0	51	4	US-09-443-199C-567	Sequence
60.0	38	4	US-09-474-432B-1384	Sequence 1384, App	c 506	10.2	60.0	53	4	US-09-012-895-11	Sequence
60.0	38	4	US-09-474-432B-1393	Sequence 1393, App	c 507	10.2	60.0	53	4	US-08-390-850-1089	Sequence
60.0	38	4	US-09-474-432B-1394	Sequence 1394, App	508	10.2	60.0	54	1	US-08-435-634-1089	Sequence
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60.0	38	4	US-09-474-432B-1443	Sequence 1443, App	513	10.2	60.0	57	1	US-08-330-163-35	Sequence
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60.0	38	4	US-09-476-387-1147	Sequence 1147, App	515	10.2	60.0	57	1	US-08-482-111-35	Sequence
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60.0	38	4	US-09-476-387-1150	Sequence 1150, App	517	10.2	60.0	60	4	US-08-407-620A-36	Sequence
60.0	38	4	US-09-476-387-1154	Sequence 1154, App	518	10.2	60.0	60	4	US-08-182-968A-247	Sequence
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60.0	38	4	US-09-476-387-1340	Sequence 1340, App	530	10	58.8	18	4	US-09-339-972-41	Sequence
60.0	38	4	US-09-476-387-1341	Sequence 1341, App	c 531	10	58.8	20	2	US-08-417-629B-2	Sequence
60.0	38	4	US-09-476-387-1347	Sequence 1347, App	532	10	58.8	20	2	US-09-203-860-3	Sequence
60.0	38	4	US-09-476-387-1356	Sequence 1356, App	c 533	10	58.8	20	3	US-08-630-019A-37	Sequence
60.0	38	4	US-09-476-387-1371	Sequence 1371, App	c 534	10	58.8	20	3	US-08-357-071-36	Sequence
60.0	38	4	US-09-476-387-1383	Sequence 1383, App	c 535	10	58.8	20	3	US-08-838-545-42	Sequence
60.0	38	4	US-09-476-387-1392	Sequence 1392, App	c 537	10	58.8	20	3	US-08-838-545-47	Sequence
60.0	38	4	US-09-476-387-1393	Sequence 1393, App	c 538	10	58.8	20	3		



58.8	20	3	US-09-487-445-30	Sequence 30, Appl	612	9.8	57.6	19	4	US-09-422-978-5995	Sequence
58.8	20	3	US-09-349-532-42	Sequence 42, Appl	c 613	9.8	57.6	19	4	US-09-422-978-9121	Sequence
58.8	20	3	US-09-349-532-47	Sequence 47, Appl	614	9.8	57.6	19	4	US-09-747-391-229	Sequence
58.8	20	4	US-08-469-260A-670	Sequence 670, Appl	c 615	9.8	57.6	20	1	US-08-308-892A-2	Sequence
58.8	20	4	US-08-488-446-670	Sequence 670, App	c 616	9.8	57.6	20	2	US-08-117-952-435	Sequence
58.8	20	4	US-09-138-452A-4312	Sequence 4312, Ap	617	9.8	57.6	20	3	US-09-487-445-39	Sequence
58.8	20	4	US-09-138-452A-5714	Sequence 5714, Ap	618	9.8	57.6	20	3	US-09-487-368A-230	Sequence
58.8	20	4	US-08-467-344A-670	Sequence 670, App	c 619	9.8	57.6	20	3	US-09-489-868A-26	Sequence
58.8	21	4	US-09-557-910-4	Sequence 4, Appli	620	9.8	57.6	20	4	US-09-517-467B-300	Sequence
58.8	22	4	US-09-535-008-12	Sequence 12, Appl	621	9.8	57.6	20	4	US-09-517-467B-343	Sequence
58.8	22	4	US-09-636-735A-24	Sequence 24, Appl	622	9.8	57.6	20	4	US-09-091-952A-190	Sequence
58.8	27	3	US-08-985-162-850	Sequence 850, App	623	9.8	57.6	20	4	US-09-629-644A-230	Sequence
58.8	27	4	US-09-401-063-850	Sequence 850, App	c 624	9.8	57.6	20	4	US-09-060-239-252	Sequence
58.8	28	2	US-08-859-998-1194	Sequence 1194, App	c 625	9.8	57.6	20	4	US-09-402-923A-252	Sequence
58.8	28	4	US-09-225-928-1194	Sequence 1194, Ap	c 626	9.8	57.6	20	4	US-09-198-452A-2140	Sequence
58.8	28	4	US-09-225-201B-1194	Sequence 1194, Ap	c 627	9.8	57.6	20	4	US-09-198-452A-4476	Sequence
58.8	29	1	US-08-073-197-15	Sequence 15, Appl	628	9.8	57.6	20	4	US-09-909-595-23	Sequence
58.8	29	1	US-08-073-197-20	Sequence 20, Appl	629	9.8	57.6	20	4	US-09-629-644A-230	Sequence
58.8	29	1	US-08-451-313-15	Sequence 15, Appl	630	9.8	57.6	21	3	US-08-952-796-7	Sequence
58.8	29	1	US-08-451-313-20	Sequence 20, Appl	c 631	9.8	57.6	21	4	US-09-162-631-4	Sequence
58.8	30	1	US-08-266-451B-13	Sequence 13, Appl	c 632	9.8	57.6	21	4	US-09-328-174A-6	Sequence
58.8	30	2	US-08-608-584-25	Sequence 25, Appl	c 633	9.8	57.6	21	4	US-09-328-174A-24	Sequence
58.8	30	2	US-08-748-725-13	Sequence 13, Appl	634	9.8	57.6	21	4	US-09-422-978-8744	Sequence
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58.8	31	1	US-08-390-850-276	Sequence 276, App	c 636	9.8	57.6	22	2	US-08-596-387B-119	Sequence
58.8	31	1	US-08-390-850-277	Sequence 277, App	c 637	9.8	57.6	22	2	US-08-874-266-31	Sequence
58.8	31	1	US-08-390-850-278	Sequence 278, App	c 638	9.8	57.6	22	4	US-09-067-615-119	Sequence
58.8	31	1	US-08-390-850-279	Sequence 279, App	c 639	9.8	57.6	22	5	PCT-US95-09816A-119	Sequence
58.8	31	1	US-08-390-850-280	Sequence 280, App	c 640	9.8	57.6	23	1	US-08-446-918A-8	Sequence
58.8	31	1	US-08-390-850-281	Sequence 281, App	c 641	9.8	57.6	23	2	US-08-580-806-8	Sequence
58.8	31	1	US-08-435-634-275	Sequence 275, App	c 642	9.8	57.6	23	4	US-09-564-805-208	Sequence
58.8	31	1	US-08-435-634-276	Sequence 276, App	c 643	9.8	57.6	24	3	US-09-046-158A-24	Sequence
58.8	31	1	US-08-435-634-277	Sequence 277, App	644	9.8	57.6	24	6	5164366-9	Patent No
58.8	31	1	US-08-435-634-278	Sequence 278, App	645	9.8	57.6	25	3	US-08-996-441B-88	Sequence
58.8	31	1	US-08-435-634-279	Sequence 279, App	646	9.8	57.6	25	3	US-08-993-722A-88	Sequence
58.8	31	1	US-08-435-634-280	Sequence 280, App	647	9.8	57.6	25	3	US-08-993-170A-88	Sequence
58.8	31	1	US-08-435-634-281	Sequence 281, App	648	9.8	57.6	25	3	US-08-993-775B-88	Sequence
58.8	33	1	US-08-255-670A-8	Sequence 8, Appli	649	9.8	57.6	25	4	US-09-427-770-88	Sequence
58.8	38	4	US-09-371-772B-12197	Sequence 12197, A	650	9.8	57.6	25	4	US-09-427-769-88	Sequence
58.8	38	4	US-09-371-772B-13772	Sequence 13772, A	651	9.8	57.6	25	4	US-09-866-108A-15480	Sequence
58.8	39	2	US-08-841-178-16	Sequence 16, Appl	652	9.8	57.6	25	4	US-09-866-108A-15481	Sequence
58.8	42	1	US-07-931-473B-178	Sequence 178, App	653	9.8	57.6	25	4	US-09-866-108A-15482	Sequence
58.8	42	1	US-07-744-131C-178	Sequence 178, App	654	9.8	57.6	25	4	US-09-866-108A-15483	Sequence
58.8	42	1	US-08-412-110-178	Sequence 178, App	655	9.8	57.6	25	4	US-09-866-108A-15484	Sequence
58.8	42	1	US-08-409-442A-178	Sequence 178, App	656	9.8	57.6	25	4	US-09-866-108A-15485	Sequence
58.8	42	2	US-08-469-609A-178	Sequence 178, App	657	9.8	57.6	25	4	US-09-866-108A-15486	Sequence
58.8	42	2	US-09-143-190-178	Sequence 178, App	658	9.8	57.6	25	4	US-09-866-108A-15487	Sequence
58.8	42	4	US-09-502-344-178	Sequence 178, App	659	9.8	57.6	25	4	US-09-866-108A-15488	Sequence
58.8	47	4	US-09-671-317-640	Sequence 640, App	660	9.8	57.6	25	4	US-09-866-108A-15489	Sequence
58.8	47	4	US-09-422-978-1646	Sequence 1646, Ap	661	9.8	57.6	25	4	US-09-866-108A-15490	Sequence
57.6	16	1	US-08-218-303-14	Sequence 14, Appl	662	9.8	57.6	25	4	US-09-866-108A-15491	Sequence
57.6	17	4	US-08-584-040-5411	Sequence 5411, Ap	663	9.8	57.6	25	4	US-09-866-108A-15492	Sequence
57.6	17	4	US-08-584-040-7272	Sequence 7272, Ap	664	9.8	57.6	26	1	US-08-379-078-619	Sequence
57.6	17	4	US-08-584-040-7273	Sequence 7273, Ap	665	9.8	57.6	26	4	US-07-974-409C-619	Sequence
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57.6	17	4	US-09-371-772B-2310	Sequence 2310, Ap	667	9.8	57.6	26	5	PCT-US93-00977-619	Sequence
57.6	17	4	US-09-371-772B-3081	Sequence 3081, Ap	c 668	9.8	57.6	27	1	US-08-464-531-33	Sequence
57.6	17	4	US-09-371-772B-3082	Sequence 3082, Ap	c 669	9.8	57.6	27	2	US-08-461-598-33	Sequence
57.6	17	4	US-09-371-772B-3083	Sequence 3083, Ap	670	9.8	57.6	27	3	US-08-985-162-1335	Sequence
57.6	17	4	US-09-866-108A-10588	Sequence 10588, A	c 671	9.8	57.6	27	3	US-08-467-023-181	Sequence
57.6	17	4	US-09-866-108A-10589	Sequence 10589, A	c 672	9.8	57.6	27	3	US-08-322-137-33	Sequence
57.6	17	4	US-09-866-108A-10590	Sequence 10590, A	c 673	9.8	57.6	27	4	US-09-508-264A-11	Sequence
57.6	17	4	US-09-866-108A-10591	Sequence 10591, A	674	9.8	57.6	28	4	US-09-401-063-1335	Sequence
57.6	17	4	US-09-866-108A-10592	Sequence 10592, A	c 675	9.8	57.6	28	4	US-09-417-197-19	Sequence
57.6	18	1	US-08-139-862-5	Sequence 5, Appli	c 676	9.8	57.6	29	1	US-08-683-877-12	Sequence
57.6	18	2	US-08-117-952-34	Sequence 34, Appl	c 677	9.8	57.6	29	3	US-09-257-799-21	Sequence
57.6	18	3	US-08-150-805-12	Sequence 12, Appl	c 678	9.8	57.6	29	3	US-08-320-919A-21	Sequence
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57.6	18	4	US-09-721-822A-102	Sequence 102, App	680	9.8	57.6	30	1	US-08-367-175A-11	Sequence
57.6	18	4	US-09-357-487B-35	Sequence 35, Appl	681	9.8	57.6	30	1	US-08-555-678-63	Sequence
57.6	18	4	US-09-555-554-12	Sequence 12, Appl	682	9.8	57.6	30	2	US-08-117-952-647	Sequence
57.6	18	4	US-09-897-259C-8	Sequence 8, Appli	683	9.8	57.6	30	2	US-08-479-275D-48	Sequence
57.6	19	4	US-09-422-978-5785	Sequence 5785, Ap	684	9.8	57.6	30	2		

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57.6	30	2	US-08-701-339-11	Sequence 11, Appl	759	9.8	57.6	42	4	US-09-214-909-19	Sequence
57.6	30	3	US-08-746-397-5	Sequence 5, Appl	c 760	9.8	57.6	43	1	US-07-763-512-8	Sequence
57.6	30	3	US-08-746-397-9	Sequence 9, Appl	761	9.8	57.6	43	1	US-07-931-473B-256	Sequence
57.6	30	3	US-08-523-894-56	Sequence 56, Appl	762	9.8	57.6	43	1	US-07-714-131C-256	Sequence
57.6	30	4	US-09-359-361-5	Sequence 5, Appl	763	9.8	57.6	43	1	US-08-412-110-256	Sequence
57.6	30	4	US-09-462-843A-18	Sequence 18, Appl	764	9.8	57.6	43	1	US-08-409-442A-256	Sequence
57.6	30	4	US-09-937-832-3	Sequence 3, Appl	765	9.8	57.6	43	2	US-08-469-609A-256	Sequence
57.6	30	5	PCT-US95-05265-63	Sequence 63, Appl	766	9.8	57.6	43	3	US-09-143-190-256	Sequence
57.6	31	1	US-08-066-281-3	Sequence 3, Appl	767	9.8	57.6	43	4	US-09-502-344-256	Sequence
57.6	31	1	US-08-066-281-7	Sequence 7, Appl	c 768	9.8	57.6	43	4	US-09-390-134B-26	Sequence
57.6	31	2	US-09-018-628-21	Sequence 21, Appl	769	9.8	57.6	45	2	US-08-379-057-5	Sequence
57.6	31	3	US-09-273-378-21	Sequence 21, Appl	770	9.8	57.6	45	3	US-08-989-251-16	Sequence
57.6	31	3	US-09-280-766-7	Sequence 7, Appl	771	9.8	57.6	45	3	US-08-340-250-16	Sequence
57.6	31	3	US-09-303-064-10	Sequence 10, Appl	772	9.8	57.6	45	4	US-09-528-108-16	Sequence
57.6	31	3	US-09-018-635-52	Sequence 52, Appl	773	9.8	57.6	46	4	US-09-486-241-19	Sequence
57.6	31	4	US-09-086-503-10	Sequence 10, Appl	c 774	9.8	57.6	47	4	US-09-641-638-981	Sequence
57.6	31	4	US-09-813-781-71	Sequence 71, Appl	775	9.8	57.6	47	4	US-09-486-241-11	Sequence
57.6	31	4	US-09-912-962-52	Sequence 52, Appl	c 776	9.8	57.6	47	4	US-09-422-978-1174	Sequence
57.6	32	3	US-09-358-382-4	Sequence 4, Appl	c 777	9.8	57.6	47	4	US-09-422-978-1370	Sequence
57.6	33	1	US-08-138-608-41	Sequence 41, Appl	778	9.8	57.6	47	4	US-09-422-978-1420	Sequence
57.6	33	1	US-08-583-318-6	Sequence 38, Appl	779	9.8	57.6	47	4	US-09-422-978-1682	Sequence
57.6	33	2	US-08-479-275D-38	Sequence 39, Appl	780	9.8	57.6	49	1	US-08-171-389-136	Sequence
57.6	33	2	US-08-479-275D-39	Sequence 39, Appl	781	9.8	57.6	49	1	US-08-123-936-136	Sequence
57.6	33	2	US-08-488-271B-38	Sequence 38, Appl	782	9.8	57.6	49	2	US-08-475-228A-136	Sequence
57.6	33	2	US-08-488-271B-39	Sequence 39, Appl	783	9.8	57.6	49	3	US-08-482-080A-136	Sequence
57.6	33	2	US-08-488-271B-40	Sequence 40, Appl	784	9.8	57.6	49	4	US-09-354-947-136	Sequence
57.6	33	2	US-08-488-271B-41	Sequence 41, Appl	785	9.8	57.6	49	4	US-09-350-969-35	Sequence
57.6	33	2	US-08-667-939A-25	Sequence 25, Appl	786	9.8	57.6	49	5	PCT-US93-12388-136	Sequence
57.6	33	3	US-08-722-719-51	Sequence 51, Appl	787	9.8	57.6	50	4	US-08-849-567A-57	Sequence
57.6	33	3	US-08-840-316-107	Sequence 107, Appl	788	9.8	57.6	50	4	US-08-849-567A-72	Sequence
57.6	33	3	US-09-232-468A-38	Sequence 38, Appl	c 789	9.8	57.6	51	4	US-09-443-199C-34	Sequence
57.6	33	3	US-08-809-523-107	Sequence 107, Appl	c 790	9.8	57.6	51	4	US-09-443-199C-709	Sequence
57.6	33	3	US-08-471-971-107	Sequence 107, Appl	c 791	9.8	57.6	51	4	US-09-443-199C-710	Sequence
57.6	33	4	US-08-433-123-25	Sequence 25, Appl	c 792	9.8	57.6	51	4	US-09-443-199C-1111	Sequence
57.6	33	4	US-09-334-951-51	Sequence 51, Appl	c 793	9.8	57.6	51	4	US-09-443-199C-1112	Sequence
57.6	33	4	US-09-402-776-107	Sequence 107, Appl	c 794	9.8	57.6	51	6	5198542-16	Patent No
57.6	33	4	US-09-334-923A-51	Sequence 51, Appl	c 795	9.8	57.6	52	1	US-08-260-202A-27	Sequence
57.6	33	4	US-09-170-496D-135	Sequence 135, Appl	c 796	9.8	57.6	52	1	US-08-608-151A-24	Sequence
57.6	33	4	US-09-784-984B-32	Sequence 32, Appl	c 797	9.8	57.6	52	2	US-08-479-275D-45	Sequence
57.6	33	4	US-09-334-954A-51	Sequence 51, Appl	798	9.8	57.6	54	2	US-08-488-271B-45	Sequence
57.6	35	1	US-08-591-989-87	Sequence 87, Appl	799	9.8	57.6	54	2	US-08-701-339-8	Sequence
57.6	35	2	US-08-334-545-12	Sequence 12, Appl	c 800	9.8	57.6	55	3	US-08-485-355B-16	Sequence
57.6	35	4	US-09-450-072-37	Sequence 37, Appl	801	9.8	57.6	56	3	US-09-150-805-2	Sequence
57.6	35	4	US-09-351-348-37	Sequence 37, Appl	802	9.8	57.6	56	3	US-08-996-069A-2	Sequence
57.6	36	2	US-08-809-267-27	Sequence 27, Appl	c 803	9.8	57.6	56	3	US-09-390-867A-45	Sequence
57.6	36	3	US-09-232-468A-15	Sequence 15, Appl	c 804	9.8	57.6	56	3	US-09-390-867A-46	Sequence
57.6	36	3	US-09-338-420-8	Sequence 8, Appl	c 805	9.8	57.6	56	4	US-09-548-260-45	Sequence
57.6	36	4	US-09-158-863C-29	Sequence 29, Appl	c 806	9.8	57.6	56	4	US-09-548-260-46	Sequence
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57.6	36	5	PCT-US95-13662A-27	Sequence 27, Appl	c 808	9.8	57.6	60	2	US-07-662-764D-22	Sequence
57.6	37	4	US-09-813-781-16	Sequence 16, Appl	809	9.8	57.6	60	2	US-07-662-764D-34	Sequence
57.6	38	4	US-09-373-845-13	Sequence 13, Appl	c 810	9.8	57.6	60	2	US-07-662-764D-34	Sequence
57.6	38	4	US-09-483-846B-3	Sequence 3, Appl	811	9.8	57.6	60	3	US-09-150-805-1	Sequence
57.6	38	4	US-09-348-953-8	Sequence 8, Appl	812	9.8	57.6	60	3	US-08-996-069A-1	Sequence
57.6	39	1	US-08-232-537-3	Sequence 3, Appl	813	9.8	57.6	60	4	US-09-193-390A-22	Sequence
57.6	39	2	US-08-782-760-7	Sequence 7, Appl	c 814	9.8	57.6	60	4	US-09-193-390A-22	Sequence
57.6	39	3	US-08-435-568A-28	Sequence 28, Appl	815	9.8	57.6	60	4	US-09-193-390A-34	Sequence
57.6	39	3	US-09-306-290-40	Sequence 40, Appl	c 816	9.8	57.6	60	4	US-09-193-390A-34	Sequence
57.6	39	3	US-09-367-953B-14	Sequence 14, Appl	817	9.6	56.5	17	4	US-09-866-108A-455	Sequence
57.6	39	4	US-08-417-551-5	Sequence 5, Appl	818	9.6	56.5	17	4	US-09-866-108A-456	Sequence
57.6	39	4	US-09-097-319A-22	Sequence 22, Appl	819	9.6	56.5	18	2	US-09-200-141-39	Sequence
57.6	39	4	US-09-813-781-58	Sequence 58, Appl	c 820	9.6	56.5	18	3	US-08-912-272-73	Sequence
57.6	39	4	US-08-316-385-5	Sequence 5, Appl	c 821	9.6	56.5	18	3	US-09-205-143-20	Sequence
57.6	39	5	PCT-US96-00995-7	Sequence 7, Appl	822	9.6	56.5	18	3	US-08-784-582-68	Sequence
57.6	40	1	US-07-938-084-8	Sequence 8, Appl	c 823	9.6	56.5	18	3	US-09-723-534-39	Sequence
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57.6	40	3	US-08-748-547-15	Sequence 15, Appl	c 826	9.6	56.5	18	4	US-09-025-039-73	Sequence
57.6	40	3	US-08-748-547-16	Sequence 16, Appl	c 827	9.6	56.5	19	4	US-09-143-571-31	Sequence
57.6	40	4	US-09-060-299-253	Sequence 253, Appl	828	9.6	56.5	19	4	US-09-563-826-5	Sequence
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57.6	41	2	US-08-343-443B-21	Sequence 21, Appl	c 830	9.6	55.5	20	2	US-08-904-901-119	Sequence

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## ALIGNMENTS

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825/c Application US/09198452A
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ATTENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
ATTENTION: thereof and uses thereof, in particular for the diagnosis, prevention
ATTENTION: and treatment of infection
E: 9710-003-999
CATION NUMBER: US/09/198,452A
IG DATE: 1998-11-24
ID NOS: 6849

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lamydia pneumoniae
825

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Conservative 93.3%; Pred. No. 2.2e+02; Mismatches 1; Indels 0; Gaps 0;

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10/c Application US/07807529A
17669
ATTENTION:

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Rogers, Bruce L.
Morgenstern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm
ATTENTION: RECOMBITOPE PEPTIDES
SEQUENCES: 76
ENCE ADDRESS:
3: IMMULOGIC PHARMACEUTICAL CORPORATION

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STREET: One Kendall Square, Building 600
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Channing, Stacey L.
REGISTRATION NUMBER: 31,095
REFERENCE/DOCKET NUMBER: IPC-027/imi-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-807-529A-70
Query Match 72.9%; Score 12.4; DB 1; Length 32;
Best Local Similarity 92.9%; Pred. No. 8.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0;

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Db 14 GAGTGAAGATCCCC 1

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Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

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us-10-090-326-17.max.rni

E. MANDRAGOURAS  
ON NUMBER: 36,207  
DOCKET NUMBER: 002.6US(IMI-044)  
ACTION INFORMATION:  
(617) 227-7400  
(617) 227-5941  
OR SEQ ID NO: 101:  
CHARACTERISTICS:  
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leic acid  
SS: single  
linear  
PE: CDNA  
YES  
11

72.9%; Score 12.4; DB 3; Length 32;  
larity 92.9%; Pred. No. 8.3e+02;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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11/c  
Application US/08430944D  
1162  
ACTION:  
Bruce L. Rogers et al.  
VENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN  
SEQUENCES: 103  
ICE ADDRESS:  
LAHIVE & COCKFIELD, LLP  
18 State Street  
Boston  
Massachusetts  
USA  
09

ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patent In Release #1.0, Version #1.25  
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IN NUMBER: US/08/430,944D  
PE: 28-APR-1995  
ACTION DATA:  
IN NUMBER: US 08/430,014  
PE: 27-APR-1995  
ACTION DATA:  
IN NUMBER: US 08/300,928  
PE: 02-SEPT-1994  
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E. Mandragouras  
ON NUMBER: 36,207  
DOCKET NUMBER: IMI-044DV2  
ACTION INFORMATION:  
(617) 227-7400  
(617) 742-4214  
OR SEQ ID NO: 101:  
CHARACTERISTICS:  
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SS: single  
linear  
PE: CDNA  
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Best Local Similarity 92.9%; Pred. No. 8.3e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;

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DB 14 GAGTGAAGATCCCC 1

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; Sequence 101, Application US/08430014  
; Patent No. 6048962  
; GENERAL INFORMATION:  
; APPLICANT: GEFFER, Malcolm L. et al.  
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE  
; TITLE OF INVENTION: PROTEIN (TRFP)  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02145  
; COMPUTER READABLE FORM:  
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; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/300,928  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: AMY E. MANDRAGOURAS  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: 002.6US(IMI-044)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 101:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ANTI-SENSE: YES  
US-08-430-014-101

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Best Local Similarity 92.9%; Pred. No. 8.3e+02;  
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; APPLICANT: Bruce L. Rogers et al.  
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:

09:38:23 2004

us-10-090-326-17.max.rni

LAHIVE & COCKFIELD, LLP  
28 State Street  
Boston  
Massachusetts  
USA  
09

ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
Patent In Release #1.0, Version #1.25  
LITIGATION DATA:  
ON NUMBER: US/08/431,184  
TE: 28-APR-1995  
CATION DATA:  
ON NUMBER: US 08/430,014  
TE: 27-APR-1995  
CATION DATA:  
ON NUMBER: US 08/300,328  
TE: 02-SEPT-1994  
ENT INFORMATION:  
IV E. Mandragouras  
ION NUMBER: 36,207  
/DOCKET NUMBER: IMI-044DV3  
CATION INFORMATION:  
: (617)227-7400  
(617)742-4214  
OR SEQ ID NO: 101:  
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ESS: single  
linear  
PE: cDNA  
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72.9%; Score 12.4; DB 3; Length 32;  
ilarity 92.9%; Pred. No. 8.3e+02;  
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65 Application US/09474432B  
8640  
ATION:  
bozyme Pharmaceuticals, Inc.  
eigelman, Leo  
urgin, Alex  
eaudry, Amber  
arpeisky, Alex  
ademic, Jasenka  
weedler, David  
innen, Shawn  
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E: MBH00-831-B (247/276)  
CATION NUMBER: US/09/474,432B  
G DATE: 1999-12-19  
ATION NUMBER: US 60/064,866  
DATE: 1997-11-05  
ATION NUMBER: US 60/084,727  
DATE: 1998-04-29  
ATION NUMBER: US 09/186,675  
DATE: 1998-11-04  
ATION NUMBER: US 09/301,511  
DATE: 1999-04-28  
Q ID NOS: 1526  
entin version 3.0

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NAME/KEY: misc feature  
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US-09-474-432B-265

Query Match 71.8%; Score 12.2; DB 4; Length 36;  
Best Local Similarity 58.8%; Pred. No. 1.1e+03;  
Matches 10; Conservative 4; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCCCTT 17  
|||||  
Db 17 CGAGTGAAGGUCUCCU 33

RESULT 8  
US-09-476-387-264  
Sequence 264, Application US/09476387  
Patent No. 6617438  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Beigelman, Leo  
APPLICANT: Beaudry, Amber  
APPLICANT: Karpeisky, Alex  
APPLICANT: Adamic, Jasenka Matulic  
APPLICANT: Sweedler, Dave  
APPLICANT: Zinnen, Shawn  
TITLE OF INVENTION: Nucleotide Triphosphate and their incorporation  
FILE REFERENCE: MBH00-831-C (249/073)  
CURRENT APPLICATION NUMBER: US/09/476,387  
CURRENT FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: 09/474,432  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: 09/301,511  
PRIOR FILING DATE: 1999-04-28  
PRIOR APPLICATION NUMBER: 09/186,675  
PRIOR FILING DATE: 1998-11-04  
PRIOR APPLICATION NUMBER: 60/083,727  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/064,866  
PRIOR FILING DATE: 1997-11-05

ID NOS: 1524  
antIn version 3.0

# Official Sequence

ATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

sc feature

1) ..(4)

ATION: Phosphorothioate 3'-Internucleotide Linkage

sc feature

1) ..(7)

ATION: 2'-O-Methyl

sc feature

1) ..(15)

ATION: 2'-O-Methyl

sc feature

9) ..(19)

ATION: 2'-O-Methyl

sc feature

1) ..(24)

ATION: 2'-O-Methyl

sc feature

7) ..(27)

ATION: 2'-O-Methyl

sc feature

9) ..(36)

ATION: 2'-O-Methyl

sc feature

7) ..(17)

ATION: 2'-deoxy-2'-amino

sc feature

3) ..(28)

ATION: 2'-deoxy-2'-amino

sc feature

7) ..(37)

ATION: n stands for inverted deoxyabasic derivative

4

71.8%; Score 12.2; DB 4; Length 37;  
ilarity 58.8%; Pred. No. 1.1e+03; DB 4; Length 38;  
Conservative 4; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17

AGUCAAGGUCUCUU 33

199

Application US/09474432B

9640

ATION:

bozyme Pharmaceuticals, Inc.

igelman, Leo

irgin, Alex

audry, Amber

arpeisky, Alex

amic, Jasenka

weedler, David

innen, Shawn

ATION: Nucleotide triphosphate and their incorporation into oligonucleot

E: MBH00-831-B (247/276)

CATION NUMBER: US/09474,432B

G DATE: 1999-12-19

TION NUMBER: US 60/064,866

DATE: 1997-11-05

TION NUMBER: US 60/084,727

DATE: 1998-04-29

TION NUMBER: US 09/186,675

DATE: 1998-11-04

TION NUMBER: US 09/301,511

; PRIOR FILING DATE: 1999-04-28  
; NUMBER OF SEQ ID NOS: 1526  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1199  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymati  
US-09-474-432B-1199

Query Match 71.8%; Score 12.2; DB 4; Length 38;  
Best Local Similarity 58.8%; Pred. No. 1.1e+03;  
Matches 10; Conservative 4; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17

Db 18 CGAGUCAAGGUCUCUU 34

RESULT 10

US-09-474-432B-1257  
; Sequence 1257, Application US/09474432B  
; Patent No. 6528640  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Beigelman, Leo  
; APPLICANT: Burgin, Alex  
; APPLICANT: Beaudry, Amber  
; APPLICANT: Karpeisky, Alex  
; APPLICANT: Adamic, Jasenka  
; APPLICANT: Sweedler, David  
; APPLICANT: Zinnen, Shawn  
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporati  
; FILE REFERENCE: MBH00-831-B (247/276)  
; CURRENT APPLICATION NUMBER: US/09474,432B  
; CURRENT FILING DATE: 1999-12-19  
; PRIOR APPLICATION NUMBER: US 60/064,866  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: US 60/084,727  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: US 09/186,675  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: US 09/301,511  
; PRIOR FILING DATE: 1999-04-28  
; NUMBER OF SEQ ID NOS: 1526  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1257  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymati  
US-09-474-432B-1257

Query Match 71.8%; Score 12.2; DB 4; Length 38;  
Best Local Similarity 58.8%; Pred. No. 1.1e+03;  
Matches 10; Conservative 4; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17

Db 18 CGAGUCAAGGUCUCUU 34

RESULT 11

US-09-474-432B-1303  
; Sequence 1303, Application US/09474432B  
; Patent No. 6528640  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Beigelman, Leo  
; APPLICANT: Burgin, Alex  
; APPLICANT: Beaudry, Amber

arpeisky, Alex  
adamic, Jasenka  
weedler, David  
innen, Shawn  
NTION: Nucleotide triphosphate and their incorporation into oligonucleot  
E: MBHB00-831-B (247/276)  
CATION NUMBER: US/09/474,432B  
IG DATE: 1999-12-19  
TION NUMBER: US 60/064,866  
DATE: 1997-11-05  
TION NUMBER: US 60/084,727  
DATE: 1998-04-29  
TION NUMBER: US 09/186,675  
DATE: 1998-11-04  
TION NUMBER: US 09/301,511  
DATE: 1999-04-28  
ID NOS: 1526  
entIn version 3.0

## tificial Sequence

ATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
.303

71.8%; Score 12.2; DB 4; Length 38;  
ilarity 58.8%; Pred.No.1.le+03;  
Conservative 4; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||: |||: |||:  
AGUCAGGUCUCCUU 34

1332  
Application US/09474432B

28640  
ATION:  
ibozyme Pharmaceuticals, Inc.

Beigelman, Leo  
Burgin, Alex  
Beaudry, Amber  
Karpeisky, Alex  
Adamic, Jasenka  
Sweedler, David  
Zinnen, Shawn

ENTION: Nucleotide triphosphate and their incorporation into oligonucleot  
CE: MBHB00-831-B (247/276)

ICATION NUMBER: US/09/474,432B

NG DATE: 1999-12-19

ATION NUMBER: US 60/064,866

DATE: 1997-11-05

ATION NUMBER: US 60/084,727

DATE: 1998-04-29

ATION NUMBER: US 09/186,675

DATE: 1998-11-04

ATION NUMBER: US 09/301,511

DATE: 1999-04-28

ID NOS: 1526

tentIn version 3.0

2

## artificial Sequence

ATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
.1332

71.8%; Score 12.2; DB 4; Length 38;  
milarity 58.8%; Pred.No.1.le+03;  
Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 CGAGTGAAGATCCCTT 17  
|||: |||: |||:  
Db 18 CGAGUCAGGUCUCCUU 34

## RESULT 13

US-09-476-387-1198  
; Sequence 1198, Application US/09476387  
; Patent No. 6617438  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Beigelman, Leo  
; APPLICANT: Beaudry, Amber  
; APPLICANT: Karpeisky, Alex  
; APPLICANT: Adamic, Jasenka Matulic  
; APPLICANT: Sweedler, Dave  
; APPLICANT: Zinnen, Shawn  
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporat  
; FILE REFERENCE: MBHB00-831-C (249/073)  
; CURRENT APPLICATION NUMBER: US/09/476,387  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 09/474,432  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/301,511  
; PRIOR FILING DATE: 1999-04-28  
; PRIOR APPLICATION NUMBER: 09/186,675  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: 60/083,727  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/064,866  
; PRIOR FILING DATE: 1997-11-05  
; NUMBER OF SEQ ID NOS: 1524  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1198  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymat  
US-09-476-387-1198

Query Match 71.8%; Score 12.2; DB 4; Length 38;  
Best Local Similarity 58.8%; Pred.No.1.le+03;  
Matches 10; Conservative 4; Mismatches 3; Indels 0;

OY 1 CGAGTGAAGATCCCTT 17  
|||: |||: |||:  
Db 18 CGAGUCAGGUCUCCUU 34

## RESULT 14

US-09-476-387-1256  
; Sequence 1256, Application US/09476387  
; Patent No. 6617438  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Beigelman, Leo  
; APPLICANT: Beaudry, Amber  
; APPLICANT: Karpeisky, Alex  
; APPLICANT: Adamic, Jasenka Matulic  
; APPLICANT: Sweedler, Dave  
; APPLICANT: Zinnen, Shawn  
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporat  
; FILE REFERENCE: MBHB00-831-C (249/073)  
; CURRENT APPLICATION NUMBER: US/09/476,387  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 09/474,432  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/301,511  
; PRIOR FILING DATE: 1999-04-28  
; PRIOR APPLICATION NUMBER: 09/186,675  
; PRIOR FILING DATE: 1998-11-04



us-10-090-326-17.max.rni

; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Beigelman, Leo  
 ; APPLICANT: Beaudry, Amber  
 ; APPLICANT: Karpeisky, Alex  
 ; APPLICANT: Adamic, Jasenka Matulic  
 ; APPLICANT: Sneedler, Dave  
 ; APPLICANT: Zinner, Shawn

; AFFILIANT: ZIMMER, SHAWN  
 ; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporati  
 ; FILE REFERENCE: MEHH00-831-C (249/073)

; CURRENT APPLICATION NUMBER: US/09/476,387

; CURRENT FILING DATE: 2001-04-04  
 ; PRIOR APPLICATION NUMBER: 09/474,432  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: 09/301,511

```

; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1331

```

```

;
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence

```

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic
US-09-476-387-1331

```

Query Match 71.8%; Score 12.2; DB 4; Length 38;  
Best Local Similarity 58.8%; Pred. No. 1.1e+03;  
Matches 10; Conservative 4; Mismatches 3; Indels

QY 1 CGAGTGAAGATCCCCCTT 17

DB 18 CGAGUCAAGGUCUCUU 34

RESULT 17  
US-09-070-408-67/c

; Sequence 67, Application US/09070408  
; Patent No. 6180341

; GENERAL INFORMATION:  
; APPLICANT: Iverson, Brent L.

APPLICANT: Georgiou, George  
APPLICANT: Burks, Elizabeth A.

; TITLE OF INVENTION: IN VITRO SCANNING SATURATION MUTAGENESIS  
; TITLE OF INVENTION: OF PROTEINS

ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433

CITY: Houston  
STATE: Texas; COUNTRY: USA  
; ZIP: 77210

```

;
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible

```

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.30

```

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,408  
FILING DATE: Concurrently Herewith

09:38:23 2004

us-10-090-326-17.max.ini

DOCKET NUMBER: UTBS:593  
CATION INFORMATION:  
: 512/418-3000  
OR SEQ ID NO: 67:  
ARACTERISTICS:  
46 base pairs  
cleic acid  
ESS: single  
linear

71.8%; Score 12.2; DB 3; Length 46;  
ilarity 82.4%; Pred. No. 1.1e+03;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAGATCCCCCTT 17  
|||||  
GGTGATGATCCCCAT 19

C  
plication US/09302357  
0070

ATION:  
KAJIMA, Hiroki  
GASAWA, Akitsu  
ANTION: METHOD FOR GIVING RESISTANCE TO WEED CONTROL COMPOUNDS  
NTION: TO PLANTS  
E: 20-4555P  
CATION NUMBER: US/09/302,357  
G DATE: 1999-04-30  
ID NOS: 65  
entIn Ver. 2.0

tificial Sequence

ATION: Description of Artificial Sequence: Synthetic  
ATION: Oligonucleotide Primer to amplify bchH gene

70.6%; Score 12; DB 4; Length 31;  
ilarity 100.0%; Pred. No. 1.4e+03;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

HAGTGAGATC 12  
|||||  
HAGTGAGATC 12

plication US/07936533A

ATION:  
Philip Hammond  
Anthony Endozo  
VENTION: NUCLEIC ACID PROBES  
VENTION: TO CHLAMYDIA PNEUMONIAE  
SEQUENCES: 40  
ENCE ADDRESS:  
3: Lyon & Lyon  
611 West Sixth Street  
s Angeles  
California  
USA  
317  
EADABLE FORM:  
YPE: 3.5" Diskette, 1.44 Mb  
: IBM Compatible

OPERATING SYSTEM: IBM P.C.DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/936,533A  
FILING DATE: 19920826  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 198/175  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-936-533A-3

Query Match 70.6%; Score 12; DB 1; Length 43;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;

QY 6 GAAGATCCCCCTT 17  
|||||

DB 14 GAAGATCCCCCTT 25  
|||||

RESULT 20

US-07-936-533A-32/c  
Sequence 32, Application US/07936533A  
Patent No. 5374718  
GENERAL INFORMATION:  
APPLICANT: Philip Hammond  
APPLICANT: Anthony Endozo  
TITLE OF INVENTION: NUCLEIC ACID PROBES  
TITLE OF INVENTION: TO CHLAMYDIA PNEUMONIAE  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C.DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/936,533A  
FILING DATE: 19920826  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 198/175  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600

09:38:23 2004

us-10-090-326-17.max.rni

```
(213) 955-0440
7-3510
OR SEQ ID NO: 32:
CHARACTERISTICS:
3
NLEIC ACID
SS: single
linear
;

70.6%; Score 12; DB 1; Length 43;
ilarity 100.0%; Pred. No. 1.4e+03;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGATCCCTT 17
|||||
AGATCCCTT 19

plication US/08344257A
870
ACTION:
Philip Hammond
Anthony Ednoza
VENTION: NUCLEIC ACID PROBES
VENTION: TO CHLAMYDIA PNEUMONIAE
SEQUENCES: 30
ICE ADDRESS:
; Lyon & Lyon
333 West Fifth Street
Suite 4700
; Angeles
; California
; U.S.A.
;

ADABLE FORM:
PE: 3.5" Diskette, 1.44 Mb
PE: storage
IBM Compatible
SYSTEM: IBM P.C. DOS 5.0
Word Perfect 5.1
ICATION DATA:
ON NUMBER: US/08/344,257A
PE: No. 5683870ember 23, 1994
ATION: 435
ATION DATA:
ATION DATA: including application
ATION DATA: described below:
ATION: 435
ENT INFORMATION:
per, Sheldon O
ION NUMBER: 38,179
/DOCKET NUMBER: 209/248
ATION INFORMATION:
: (213) 489-1600
(213) 955-0440
7-3510
OR SEQ ID NO: 3:
CHARACTERISTICS:
3
leic acid
SS: single
linear

70.6%; Score 12; DB 1; Length 43;
ilarity 100.0%; Pred. No. 1.4e+03;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGATCCCTT 17
|||||
```

```
Db 14 GAAGATCCCTT 25

RESULT 22
US-08-638-931-17
; Sequence 17, Application US/08638931
; Patent No. 6194145
; GENERAL INFORMATION:
; APPLICANT: HEIDRICH, Bj rn
; APPLICANT: ROBINSON, Peter-Nicholas
; APPLICANT: TIECKE, Frank
; APPLICANT: ROLFS, Arndt
; TITLE OF INVENTION: Genus and species-specific identification
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaído, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,931
; FILING DATE: 25-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 15 891.1
; FILING DATE: 29-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; US-08-638-931-17

Query Match 69.4%; Score 11.8; DB 3; Length 27;
Best Local Similarity 86.7%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 2 GAGTGAAGATCCCTT 16
|||
Db 5 GAATGAATATCCCTT 19

RESULT 23
US-09-462-941-25/c
; Sequence 25, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Pro
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
```

## Artificial Sequence

ATON: Description of Artificial Sequence:PCR Primer

69.4%; Score 11.8; DB 4; Length 33;  
ilarity 86.7%; Pred. No. 1.8e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCCC 15  
|||||  
AGTGAGGATCCCC 2

## 4/c

Application US/09182145B  
7657

## INVENTOR:

stein, David A.

hen, Robert

ddard, Audrey

dney, Austin L.

llan, Kenneth J.

wrence, David A.

vine, Arnold J.

nnica, Diane

y, Margaret Ann

od, William I.

NTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

E: P117682

CATION NUMBER: US/09/182,145B

IG DATE: 1998-10-29

CATION NUMBER: US 60/063,704

IG DATE: 1997-10-29

CATION NUMBER: US 60/073,612

IG DATE: 1998-02-04

CATION NUMBER: US 60/081,695

IG DATE: 1998-04-14

ID NOS: 156

## Artificial sequence

## .sc.feature

50-

ATION: Sequence is synthesized.

7657

4

69.4%; Score 11.8; DB 4; Length 50;  
ilarity 86.7%; Pred. No. 1.9e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCCC 15  
|||||  
AGTGAGGATCCCC 35

## 2265/c

Application US/08956171E

93114

## INVENTOR:

ANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides a  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 2265:

SEQUENCE CHARACTERISTICS:

LENGTH: 52 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2265:

US-08-956-171E-2265

Query Match 69.4%; Score 11.8; DB 4; Length 52;

Best Local Similarity 86.7%; Pred. No. 1.9e+03;

Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 3 AGTGAAGATCCCCCT 17

Db 39 AGTTAAGCTCCCTT 25

## RESULT 26

US-08-908-643C-56

; Sequence 56, Application US/08908643C

; Patent No. 6120995

; GENERAL INFORMATION:

; APPLICANT: Waldman, Scott A.

; Pearlman, Joshua M.

; Barber, Michael T.

; Schultz, Stephanie

; Parkinson, Scott J.

; TITLE OF INVENTION: COMPOSITIONS THAT SPECIFICALLY BIND TO

; COLORECTAL CANCER CELLS AND METHODS OF

; USING THE SAME

; NUMBER OF SEQUENCES: 85

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6;

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

; COMPUTER: IBM PC compatible

BRATING SYSTEM: PC-DOS/MS-DOS  
 TWARE: WordPerfect 6.1  
 APPLICATION DATA:  
 APPLICATION NUMBER: US/08/908,643C  
 FILING DATE: 07-Aug-1997  
 ASSIFICATION: N/A  
 APPLICATION DATA:  
 APPLICATION NUMBER: <Unknown>  
 FILING DATE: <Unknown>  
 //AGENT INFORMATION:  
 NAME: Mark Deluca  
 REGISTRATION NUMBER: 33,229  
 REFERENCE/DOCKET NUMBER: TJU-2209  
 APPLICATION INFORMATION:  
 TELEPHONE: 215-568-3100  
 TELEFAX: 215-568-3439  
 FOR SEQ ID NO: 56:  
 3 CHARACTERISTICS:  
 LENGTH: 57 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 DESCRIPTION: SEQ ID NO: 56:

69.4%; Score 11.8; DB 3; Length 57;  
 Similarity 86.7%; Pred. No. 1.9e+03;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAAGATCCCT 16  
 |||||  
 TAGAGATCCCT 42

l/c  
 Application US/08390850  
 3215

ATION:  
 Draper, Kenneth G.  
 Pavco, Pamela  
 McSwiggen, James  
 Gustofson, John  
 Stinchcomb, Dan T.  
 VENTION: METHOD AND REAGENT FOR TREATMENT  
 OF ARTHRITIC CONDITIONS  
 SEQUENCES: 1151  
 ADDRESS:  
 : Lyon & Lyon  
 533 West Fifth Street  
 Suite 4700  
 Angeles  
 alifornia  
 U.S.A.  
 71

ADABLE FORM:  
 PE: 3.5" Diskette, 1.44 Mb  
 PE: storage  
 IBM Compatible  
 SYSTEM: IBM P.C. DOS 5.0  
 FASTSEQ Version 1.5  
 LICATION DATA:  
 ON NUMBER: US/08/390,850  
 TE: February 17, 1995  
 CATION DATA:  
 ON NUMBER: 08/354,920  
 TE: December 13, 1994  
 ON NUMBER: 08/152,487  
 TE: No. 5612215ember 12, 1993  
 ON NUMBER: 07/989,848  
 TE: December 7, 1992  
 ENT INFORMATION:  
 tburg, Richard

REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 211/084  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 641:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-390-850-641  
 Query Match 67.1%; Score 11.4; DB 1; Length 17;  
 Best Local Similarity 92.3%; Pred. No. 2.7e+03;  
 Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 4 GTGAAGATCCCT 16  
 |||||  
 Db 14 GTGAAGATCCACT 2

## RESULT 28

US-08-435-634-641/c  
 ; Sequence 641, Application US/08435634  
 ; Patent No. 5731295  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Draper, Kenneth G.  
 ; APPLICANT: Pavco, Pamela  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Gustofson, John  
 ; APPLICANT: Stinchcomb, Dan T.  
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
 ; OF ARTHRITIC CONDITIONS  
 ; NUMBER OF SEQUENCES: 1151  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FastSEQ Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/435,634  
 ; FILING DATE: 05-MAY-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/390,850  
 ; FILING DATE: February 17, 1995  
 ; APPLICATION NUMBER: 08/354,920  
 ; FILING DATE: December 13, 1994  
 ; APPLICATION NUMBER: 08/152,487  
 ; FILING DATE: No. 5731295ember 12, 1993  
 ; APPLICATION NUMBER: 07/989,848  
 ; FILING DATE: December 7, 1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 211/084  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 641:  
 ; SEQUENCE CHARACTERISTICS:

352/c

09:38:23 2004

us-10-090-326-17.max.rni

VENTION: CHICKEN NEUROPEPTIDE GENE USEFUL  
VENTION: FOR IMPROVED POULTRY PRODUCTION  
SEQUENCES: 20

ICE ADDRESS:  
Klarquist Sparkman Campbell Leigh &  
Whinston, LLP

One World Trade Center  
21 S.W. Salmon Street  
Suite 1600  
Portland, Oregon 97204

United States of America

4-2988

ADABLE FORM:  
RE: Disk, 3-1/2 inch

IBM PC compatible

SYSTEM: Windows NT

WordPerfect 7.0 & ASCII

LOCATION DATA: US/08/789,329C

RE: 01/23/97

ATION: 435

ATION DATA:

RE: NUMBER:

INT INFORMATION:

ON NUMBER: 41,401

DOCKET NUMBER: 2847-46468/DJE

ATION INFORMATION:

(503) 226-7391

(503) 228-9446

AR SEQ ID NO: 15:

CHARACTERISTICS:

leuc acid

SS: single

linear

67.1%; Score 11.4; DB 3; Length 26;

larity 92.3%; Pred. No. 2.8e+03;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AAAGATCCCT 16

|||||

AAAGATCCCAT 8

)/c

Application US/09013895A

363

ATION:

Ni, Jian

Rosen, Craig A.

Pan, James G.

Gentz, Reiner L.

Dixit, Vishva M.

VENTION: Death Domain Containing Receptor 4 (DR4: Death

VENTION: Receptor 4), Member of the TNF-Receptor

VENTION: Superfamily and Binding to Trail (AP02-L)

SEQUENCES: 12

ICE ADDRESS:

: HUMAN GENOME SCIENCES, INC.

9410 KEY WEST AVENUE

EVILLE

US

50

ADABLE FORM:

RE: Floppy disk

IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/013,895A  
FILING DATE: 27-JAN-1998  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1300002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-013-895A-10

Query Match 67.1%; Score 11.4; DB 4; Length 33;

Best Local Similarity 92.3%; Pred. No. 2.9e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCC 14

|||||

Db 15 GAGTGAAGATCCC 3

RESULT 35

US-09-565-918-11/c

; Sequence 11, Application US/09565918

; Patent No. 6433147

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; APPLICANT: Rosen, Craig A.

; APPLICANT: Pan, James G.

; APPLICANT: Gentz, Reiner L.

; APPLICANT: Dixit, Vishva M.

; TITLE OF INVENTION: Death Domain Containing Receptor 4

; FILE REFERENCE: 1488.1300005

; CURRENT APPLICATION NUMBER: US/09/565,918

; CURRENT FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: US 60/132,922

; PRIOR FILING DATE: 1999-05-06

; PRIOR APPLICATION NUMBER: US 09/013,895

; PRIOR FILING DATE: 1998-01-27

; PRIOR APPLICATION NUMBER: US 60/037,829

; PRIOR FILING DATE: 1997-02-05

; PRIOR APPLICATION NUMBER: US 60/035,722

; PRIOR FILING DATE: 1997-01-28

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 33

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: DNA Prime;

US-09-565-918-11

Query Match 67.1%; Score 11.4; DB 4; Length 33;

Best Local Similarity 92.3%; Pred. No. 2.9e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 2 GAGTGAAGATCCC 14

|||||

Db 15 GAGTGAAGATCCC 3

RESULT 36

09:38:23 2004

us-10-090-326-17.max.rni

/c  
pplication US/09448868  
1823  
MATION:  
Ni, Jian  
Rosen, Craig A.  
Pan, James G.  
Gentz, Reiner L.  
Dixit, Vishva M.  
VENTION: Death Domain Containing Receptor 4 (DR4: Death  
VENTION: Receptor 4), Member of the TNF-Receptor  
VENTION: Superfamily and Binding to Trail (AP02-L)  
SEQUENCES: 12  
NCE ADDRESS:  
: HUMAN GENOME SCIENCES, INC.  
9410 KEY WEST AVENUE  
CKVILLE  
D  
US  
50  
ADABLE FORM:  
PE: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.30  
LOCATION DATA:  
ON NUMBER: US/09/448,868  
TE: HEREWITH  
ACTION:  
CATION DATA:  
ON NUMBER: 09/013,895  
TE: 27-JAN-1998  
ACTION:  
ENT INFORMATION:  
EFEFE, ERIC K.  
ION NUMBER: 36,688  
/DOCKET NUMBER: 1498.1300004  
CATION INFORMATION:  
: (202) 371-2540  
OR SEQ ID NO: 10:  
33 base pairs  
nucleic acid  
ESS: single  
linear  
PE: DNA (genomic)  
67.1%; Score 11.4; DB 4; Length 33;  
ilarity 92.3%; Pred.No.2.9e+03;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
GTGAAGATCCC 14  
|||||  
GTGAGGATCCC 3  
/c  
pplication US/09144428  
13108  
NATION:  
BAYER CORPORATION, The  
TAMBURINI, Paul P  
DAVIS, Gary  
DELARIA, Katherine A  
MARLOR, Christopher W  
MULLER, Daniel K  
VENTION: HUMAN BIKUNIN  
SEQUENCES: 71  
NCE ADDRESS:  
3: McDonnell Boehnen Hulbert & Berghoff

STREET: 30C S. Wacker Drive Suite 3200  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/144,428  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/03894  
FILING DATE: 10-MAR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/013,106  
FILING DATE: 11-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/019,793  
FILING DATE: 14-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/725,251  
FILING DATE: 04-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: CHAO, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 96,223-II  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 913-0001  
TELEFAX: (312) 913-0002  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
US-09-144-428-31  
Query Match 67.1%; Score 11.4; DB 4; Length 35;  
Best Local Similarity 92.3%; Pred.No.2.9e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0;  
QY 3 AGTGAAGATCCCC 15  
|||||  
Db 13 AGTGAGGATCCCC 1  
RESULT 38  
US-08-299-498A-29  
; Sequence 29, Application US/08299498A  
; Patent No. 5688670  
; GENERAL INFORMATION:  
; APPLICANT: Szostak, Jack W.  
; APPLICANT: Lorsch, Jon R.  
; APPLICANT: Wilson, Charles  
; TITLE OF INVENTION: NOVEL RIBOZYMES AND NOVEL RIBOZYME  
; TITLE OF INVENTION: SELECTION SYSTEMS  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible



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us-10-090-326-17.max.rni

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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30B
ICATION DATA:
N NUMBER: US/08/299,498A
E: 01-SEP-1994
TION: 435
NT INFORMATION:
rk, Paul T.
ON NUMBER: 30,162
DOCKET NUMBER: 00786/245001
ATION INFORMATION:
(617) 542-5070
(617) 542-8906
0154
R SEQ ID NO: 29:
RACTERISTICS:
16 base pairs
leic acid
SS: single
linear
),
67.1%; Score 11.4; DB 1; Length 36;
larity 84.6%; Pred.No.2.9e+03;
Conservative 1; Mismatches 1; Indels 0; Gaps 0;
AGTGAAGATCC 13
|||||:|
GGGAGAUCC 14
),
plication PC/TUS9510813
ATION:
Szostak, Jack W.
Lorsch, Jon R.
Wilson, Charles
ENTION: NOVEL RIBOZYMES AND NOVEL RIBOZYME
ENTION: SELECTION SYSTEMS
SEQUENCES: 91
ACE ADDRESS:
: Fish & Richardson
125 Franklin Street
ston
ssachusetts
U.S.A.
10-2804
ADABLE FORM:
E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30B
ICATION DATA:
N NUMBER: PC/US95/10813
E:
TION:
ATION DATA:
N NUMBER: 08/299,498
E: 01-SEP-1994
ENT INFORMATION:
ark, Paul T.
ION NUMBER: 30,162
/DOCKET NUMBER: 00786/245001
ATION INFORMATION:
: (617) 542-5070
(617) 542-8906
0154
R SEQ ID NO: 29:
RACTERISTICS:
16 base pairs
leic acid
SS: single
```

```
TOPOLOGY: linear
PCT-US95-10813-29
Query Match 67.1%; Score 11.4; DB 5; Length 36;
Best Local Similarity 84.6%; Pred.No.2.9e+03;
Matches 11; Conservative 1; Mismatches 1; Indels 0;
QY 1 CGAGTGAAGATCC 13
|||:|||||
Db 2 CGAGGAGAUCC 14
RESULT 40
US-08-681-935-15
; Sequence 15, Application US/08681935
; Patent No. 5710248
; GENERAL INFORMATION:
; APPLICANT: GROSE, CHARLES F.
; TITLE OF INVENTION: PEPTIDE TAG FOR IMMUNODETECTION AND
; TITLE OF INVENTION: IMMUNOPURIFICATION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 201
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,935
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCORMACK, MYRA H.
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 140.00040101
; TELEPHONE: 612-305-1225
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-681-935-15
Query Match 67.1%; Score 11.4; DB 1; Length 41;
Best Local Similarity 92.3%; Pred.No.3e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0;
QY 5 TGAAGATCCCTT 17
|||||:|
Db 4 TGAAGATCACCIT 16
RESULT 41
US-08-939-323-15
; Sequence 15, Application US/08939323
; Patent No. 6255462
; GENERAL INFORMATION:
; APPLICANT: GROSE, CHARLES F.
; TITLE OF INVENTION: PEPTIDE TAG FOR IMMUNODETECTION AND
; TITLE OF INVENTION: IMMUNOPURIFICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
```

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us-10-090-326-17.max.rni

119 NORTH FOURTH STREET, SUITE 203  
MINNEAPOLIS

USA

ADABLE FORM:

PE: Floppy disk

SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

PLICATION DATA:

ON NUMBER: US/08/939,323

TE: 29-SEP-1997

ATION: 435

CATION DATA:

ON NUMBER: US 08/681,935

TE: 29-JUL-1996

ENT INFORMATION:

ETING MS., ANN M.

ION NUMBER: 33,977

/DOCKET NUMBER: 140.00040102

CATION INFORMATION:

: (612) 305-1217

OR SEQ ID NO: 15:

ARACTERISTICS:

41 base pairs

cleic acid

RSS: single

linear

PE: other nucleic acid

67.1%; Score 11.4; DB 3; Length 41;

ilarity 92.3%; Pred. No. 3e+03; 1; Indels 0; Gaps 0;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AAGATCCCTT 17

|||||

AAGATCACCTT 16

/c

plication us/08681935

0248

MATION:

GROSE, CHARLES F.

VENTION: PEPTIDE TAG FOR IMMUNODETECTION AND

VENTION: IMMUNOPURIFICATION

SEQUENCES: 18

NCE ADDRESS:

: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.

119 NORTH FOURTH STREET, SUITE 201

MINNEAPOLIS

MINNESOTA

USA

01

ADABLE FORM:

PE: Floppy disk

SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

PLICATION DATA:

ON NUMBER: US/08/681,935

TE:

ATION: 435

ENT INFORMATION:

CORMACK, MYRA H.

ION NUMBER: 36,602

/DOCKET NUMBER: 140.00040101

CATION INFORMATION:

: 612-305-1225

TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-681-935-14

Query Match

Best Local Similarity 67.1%; Score 11.4; DB 1; Length 42;

Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 5 TGAAGATCCCTT 17

|||||

Db 23 TGAAGATCACCTT 11

RESULT 43

US-08-939-323-14/c

Sequence 14, Application US/08939323

Patent No. 6255462

GENERAL INFORMATION:

APPLICANT: GROSE, CHARLES F.

TITLE OF INVENTION: PEPTIDE TAG FOR IMMUNODETECTION AND

TITLE OF INVENTION: IMMUNOPURIFICATION

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MN

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,323

FILING DATE: 29-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/681,935

FILING DATE: 29-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: MUETING MS., ANN M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 140.00040102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 305-1217

TELEFAX: (612) 305-1228

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

US-08-939-323-14

Query Match

Best Local Similarity 67.1%; Score 11.4; DB 3; Length 42;

Matches 12; Conservative 0; Mismatches 1; Indels 0;

QY 5 TGAAGATCCCTT 17

|||||

Db 23 TGAAGATCACCTT 11

RESULT 44

09:38:23 2004

us-10-090-326-17.max.rni

publication US/09302620B  
420  
TION:  
son, C. Ron  
aft, David L.  
rich, Dudley  
hoo, Mark  
dduri, Krishna M.  
rnett, Cathy A.  
enner, Alfred A.  
ng, Maria  
per, John C.  
eeson, Martin  
TION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450  
TION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA  
TION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS  
TION: RELATING THERETO  
:: 1010-16.seq  
ATION NUMBER: US/09/302,620B  
DATE: 1999-04-30  
ID NOS: 109  
ntIn Ver. 2.1

ificial Sequence

TION: Description of Artificial Sequence: Primer

67.1%; Score 11.4; DB 4; Length 42;  
larity 92.3%; Pred. No. 3e+03; 1; Indels 0; Gaps 0;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AGATCCCCCT 16  
|||||||  
AGATCCCCAT 18

lication US/08434730  
463  
ATION:  
Dalton, Stephen  
Kochan, Jarema P  
Osborne, Mark A  
ENTION: METHOD TO DETECT PROTEIN-PROTEIN  
ENTION: INTERACTIONS  
QUENCES: 16  
ICE ADDRESS:  
Hoffmann-La Roche Inc  
40 Kingsland Street  
ley

USA  
.0  
DABLE FORM:  
E: Floppy disk  
IBM PC compatible  
SYSTEM: PC-DOS/MS-DOS  
PatentIn Release #1.0, Version #1.30  
ICATION DATA:  
N NUMBER: US/08/434,730  
E: 04-MAY-1995  
TION: 435  
NT INFORMATION:  
ilonow, Raina  
ON NUMBER: 39022  
DOCKET NUMBER: 9069  
ATION INFORMATION:  
(201)235-4391

TELEFAX: (201)235-2363  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-434-730-1  
  
Query Match 67.1%; Score 11.4; DB 1; Length 45;  
Best Local Similarity 92.3%; Pred. No. 3e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0;  
  
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Search completed: February 29, 2004, 11:22:32  
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Listing first 1000 summaries

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#### SUMMARIES

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75.3	25	14	US-10-098-263B-14835	Sequence 14835, A
75.3	25	14	US-10-098-263B-30891	Sequence 30891, A
75.3	25	14	US-10-098-263B-60404	Sequence 60404, A
75.3	25	14	US-10-098-263B-66622	Sequence 66622, A
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75.3	50	15	US-10-131-827-934	Sequence 934, App
75.3	60	10	US-09-908-975-31862	Sequence 31862, A
72.9	32	8	US-08-464-363-70	Sequence 70, Appl
71.8	17	10	US-09-780-533A-658	Sequence 658, App
71.8	24	10	US-09-940-185-246	Sequence 246, App
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71.8	25	14	US-10-098-263B-15429	Sequence 15429, A

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63.5	50	14	US-10-012-755A-230	Sequence 230, Appl	339	10.6	62.4	25	14	US-10-098-263B-11353	Sequence
63.5	50	14	US-10-015-386A-230	Sequence 230, Appl	c 340	10.6	62.4	25	14	US-10-098-263B-15430	Sequence
63.5	50	14	US-10-011-692A-230	Sequence 230, Appl	c 341	10.6	62.4	25	14	US-10-098-263B-30808	Sequence
63.5	50	14	US-10-006-768A-230	Sequence 230, Appl	342	10.6	62.4	25	14	US-10-098-263B-39331	Sequence
63.5	50	14	US-10-017-610A-230	Sequence 230, Appl	c 343	10.6	62.4	25	14	US-10-098-263B-45899	Sequence
63.5	50	14	US-10-006-063A-230	Sequence 230, Appl	c 344	10.6	62.4	25	14	US-10-098-263B-69666	Sequence
63.5	50	14	US-10-020-063A-230	Sequence 230, Appl	c 345	10.6	62.4	25	14	US-10-098-263B-70792	Sequence
63.5	50	14	US-10-015-391A-230	Sequence 230, Appl	c 346	10.6	62.4	25	14	US-10-098-263B-71483	Sequence
63.5	50	14	US-10-017-407A-230	Sequence 230, Appl	347	10.6	62.4	25	14	US-10-098-263B-81967	Sequence
63.5	50	14	US-10-011-833A-230	Sequence 230, Appl	c 348	10.6	62.4	25	14	US-10-098-263B-99961	Sequence
63.5	50	14	US-10-006-041A-230	Sequence 230, Appl	349	10.6	62.4	25	14	US-10-098-263B-102598	Sequence
63.5	50	14	US-10-015-822A-230	Sequence 230, Appl	c 350	10.6	62.4	25	14	US-10-098-263B-109788	Sequence
63.5	50	14	US-10-015-387A-230	Sequence 230, Appl	c 351	10.6	62.4	25	14	US-10-098-263B-114118	Sequence
63.5	50	14	US-10-006-130A-230	Sequence 230, Appl	352	10.6	62.4	25	14	US-10-098-263B-115836	Sequence
63.5	50	14	US-10-006-172A-230	Sequence 230, Appl	353	10.6	62.4	25	14	US-10-098-263B-126309	Sequence
63.5	50	14	US-10-017-253A-230	Sequence 230, Appl	c 354	10.6	62.4	25	14	US-10-098-263B-130904	Sequence
63.5	50	14	US-10-015-392A-230	Sequence 230, Appl	355	10.6	62.4	25	14	US-10-032-585-4039	Sequence
63.5	50	14	US-10-017-306A-230	Sequence 230, Appl	c 356	10.6	62.4	31	9	US-09-801-274-286	Sequence
63.5	50	14	US-10-017-867A-230	Sequence 230, Appl	357	10.6	62.4	33	14	US-10-273-762-1	Sequence
63.5	50	14	US-10-012-064A-230	Sequence 230, Appl	358	10.6	62.4	34	12	US-10-278-768-21	Sequence
63.5	50	14	US-10-032-585-3034	Sequence 3034, Ap	359	10.6	62.4	34	14	US-10-151-716-4	Sequence
63.5	50	14	US-10-013-909A-230	Sequence 230, Appl	360	10.6	62.4	35	10	US-09-825-805-300	Sequence
63.5	50	14	US-10-015-671A-230	Sequence 230, Appl	361	10.6	62.4	35	10	US-09-740-332-9370	Sequence
63.5	50	14	US-10-015-610A-230	Sequence 230, Appl	362	10.6	62.4	35	10	US-09-740-332-9432	Sequence
63.5	50	14	US-10-012-137A-230	Sequence 230, Appl	363	10.6	62.4	35	10	US-09-817-879-9370	Sequence
63.5	50	14	US-10-012-752A-230	Sequence 230, Appl	364	10.6	62.4	35	10	US-09-817-879-9432	Sequence
63.5	50	14	US-10-012-754A-230	Sequence 230, Appl	365	10.6	62.4	36	9	US-09-848-164-114	Sequence
63.5	50	14	US-10-013-910A-230	Sequence 230, Appl	366	10.6	62.4	36	9	US-09-900-379-114	Sequence
63.5	50	14	US-10-013-911A-230	Sequence 230, Appl	367	10.6	62.4	37	9	US-09-864-785-1987	Sequence
63.5	50	14	US-10-013-912A-230	Sequence 230, Appl	368	10.6	62.4	37	10	US-09-825-805-275	Sequence
63.5	50	14	US-10-015-653A-230	Sequence 230, Appl	369	10.6	62.4	37	10	US-09-740-332-9371	Sequence
63.5	50	14	US-10-012-101B-230	Sequence 230, Appl	370	10.6	62.4	37	10	US-09-740-332-9423	Sequence
63.5	50	14	US-10-015-480A-230	Sequence 230, Appl	371	10.6	62.4	37	10	US-09-817-879-9371	Sequence
63.5	50	14	US-10-015-715A-230	Sequence 230, Appl	372	10.6	62.4	37	10	US-09-817-879-9423	Sequence
63.5	50	14	US-10-012-237A-230	Sequence 230, Appl	373	10.6	62.4	37	14	US-10-092-135-32	Sequence
63.5	50	14	US-10-013-906A-230	Sequence 230, Appl	374	10.6	62.4	37	14	US-10-156-306-2570	Sequence
63.5	50	14	US-10-015-388A-230	Sequence 230, Appl	375	10.6	62.4	38	10	US-09-825-805-963	Sequence
63.5	50	14	US-10-012-753A-230	Sequence 230, Appl	376	10.6	62.4	38	10	US-09-825-805-1074	Sequence
63.5	50	14	US-10-015-385A-230	Sequence 230, Appl	377	10.6	62.4	38	10	US-09-825-805-1094	Sequence
63.5	50	14	US-10-007-236A-230	Sequence 230, Appl	378	10.6	62.4	38	10	US-09-825-805-1111	Sequence
63.5	50	14	US-10-015-389A-230	Sequence 230, Appl	379	10.6	62.4	38	10	US-09-825-805-1187	Sequence
63.5	50	15	US-10-015-519A-230	Sequence 230, Appl	380	10.6	62.4	38	10	US-09-825-805-1192	Sequence

62.4	38	10	US-09-825-805-1203	Sequence 1203, Ap	454	10.6	62.4	39	14	US-10-005-956-1382	Sequence
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62.4	38	10	US-09-825-805-1284	Sequence 1284, Ap	c 457	10.6	62.4	50	15	US-10-131-827-2284	Sequence
62.4	38	10	US-09-825-805-1290	Sequence 1290, Ap	c 458	10.6	62.4	50	15	US-10-131-827-3877	Sequence
62.4	38	10	US-09-825-805-1355	Sequence 1355, Ap	c 459	10.6	62.4	51	9	US-09-828-995B-7	Sequence
62.4	38	10	US-09-825-805-1405	Sequence 1405, Ap	c 460	10.6	62.4	51	9	US-09-828-995B-9	Sequence
62.4	38	10	US-09-825-805-1410	Sequence 1410, Ap	461	10.6	62.4	60	10	US-09-908-975-12591	Sequence
62.4	38	10	US-09-825-805-1426	Sequence 1426, Ap	462	10.6	62.4	60	10	US-09-908-975-12591	Sequence
62.4	38	10	US-09-825-805-1455	Sequence 1455, Ap	c 463	10.6	62.4	60	10	US-09-908-975-20521	Sequence
62.4	38	10	US-09-825-805-1476	Sequence 1476, Ap	c 464	10.6	62.4	60	10	US-09-908-975-21470	Sequence
62.4	38	10	US-09-730-289B-2807	Sequence 2807, Ap	c 465	10.4	61.2	12	8	US-08-424-550B-4	Sequence
62.4	38	10	US-09-730-289B-2813	Sequence 2813, Ap	c 466	10.4	61.2	12	9	US-09-751-797-6	Sequence
62.4	38	10	US-09-730-289B-2850	Sequence 2850, Ap	c 467	10.4	61.2	12	10	US-09-930-334-12	Sequence
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62.4	38	10	US-09-730-289B-2855	Sequence 2855, Ap	c 469	10.4	61.2	12	13	US-10-032-626-12	Sequence
62.4	38	10	US-09-780-533A-4516	Sequence 4516, Ap	c 470	10.4	61.2	12	13	US-10-067-813-11	Sequence
62.4	38	10	US-09-780-533A-4575	Sequence 4575, Ap	c 471	10.4	61.2	12	13	US-10-085-108-4	Sequence
62.4	38	10	US-09-780-533A-4652	Sequence 4652, Ap	c 472	10.4	61.2	12	14	US-10-235-264-9	Sequence
62.4	38	10	US-09-780-533A-4685	Sequence 4685, Ap	c 473	10.4	61.2	12	14	US-10-193-451A-12	Sequence
62.4	38	10	US-09-780-533A-4729	Sequence 4729, Ap	c 474	10.4	61.2	12	14	US-10-348-190-27	Sequence
62.4	38	10	US-09-780-533A-4742	Sequence 4742, Ap	c 475	10.4	61.2	12	14	US-10-134-345-12	Sequence
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62.4	38	10	US-09-780-533A-4764	Sequence 4764, Ap	c 477	10.4	61.2	12	14	US-10-160-237-4	Sequence
62.4	38	10	US-09-780-533A-4770	Sequence 4770, Ap	c 478	10.4	61.2	12	14	US-10-453-264-17	Sequence
62.4	38	10	US-09-780-533A-4804	Sequence 4804, Ap	c 479	10.4	61.2	12	14	US-09-780-533A-2673	Sequence
62.4	38	10	US-09-780-533A-4805	Sequence 4805, Ap	480	10.4	61.2	17	10	US-09-882-945A-308	Sequence
62.4	38	10	US-09-780-533A-4857	Sequence 4857, Ap	c 481	10.4	61.2	19	10	US-09-765-555-30	Sequence
62.4	38	10	US-09-780-533A-4862	Sequence 4862, Ap	c 482	10.4	61.2	20	13	US-10-038-984-10	Sequence
62.4	38	10	US-09-877-478-4292	Sequence 4292, Ap	c 483	10.4	61.2	20	14	US-10-305-810-47	Sequence
62.4	38	10	US-09-877-478-4393	Sequence 4393, Ap	c 484	10.4	61.2	20	15	US-10-289-762-4423	Sequence
62.4	38	10	US-09-877-478-4428	Sequence 4428, Ap	c 485	10.4	61.2	20	15	US-10-189-429-45	Sequence
62.4	38	10	US-09-877-478-4456	Sequence 4456, Ap	486	10.4	61.2	20	15	US-10-189-429-45	Sequence
62.4	38	10	US-09-877-478-4469	Sequence 4469, Ap	c 487	10.4	61.2	22	15	US-10-115-571A-52	Sequence
62.4	38	10	US-09-877-478-4485	Sequence 4485, Ap	c 488	10.4	61.2	22	15	US-10-093-463-293	Sequence
62.4	38	10	US-09-776-474-2026	Sequence 2026, Ap	c 489	10.4	61.2	22	15	US-10-093-463-296	Sequence
62.4	38	10	US-09-776-474-2045	Sequence 2045, Ap	c 490	10.4	61.2	23	14	US-10-205-951-29	Sequence
62.4	38	10	US-09-776-474-2084	Sequence 2084, Ap	c 491	10.4	61.2	24	9	US-09-848-585-36	Sequence
62.4	38	10	US-09-776-474-2085	Sequence 2085, Ap	c 492	10.4	61.2	24	10	US-09-940-185-1185	Sequence
62.4	38	10	US-09-930-423-2982	Sequence 2982, Ap	493	10.4	61.2	24	12	US-10-072-012-964	Sequence
62.4	38	10	US-09-930-423-3036	Sequence 3036, Ap	c 494	10.4	61.2	25	9	US-09-828-313-104	Sequence
62.4	38	10	US-09-930-423-3103	Sequence 3103, Ap	c 495	10.4	61.2	25	9	US-09-997-664-95	Sequence
62.4	38	10	US-09-930-423-3114	Sequence 3114, Ap	496	10.4	61.2	25	14	US-10-215-112-1842	Sequence
62.4	38	10	US-09-930-423-3117	Sequence 3117, Ap	c 497	10.4	61.2	25	14	US-10-215-112-8545	Sequence
62.4	38	10	US-09-930-423-3120	Sequence 3120, Ap	498	10.4	61.2	25	14	US-10-098-263B-95	Sequence
62.4	38	10	US-09-930-423-3148	Sequence 3148, Ap	c 499	10.4	61.2	25	14	US-10-098-263B-96	Sequence
62.4	38	10	US-09-930-423-3174	Sequence 3174, Ap	500	10.4	61.2	25	14	US-10-098-263B-13895	Sequence
62.4	38	10	US-09-930-423-3193	Sequence 3193, Ap	c 501	10.4	61.2	25	14	US-10-098-263B-14871	Sequence
62.4	38	10	US-09-930-423-3203	Sequence 3203, Ap	c 502	10.4	61.2	25	14	US-10-098-263B-14872	Sequence
62.4	38	10	US-09-930-423-3226	Sequence 3226, Ap	c 503	10.4	61.2	25	14	US-10-098-263B-22214	Sequence
62.4	38	10	US-09-930-423-3234	Sequence 3234, Ap	c 504	10.4	61.2	25	14	US-10-098-263B-25357	Sequence
62.4	38	10	US-09-780-164-1852	Sequence 1852, Ap	505	10.4	61.2	25	14	US-10-098-263B-30870	Sequence
62.4	38	10	US-09-780-164-1863	Sequence 1863, Ap	c 506	10.4	61.2	25	14	US-10-098-263B-40248	Sequence
62.4	38	10	US-09-780-164-1878	Sequence 1878, Ap	c 507	10.4	61.2	25	14	US-10-098-263B-42126	Sequence
62.4	38	10	US-09-780-164-1933	Sequence 1933, Ap	c 508	10.4	61.2	25	14	US-10-098-263B-43610	Sequence
62.4	38	10	US-09-792-818-1490	Sequence 1490, Ap	509	10.4	61.2	25	14	US-10-098-263B-62891	Sequence
62.4	38	10	US-09-792-818-1493	Sequence 1493, Ap	c 510	10.4	61.2	25	14	US-10-098-263B-62892	Sequence
62.4	38	10	US-09-792-818-1542	Sequence 1542, Ap	c 511	10.4	61.2	25	14	US-10-098-263B-65535	Sequence
62.4	38	10	US-09-792-818-1586	Sequence 1586, Ap	c 512	10.4	61.2	25	14	US-10-098-263B-66895	Sequence
62.4	38	10	US-09-745-237A-2982	Sequence 2982, Ap	c 513	10.4	61.2	25	14	US-10-098-263B-66896	Sequence
62.4	38	10	US-09-745-237A-3036	Sequence 3036, Ap	515	10.4	61.2	25	14	US-10-098-263B-70971	Sequence
62.4	38	10	US-09-745-237A-3103	Sequence 3103, Ap	c 516	10.4	61.2	25	14	US-10-098-263B-72474	Sequence
62.4	38	10	US-09-745-237A-3114	Sequence 3114, Ap	517	10.4	61.2	25	14	US-10-098-263B-75770	Sequence
62.4	38	10	US-09-745-237A-3117	Sequence 3117, Ap	c 518	10.4	61.2	25	14	US-10-098-263B-80185	Sequence
62.4	38	10	US-09-745-237A-3120	Sequence 3120, Ap	c 519	10.4	61.2	25	14	US-10-098-263B-81950	Sequence
62.4	38	10	US-09-745-237A-3148	Sequence 3148, Ap	c 520	10.4	61.2	25	14	US-10-098-263B-88005	Sequence
62.4	38	10	US-09-745-237A-3174	Sequence 3174, Ap	c 521	10.4	61.2	25	14	US-10-098-263B-88006	Sequence
62.4	38	10	US-09-745-237A-3193	Sequence 3193, Ap	522	10.4	61.2	25	14	US-10-098-263B-90137	Sequence
62.4	38	10	US-09-745-237A-3203	Sequence 3203, Ap	523	10.4	61.2	25	14	US-10-098-263B-90697	Sequence
62.4	38	10	US-09-745-237A-3226	Sequence 3226, Ap	524	10.4	61.2	25	14	US-10-098-263B-97642	Sequence
62.4	38	10	US-09-745-237A-3234	Sequence 3234, Ap	525	10.4	61.2	25	14	US-10-098-263B-112721	Sequence
62.4	38	10			c 526	10.4	61.2	25	14	US-10-098-263B-112722	Sequence

25	14	US-10-098-263B-113768	Sequence 113768,	c 600	10.2	60.0	17	10	US-09-817-879-3828	Sequence
25	14	US-10-098-263B-114170	Sequence 114170,	c 601	10.2	60.0	17	14	US-10-060-998-924	Sequence
25	14	US-10-098-263B-118332	Sequence 118332,	c 602	10.2	60.0	17	14	US-10-060-998-925	Sequence
25	14	US-10-098-263B-119425	Sequence 119425,	c 603	10.2	60.0	17	14	US-10-060-998-926	Sequence
25	14	US-10-098-263B-120505	Sequence 120505,	c 604	10.2	60.0	17	14	US-10-156-306-2808	Sequence
25	14	US-10-098-263B-120506	Sequence 120506,	c 605	10.2	60.0	18	15	US-10-297-068-1094	Sequence
25	14	US-10-098-263B-122705	Sequence 122705,	c 606	10.2	60.0	19	9	US-09-948-777-3	Sequence
25	14	US-10-098-263B-124534	Sequence 124534,	c 607	10.2	60.0	19	9	US-10-349-143-4438	Sequence
25	14	US-10-199-820-1	Sequence 1, Appli	c 608	10.2	60.0	20	10	US-09-931-375A-11	Sequence
25	15	US-10-464-952-95	Sequence 95, Appl	c 609	10.2	60.0	20	10	US-09-865-879-24	Sequence
26	12	US-10-451-892-4	Sequence 4, Appli	c 610	10.2	60.0	20	13	US-10-078-808-14	Sequence
27	10	US-09-911-904-78	Sequence 78, Appl	c 611	10.2	60.0	20	13	US-10-078-808-14	Sequence
30	9	US-09-843-245-13	Sequence 13, Appl	c 612	10.2	60.0	20	14	US-10-013-598-2	Sequence
31	9	US-09-801-274-233	Sequence 233, App	c 613	10.2	60.0	20	15	US-10-289-762-4378	Sequence
31	9	US-09-801-274-518	Sequence 518, App	c 614	10.2	60.0	21	13	US-10-016-283-19	Sequence
31	10	US-09-904-968A-5	Sequence 5, Appli	c 615	10.2	60.0	21	14	US-10-013-598-4	Sequence
31	14	US-10-245-802-4	Sequence 4, Appli	c 616	10.2	60.0	21	14	US-10-093-311-48	Sequence
31	14	US-10-128-463-11	Sequence 11, Appl	c 617	10.2	60.0	21	15	US-10-349-143-10728	Sequence
32	9	US-09-923-246-62	Sequence 62, Appl	c 618	10.2	60.0	22	14	US-10-079-528-3	Sequence
32	9	US-09-923-246-71	Sequence 71, Appl	c 619	10.2	60.0	22	14	US-10-339-740-109	Sequence
32	9	US-09-923-246-75	Sequence 75, Appl	c 620	10.2	60.0	23	15	US-10-321-033-449	Sequence
32	9	US-09-982-091A-10	Sequence 10, Appl	c 621	10.2	60.0	24	10	US-09-940-185-213	Sequence
32	12	US-10-270-176-68	Sequence 68, Appl	c 622	10.2	60.0	24	10	US-09-940-185-213	Sequence
32	14	US-10-295-723-62	Sequence 62, Appl	c 623	10.2	60.0	24	10	US-09-902-176A-27	Sequence
32	14	US-10-295-723-71	Sequence 71, Appl	c 624	10.2	60.0	24	14	US-10-085-906-536	Sequence
32	14	US-10-295-723-75	Sequence 75, Appl	c 625	10.2	60.0	24	14	US-10-288-104-23	Sequence
32	14	US-10-282-622-22	Sequence 22, Appl	c 626	10.2	60.0	24	14	US-10-168-445-8	Sequence
33	14	US-10-223-646-21	Sequence 21, Appl	c 627	10.2	60.0	24	14	US-10-084-839-3687	Sequence
34	9	US-09-996-140-20	Sequence 20, Appl	c 628	10.2	60.0	24	14	US-10-084-839-3687	Sequence
34	15	US-10-421-138A-20	Sequence 20, Appl	c 629	10.2	60.0	25	9	US-09-866-108-15374	Sequence
35	14	US-10-004-551-49	Sequence 49, Appl	c 630	10.2	60.0	25	9	US-09-866-108-15374	Sequence
36	9	US-09-966-955A-51	Sequence 51, Appl	c 631	10.2	60.0	25	9	US-09-866-108-15375	Sequence
41	14	US-10-224-683-105	Sequence 105, App	c 632	10.2	60.0	25	9	US-09-866-108-15376	Sequence
47	15	US-10-349-143-221	Sequence 221, App	c 633	10.2	60.0	25	9	US-09-866-108-15377	Sequence
47	15	US-10-349-143-1315	Sequence 1315, Ap	c 634	10.2	60.0	25	9	US-09-866-108-15377	Sequence
47	15	US-10-349-143-2778	Sequence 2778, Ap	c 635	10.2	60.0	25	9	US-09-866-108-15379	Sequence
50	15	US-10-131-827-1331	Sequence 1331, Ap	c 636	10.2	60.0	25	9	US-09-866-108-15380	Sequence
50	15	US-10-131-827-2434	Sequence 2434, Ap	c 637	10.2	60.0	25	9	US-09-866-108-15381	Sequence
50	15	US-10-131-827-4839	Sequence 4839, Ap	c 638	10.2	60.0	25	9	US-09-866-108-15382	Sequence
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51	10	US-09-963-761B-20	Sequence 20, Appl	c 640	10.2	60.0	25	9	US-09-851-501-27	Sequence
57	9	US-09-923-246-65	Sequence 65, Appl	c 641	10.2	60.0	25	10	US-09-883-152-84	Sequence
57	14	US-10-295-723-65	Sequence 65, Appl	c 642	10.2	60.0	25	10	US-09-940-185-4194	Sequence
57	15	US-10-027-632-175875	Sequence 175875,	c 643	10.2	60.0	25	14	US-10-142-722-27	Sequence
57	15	US-10-027-632-175882	Sequence 175882,	c 644	10.2	60.0	25	14	US-10-142-722-27	Sequence
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17	10	US-09-877-478-1932	Sequence 1922, Ap	c 667	10.2	60.0	25	14	US-10-098-263B-29953	Sequence
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17	10	US-09-740-332-3828	Sequence 3828, Ap	c 669	10.2	60.0	25	14	US-10-098-263B-37287	Sequence
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## ALIGNMENTS

4 Application US/10351157  
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 recher, Cindy A.  
 ao, Zeren  
 uijper, Joseph L.  
 asovich, Maria M.  
 rant, Francis J.  
 reenell, Scott R.  
 hitmore, Theodore E.  
 ammond, Angela K.  
 o. US20030215838A1ak, Julia E.  
 ross, Jane A.  
 illon, Stacey R.  
 NITION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS  
 E: 02-02  
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 G DATE: 2003-01-21  
 TION NUMBER: US 60/435,361  
 DATE: 2002-12-19  
 TION NUMBER: US 60/389,108  
 DATE: 2002-06-14  
 TION NUMBER: US 60/350,325  
 DATE: 2002-01-18  
 ID NOS: 183  
 tSEQ for Windows Version 4.0

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 Sequence 51, Appl  
 Sequence 9, Appl  
 Sequence 17, Appl  
 Sequence 104, Appl  
 Sequence 104, Appl  
 Sequence 56, Appl  
 Sequence 106, Appl  
 Sequence 106, Appl  
 Sequence 3804, Ap  
 Sequence 40, Appl  
 Sequence 178, Appl  
 Sequence 178, Appl  
 Sequence 1646, Ap  
 Sequence 1175, Ap  
 Sequence 1266, Ap  
 Sequence 6440, Ap  
 Sequence 6638, Ap  
 Sequence 6830, Ap  
 Sequence 7028, Ap  
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 ; Publication No. US20040006218A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Griffiths, R.  
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and po.  
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for  
 ; FILE REFERENCE: 9710-003-999  
 ; CURRENT APPLICATION NUMBER: US/10/289,762  
 ; CURRENT FILING DATE: 2003-03-27  
 ; NUMBER OF SEQ ID NOS: 6849  
 ; SEQ ID NO 5825  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Chlamydia pneumoniae  
 US-10-289-762-5825  
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 Best Local Similarity 93.3%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0;  
 QY 1 CGAGTGAAGATCCCC 15  
 Db 17 CGAATGAAGATCCCC 3

RESULT 3  
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 ; Publication No. US20030104410A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mittman, Michael  
 ; TITLE OF INVENTION: Human Microarray  
 ; FILE REFERENCE: 3118.1  
 ; CURRENT APPLICATION NUMBER: US/10/098,263B  
 ; CURRENT FILING DATE: 2003-01-08  
 ; PRIOR APPLICATION NUMBER: 60/276,759  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 131066  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 121677  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-121677  
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 Best Local Similarity 93.3%; Pred. No. 1.2e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0;  
 QY 1 CGAGTGAAGATCCCC 15  
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RESULT 4  
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 ; Sequence 14835, Application US/10098263B

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. US20030104410A1
tman, Michael
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TION NUMBER: US/10/098,263B
DATE: 2003-01-08
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DATE: 2001-03-16
ID NOS: 131066
:array Probe Sequence Listing Generator V 1.1
}

75.3%; Score 12.8; DB 14; Length 25;
ilarity 87.5%; Pred. No. 2.6e+03;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCCT 16
|||||
AGTGAAGAACCTCT 23

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Application US/10098263B
US20030104410A1
TION:
tman, Michael
TION: Human Microarray
3: 3118.1
TION NUMBER: US/10/098,263B
DATE: 2003-01-08
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
:array Probe Sequence Listing Generator V 1.1
}

75.3%; Score 12.8; DB 14; Length 25;
ilarity 87.5%; Pred. No. 2.6e+03;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAAGATCCCT 16
|||||
GTGAAGAACCTCT 16

404
Application US/10098263B
US20030104410A1
TION:
tman, Michael
TION: Human Microarray
3: 3118.1
TION NUMBER: US/10/098,263B
DATE: 2003-01-08
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
:array Probe Sequence Listing Generator V 1.1
}

o sapien
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US-10-098-263B-60404

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Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCT 16
|||||
Db 8 CGAGTGAAGTCCCT 23

RESULT 7
US-10-098-263B-66622
; Sequence 66622, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 66622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-66622

Query Match 75.3%; Score 12.8; DB 14; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCT 16
|||||
Db 8 CGAGTGAAGTCCCT 23

RESULT 8
US-10-098-263B-109878/c
; Sequence 109878, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 109878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-109878

Query Match 75.3%; Score 12.8; DB 14; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCT 16
|||||
Db 16 CGAGTGAAGTCCCT 1

RESULT 9
US-10-131-827-934
; Sequence 934, Application US/10131827
; Publication No. US20040009479A1
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Application US/08464363  
US20030035815A1  
INVENTOR: Rogers, Bruce L.

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1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
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1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

UTION: Computer Generated Probe Sequence.

RESULT 17  
US-09-825-805-264  
Sequence 264, Application US/09825805  
Publication No. US20030004122A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.

Beigelman, Leo  
 Beaudry, Amber  
 Karpeisky, Alex  
 Adamic, Jasenka Matulic  
 Sweedler, Dave  
 Zinnen, Shawn  
 TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides  
 FILE REFERENCE: MBH00-831-F (400/009)  
 PUBLICATION NO. US20030004122A1  
 APPLICATION NO. US/09/825,805  
 CURRENT FILING DATE: 2001-09-27  
 PRIOR APPLICATION NUMBER: 09/476,387  
 PRIOR FILING DATE: 1999-12-30  
 PRIOR APPLICATION NUMBER: 09/474,432  
 PRIOR FILING DATE: 1999-12-29  
 PRIOR APPLICATION NUMBER: 09/301,511  
 PRIOR FILING DATE: 1999-04-28  
 PRIOR APPLICATION NUMBER: 09/186,675  
 PRIOR FILING DATE: 1998-11-04  
 PRIOR APPLICATION NUMBER: 09/083,727  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/064,866  
 PRIOR FILING DATE: 1997-11-05  
 NUMBER OF SEQ ID NOS: 1558  
 SOFTWARE: Patent in version 3.0  
 SEQ ID NO 1558

## Artificial Sequence

NAME: Description of Artificial Sequence: Enzymatic Nucleic Acid

1..(4)

NAME: Phosphorothioate 3'-Internucleotide Linkage

1..(7)

NAME: 2'-O-Methyl

1..(15)

NAME: 2'-O-Methyl

1..(19)

NAME: 2'-O-Methyl

1..(24)

NAME: 2'-O-Methyl

1..(27)

NAME: 2'-O-Methyl

1..(36)

NAME: 2'-O-Methyl

1..(17)

NAME: 2'-deoxy-2'-amino

1..(28)

NAME: 2'-deoxy-2'-amino

1..(37)

NAME: n stands for inverted deoxybasic derivative

64

Query Match 71.8%; Score 12.2; DB 10; Length 37;  
 Best Local Similarity 58.8%; Pred. No. 5.8e+03;  
 Matches 10; Conservative 4; Mismatches 3; Indels 0;

1..(17)

1..(33)

1..(33)

RESULT 18  
 US-09-825-805-1198  
 ; Sequence 1198, Application US/09825805  
 ; Publication No. US20030004122A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Beigelman, Leo  
 ; APPLICANT: Beaudry, Amber  
 ; APPLICANT: Karpeisky, Alex  
 ; APPLICANT: Adamic, Jasenka Matulic  
 ; APPLICANT: Sweedler, Dave  
 ; APPLICANT: Zinnen, Shawn  
 ; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation  
 ; FILE REFERENCE: MBH00-831-F (400/009)  
 ; CURRENT APPLICATION NUMBER: US/09/825,805  
 ; CURRENT FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: 09/578,223  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 09/476,387  
 ; PRIOR FILING DATE: 1999-12-30  
 ; PRIOR APPLICATION NUMBER: 09/474,432  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: 09/301,511  
 ; PRIOR FILING DATE: 1999-04-28  
 ; PRIOR APPLICATION NUMBER: 09/186,675  
 ; PRIOR FILING DATE: 1998-11-04  
 ; PRIOR APPLICATION NUMBER: 60/083,727  
 ; PRIOR FILING DATE: 1998-04-29  
 ; PRIOR APPLICATION NUMBER: 60/064,866  
 ; PRIOR FILING DATE: 1997-11-05  
 ; NUMBER OF SEQ ID NOS: 1558  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 1198  
 ; LENGTH: 38  
 ; TYPE: RNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymat  
 US-09-825-805-1198

Query Match 71.8%; Score 12.2; DB 10; Length 38;  
 Best Local Similarity 58.8%; Pred. No. 5.8e+03;  
 Matches 10; Conservative 4; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 17

DB 18 CGAGUCAAGGUCUCCU 34

## RESULT 19

US-09-825-805-1256  
 ; Sequence 1256, Application US/09825805  
 ; Publication No. US20030004122A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Beigelman, Leo  
 ; APPLICANT: Beaudry, Amber  
 ; APPLICANT: Karpeisky, Alex  
 ; APPLICANT: Adamic, Jasenka Matulic  
 ; APPLICANT: Sweedler, Dave  
 ; APPLICANT: Zinnen, Shawn  
 ; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation  
 ; FILE REFERENCE: MBH00-831-F (400/009)  
 ; CURRENT APPLICATION NUMBER: US/09/825,805  
 ; CURRENT FILING DATE: 2001-09-27  
 ; PRIOR APPLICATION NUMBER: 09/578,223  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 09/476,387  
 ; PRIOR FILING DATE: 1999-12-30  
 ; PRIOR APPLICATION NUMBER: 09/474,432  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: 09/301,511  
 ; PRIOR FILING DATE: 1999-04-28

AGTGAAGATCCCCTT 17  
||: ||| : | | : :  
AGUCAAGGUCUCCU 34

```

; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic
US-09-730-289B-2852

```



1 09:38:23 2004

us-10-090-326-17.max.rnpb

71.8%; Score 12.2; DB 10; Length 38;  
Similarity 58.8%; Pred. No. 5.8e+03;  
Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
GAGTGAAGATCCCTT 17  
||||:||||:|  
GAGUCAAGGUCUCCU 34

4834  
; Application US/09780533A  
; Publication No. US2003006611A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Chowrira, Bharat  
; APPLICANT: Haerberli, Pete  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene  
; FILE REFERENCE: MBH00.878-A (400/011)  
; CURRENT APPLICATION NUMBER: US/09/780,533A  
; CURRENT FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 60/181,797  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 6679  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

Artificial Sequence

ARTON: Description of Artificial Sequence: Enzymatic Nucleic Acid  
1834

71.8%; Score 12.2; DB 10; Length 38;  
Similarity 58.8%; Pred. No. 5.8e+03;  
Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
GAGTGAAGATCCCTT 17  
||||:||||:|  
GAGUCAAGGUCUCCU 34

29  
; Application US/09776474  
; Publication No. US20030087847A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Koehler, Robert  
; APPLICANT: Holman, Patricia  
; APPLICANT: Attaeey, Ali  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK1)  
; FILE REFERENCE: MBH00-955-A (400/008)  
; CURRENT APPLICATION NUMBER: US/09/776,474  
; CURRENT FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 60/179,983  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 2992  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

Artificial Sequence

ARTON: Description of Artificial Sequence: Nucleic Acid  
29

Query Match 71.8%; Score 12.2; DB 10; Length 38;  
Best Local Similarity 58.8%; Pred. No. 5.8e+03;  
Matches 10; Conservative 4; Mismatches 3; Indels 0;  
QY 1 CGAGTGAAGATCCCTT 17  
||||:||||:|  
Db 18 CGAGUCAAGGUCUCCU 34

RESULT 25  
US-09-930-423-3137  
; Sequence 3137, Application US/09930423  
; Publication No. US20030092003A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Blatt, Larry  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzh  
; FILE REFERENCE: MBH00.918-A 400/027  
; CURRENT APPLICATION NUMBER: US/09/930,423  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 4553  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 3137  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymat  
US-09-930-423-3137

Query Match 71.8%; Score 12.2; DB 10; Length 38;  
Best Local Similarity 58.8%; Pred. No. 5.8e+03;  
Matches 10; Conservative 4; Mismatches 3; Indels 0;  
QY 1 CGAGTGAAGATCCCTT 17  
||||:||||:|  
Db 18 CGAGUCAAGGUCUCCU 34

RESULT 26  
US-09-792-818-1504  
; Sequence 1504, Application US/09792818  
; Publication No. US20030134806A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: Von Carlowitz, Ira  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Hamblin, Paul  
; APPLICANT: Ellis, Jonathan  
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-  
; FILE REFERENCE: MBH00-901-A (400/013)  
; CURRENT APPLICATION NUMBER: US/09/792,818  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 2304  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 1504  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymati  
US-09-792-818-1504

Query Match 71.8%; Score 12.2; DB 10; Length 38;  
Best Local Similarity 58.8%; Pred. No. 5.8e+03;  
Matches 10; Conservative 4; Mismatches 3; Indels 0;  
QY 1 CGAGTGAAGATCCCTT 17  
||||:||||:|  
Db 18 CGAGUCAAGGUCUCCU 34

137 Application US/09745237A  
 . US20030143708A1  
 ATION: bozyme Pharmaceuticals, Inc.  
 .latt, Larry  
 McSwiggen, Jim  
 NTION: Method and Reagent for the Treatment of Alzheimer's Disease  
 E: 400/007 (MEH800-918-A)  
 CATION NUMBER: US/09/745,237A  
 G DATE: 2002-04-15  
 ID NOS: 4550  
 entIn version 3.0

## tificial Sequence

ATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
 137

ilarity 71.8%; Score 12.2; DB 10; Length 38;  
 Conservative 4; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
 |||: |||: |||:  
 AGUAGAAGUCUCCU 34

3896  
 Application US/10098263B  
 . US20030104410A1

ATION: ttman, Michael  
 NTION: Human Microarray  
 E: 3118.1  
 CATION NUMBER: US/10/098,263B  
 G DATE: 2003-01-08  
 TION NUMBER: 60/276,759  
 DATE: 2001-03-16  
 ID NOS: 131066  
 roarray Probe Sequence Listing Generator V 1.1  
 5

no sapien  
 3896

70.6%; Score 12; DB 14; Length 25;  
 ilarity 100.0%; Pred. No. 7.4e+03;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3TGAAGATCC 13  
 |||: |||: |||:  
 3TGAAGATCC 15

22706/c  
 6, Application US/10098263B  
 . US20030104410A1

ATION: ttman, Michael  
 NTION: Human Microarray  
 E: 3118.1  
 CATION NUMBER: US/10/098,263B  
 3 DATE: 2003-01-08  
 TION NUMBER: 60/276,759

; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 131066  
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 ; SEQ ID NO 122706  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-10-098-263B-122706

Query Match 70.6%; Score 12; DB 14; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0;

Qy 3 AGTGAAGATCCC 14  
 |||: |||: |||:  
 Db 21 AGTGAAGATCCC 10

## RESULT 30

US-09-780-533A-2313/c  
 ; Sequence 2313, Application US/09780533A  
 ; Publication No. US20030060611A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 ; APPLICANT: Blatt, Larry  
 ; APPLICANT: McSwiggen, Jim  
 ; APPLICANT: Chowrira, Bharat  
 ; APPLICANT: Haeblerli, Pete  
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGC  
 ; FILE REFERENCE: MEH800,878-A (400/011)  
 ; CURRENT APPLICATION NUMBER: US/09/780,533A  
 ; CURRENT FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: US 60/181,797  
 ; PRIOR FILING DATE: 2000-02-11  
 ; NUMBER OF SEQ ID NOS: 6679  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2313  
 ; LENGTH: 17  
 ; TYPE: RNA  
 ; ORGANISM: Homo sapiens

US-09-780-533A-2313

Query Match 69.4%; Score 11.8; DB 10; Length 17;  
 Best Local Similarity 86.7%; Pred. No. 9.5e+03;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0;

Qy 3 AGTGAAGATCCCTT 17  
 |||: |||: |||:  
 Db 17 AATGAATATCCCTT 3

## RESULT 31

US-10-215-112-11134/c  
 ; Sequence 11134, Application US/10215112  
 ; Publication No. US20030082596A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Michael Mittmann  
 ; TITLE OF INVENTION: Method of Genetic Analysis of Probes:  
 ; FILE REFERENCE: Test3  
 ; CURRENT APPLICATION NUMBER: US/10/215,112  
 ; CURRENT FILING DATE: 2002-08-08  
 ; NUMBER OF SEQ ID NOS: 14936  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 11134  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Oligonucleotide  
 US-10-215-112-11134

Query Match 69.4%; Score 11.8; DB 14; Length 25;

```
ilarity 86.7%; Pred. No. 9.6e+03; Indels 0; Gaps 0;
Conservative 0; Mismatches 2; Indels 0;

FTGAAGATCCCCCTT 17
|||||
FTGAAGACCCCTTT 2

32155/c
3, Application US/10098263B
2, US20030104410A1
ATION:
ttman, Michael
ENTION: Human Microarray
E: 3118.1
G DATE: 2003-01-08
CATION NUMBER: US/10/098,263B
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
roarray Probe Sequence Listing Generator V 1.1
5

mo sapien
2155

ilarity 69.4%; Score 11.8; DB 14; Length 25;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCCC 15
|||||
AGGACGATCCCC 8

2783/c
, Application US/10098263B
, US20030104410A1
ATION:
ttman, Michael
ENTION: Human Microarray
E: 3118.1
G DATE: 2003-01-08
TION NUMBER: 60/276,759
DATE: 2001-03-16
ID NOS: 131066
roarray Probe Sequence Listing Generator V 1.1
3

mo sapien
2783

ilarity 69.4%; Score 11.8; DB 14; Length 25;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCCC 15
|||||
AGGACGATCCCC 9

8974
, Application US/10098263B
, US20030104410A1
ATION:
ttman, Michael
ENTION: Human Microarray
```

```
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 68974
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-68974

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 14; Length 25;
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 3 AGTGAAGATCCCCCTT 17
|||||
DB 7 AGTGAAGATCCGTT 21

RESULT 35
US-10-098-263B-121678
; Sequence 121678, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 121678
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-121678

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 14; Length 25;
Matches 13; Conservative 0; Mismatches 2; Indels 0;

QY 1 CGAGTGAAGATCCCC 15
|||||
DB 9 CGAGAAAGATCCCC 23

RESULT 36
US-10-046-232-6/c
; Sequence 6, Application US/10046232
; Publication No. US20030119099A1
; GENERAL INFORMATION:
; APPLICANT: Helmut SCHWAB
; APPLICANT: Anton GLIEDER
; APPLICANT: Christoph KRATKY
; APPLICANT: Ingrid BREVENY
; APPLICANT: Peter FOCHLAUER
; APPLICANT: Wolfgang SKRANC
; APPLICANT: Herbert MAYRHOFER
; APPLICANT: Irma WIRTH
; APPLICANT: Rudolf NEUHOFER
; APPLICANT: Rodolfo BONA
; TITLE OF INVENTION: New genes containing a DNA sequence coding fo
; TITLE OF INVENTION: recombinant proteins derived therefrom and h
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 2001-1882A/LC/01553
; CURRENT APPLICATION NUMBER: US/10/046,232
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: A60/2001
```

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us-10-090-326-17.max.rnpb

DATE: 2001-01-16  
TION NUMBER: A523/2001  
DATE: 2001-04-03  
ID NOS: 24  
antIn Ver. 2.1

ificial Sequence

ATION: Description of the artificial sequence: Synthetic oligonucleotide

69.4%; Score 11.8; DB 14; Length 33;  
ilarity 86.7%; Pred. No. 9.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TCAGATCCCTT 17  
|||||  
AGAGATCTCTT 16

/c  
pplication US/10400377  
. US20030162949A1  
TION:  
x III, George N  
older Biotechnology, Inc.  
TION: Derivatives of Growth Hormone and Related Proteins  
3: 4152-1-PUS  
TION NUMBER: US/10/400,377  
3 DATE: 2003-03-26  
TION NUMBER: US/09/462,941  
DATE: 2000-01-14  
TION NUMBER: 60/052,516  
DATE: 1997-07-14  
ID NOS: 41  
antIn Ver. 2.0

tificial Sequence

ATION: Description of Artificial Sequence:PCR Primer

69.4%; Score 11.8; DB 14; Length 33;  
ilarity 86.7%; Pred. No. 9.7e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCCC 15  
|||||  
AGTGAGGATCCCC 2

/c  
pplication US/10400708  
US20030166865A1  
TION:  
x III, George N  
older Biotechnology, Inc.  
TION: Derivatives of Growth Hormone and Related Proteins  
8: 4152-1-PUS  
TION NUMBER: US/10/400,708  
3 DATE: 2003-03-26  
TION NUMBER: US/09/462,941  
DATE: 2000-01-14  
TION NUMBER: 60/052,516  
DATE: 1997-07-14  
ID NOS: 41  
antIn Ver. 2.0

; SEQ ID NO 25  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PCR Primer  
US-10-400-708-25

Query Match 69.4%; Score 11.8; DB 14; Length 33;  
Best Local Similarity 86.7%; Pred. No. 9.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

Qy 1 CGAGTGAAGATCCCC 15  
Db 16 CTAGTGAGGATCCCC 2

RESULT 39  
US-10-298-148-25/c  
; Sequence 25, Application US/10298148  
; Publication No. US20030171284A1  
; GENERAL INFORMATION:  
; APPLICANT: Cox III, George N  
; APPLICANT: Bolder Biotechnology, Inc.  
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Pro  
; FILE REFERENCE: 4152-1-PUS  
; CURRENT APPLICATION NUMBER: US/10/298,148  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US/09/462,941  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/052,516  
; PRIOR FILING DATE: 1997-07-14  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PCR Primer  
US-10-298-148-25

Query Match 69.4%; Score 11.8; DB 14; Length 33;  
Best Local Similarity 86.7%; Pred. No. 9.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

Qy 1 CGAGTGAAGATCCCC 15  
Db 16 CTAGTGAGGATCCCC 2

RESULT 40  
US-10-112-267-114/c  
; Sequence 114, Application US/10112267  
; Publication No. US20030068678A1  
; GENERAL INFORMATION:  
; APPLICANT: Botstein, David A.  
; APPLICANT: Cohen, Robert  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Lawrence, David A.  
; APPLICANT: Levine, Arnold J.  
; APPLICANT: Pennica, Diane  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING  
; FILE REFERENCE: P1176R2  
; CURRENT APPLICATION NUMBER: US/10/112,267  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,1  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,71

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us-10-090-326-17.max.rnpb

DATE: EARLIER FILING DATE: 1997-10-29  
ATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612  
DATE: EARLIER FILING DATE: 1998-02-04  
ATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695  
DATE: EARLIER FILING DATE: 1998-04-14  
ID NOS: 156

ntificial sequence  
sc\_feature  
-50  
ATION: Sequence is synthesized.  
.4

69.4%; Score 11.8; DB 14; Length 50;  
ilarity 86.7%; Pred. No. 9.8e+03; Indels 0; Gaps 0;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

HAGTGAAGATCCCC 15  
|||||  
HAGTGGAGACCCC 35

;79/c  
Application US/10131827  
. US20040009479A1  
ATION:  
hlgemuth, Jay  
ry, Kirk  
oodward, Robert  
y, Ngoc  
ATION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
ITION: CHRONIC INFLAMMATORY DISEASES  
E: 506612000120  
ATION NUMBER: US/10/131,827  
IG DATE: 2002-09-06  
ATION NUMBER: US 10/006,290  
DATE: 2001-10-22  
ATION NUMBER: US 60/296,764  
DATE: 2001-06-08  
ID NOS: 9090  
entIn version 3.1

omo sapiens  
.79

69.4%; Score 11.8; DB 15; Length 50;  
ilarity 86.7%; Pred. No. 9.8e+03; Indels 0; Gaps 0;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

HTGAAGATCCCCCTT 17  
|||||  
HTGAAGAAGCCTT 33

;265/c  
Application US/08781986A  
. US20030054436A1  
INATION:  
Charles Kunsch  
VENTION: Staphylococcus aureus Polynucleotides and Sequences  
SEQUENCES: 5255  
NCE ADDRESS:  
: Human Genome Sciences, Inc.  
9410 Key West Avenue  
ckville  
aryland

COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248PP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 2265:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 52 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-2265

Query Match 69.4%; Score 11.8; DB 8; Length 52;  
Best Local Similarity 86.7%; Pred. No. 9.8e+03; Indels 0;  
Matches 13; Conservative 0; Mismatches 2; Indels 0;

OY 3 AGTGAAGATCCCCCTT 17  
|||||  
DB 39 AGTTAAGCTCCCCCTT 25

RESULT 43  
US-09-908-975-8556  
Sequence 8556, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Liat  
APPLICANT: FAIGLER, Simchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRI  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 8556  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-8556

Query Match 69.4%; Score 11.8; DB 10; Length 60;  
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Matches 13; Conservative 0; Mismatches 2; Indels 0;

OY 2 GAGTGAAGATCCCCCTT 16  
|||||  
DB 33 GAATGAGGATCCCCCTT 47

09:38:23 2004

us-10-090-326-17.max.rnpb

73/c  
Application US/09908975  
US20030165843A1  
TION:  
SHAN, Avi  
SSERMAN, Alon  
NTZ, Eli  
NTZ, Liat  
IGLER, Simchon  
TION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
TION: THAT POPULATE A TRANSCRIPTOME  
: 36688-0005  
ATION NUMBER: US/09/908,975  
DATE: 2001-07-20  
ION NUMBER: US 60/287,724  
ATE: 2001-05-02  
ION NUMBER: US 60/221,607  
ATE: 2000-07-28  
ID NOS: 32337  
ntIn version 3.0

o sapiens  
73  
69.4%; Score 11.8; DB 10; Length 60;  
larity 86.7%; Pred. No. 9.8e+03;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GAAGATCCCGCTT 17  
| | | | | | | |  
GCAGATCCCGCTT 46

74/c  
Application US/09780533A  
US2003060611A1  
TION:  
Ozyme Pharmaceuticals, Inc.  
att, Larry  
Swiggen, Jim  
owrira, Bharat  
eberli, Pete  
TION: Method and Reagent for the Inhibition of NOGO Gene  
: MBHE00,878-A (400/011)  
ATION NUMBER: US/09/780,533A  
DATE: 2001-02-09  
ION NUMBER: US 60/181,797  
ATE: 2000-02-11  
ID NOS: 6679  
ntIn version 3.0

o sapiens  
74  
67.1%; Score 11.4; DB 10; Length 17;  
larity 92.3%; Pred. No. 1.6e+04;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AGATCCCGCTT 17  
| | | | | | | |  
ATATCCCGCTT 5

February 29, 2004, 13:43:02  
9 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

February 29, 2004, 08:43:19 ; Search time 1276.1 Seconds  
(without alignments)  
397.818 Million cell updates/sec

US-10-090-326-17

1 csgtgaagatccctt 17

IDENTITY NUC

3apop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 203984

length: 0

length: 60

Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

EST:\*

1: em\_estba:\*

2: em\_esthm:\*

3: em\_estm:\*

4: em\_estm:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_estc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_man:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

is the number of results predicted by chance to have a  
er than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

# SUMMARIES

Query	Match	Length	DB	ID	Description
75.3	60	9	A1116273		A1116273 ucl17g10.r
71.8	52	10	BE321851		BE321851 NFO09F111
70.6	37	14	R37577		R37577 yd02a09.sl
69.4	49	12	BM862480		BM862480 mgcm003XC

AL763440	59	29	AL763440	69.4	11.8	69.4	59	29	AL763440
CB353581	60	14	CB353581	69.4	11.8	69.4	60	14	CB353581
AZ624452	47	28	AZ624452	67.1	11.4	67.1	47	28	AZ624452
AZ769807	57	28	AZ769807	67.1	11.4	67.1	57	28	AZ769807
TA122G04P	31	29	TA122G04P	65.9	11.2	65.9	31	29	TA122G04P
CG720952	35	29	CG720952	65.9	11.2	65.9	35	29	CG720952
AZ771147	43	28	AZ771147	65.9	11.2	65.9	43	28	AZ771147
BM395597	45	12	BM395597	65.9	11.2	65.9	45	12	BM395597
AA288062	49	9	AA288062	65.9	11.2	65.9	49	9	AA288062
BU605161	51	13	BU605161	65.9	11.2	65.9	51	13	BU605161
CNS07HSH	56	13	CNS07HSH	65.9	11.2	65.9	56	13	CNS07HSH
EX771762	58	28	EX771762	65.9	11.2	65.9	58	28	EX771762
BH910991	59	10	BH910991	65.9	11.2	65.9	59	10	BH910991
AW511427	53	9	AW511427	64.7	11	64.7	53	9	AW511427
AA466912	57	28	AA466912	64.7	11	64.7	57	28	AA466912
BH800373	59	29	BH800373	64.7	11	64.7	59	29	BH800373
AL767128	60	10	AL767128	64.7	11	64.7	60	10	AL767128
BF639034	22	28	BF639034	63.5	10.8	63.5	22	28	BF639034
AZ423553	29	28	AZ423553	63.5	10.8	63.5	29	28	AZ423553
AZ994980	36	12	AZ994980	63.5	10.8	63.5	36	12	AZ994980
BJ064687	38	29	BJ064687	63.5	10.8	63.5	38	29	BJ064687
HSMC39C10	40	29	HSMC39C10	63.5	10.8	63.5	40	29	HSMC39C10
AL947310	41	28	AL947310	63.5	10.8	63.5	41	28	AL947310
AZ598104	43	29	AZ598104	63.5	10.8	63.5	43	29	AZ598104
EX001610	44	13	EX001610	63.5	10.8	63.5	44	13	EX001610
EX625656	44	29	EX625656	63.5	10.8	63.5	44	29	EX625656
AL947311	46	9	AL947311	63.5	10.8	63.5	46	9	AL947311
AA410197	46	28	AA410197	63.5	10.8	63.5	46	28	AA410197
BH759458	46	29	BH759458	63.5	10.8	63.5	46	29	BH759458
EX285225	46	29	EX285225	63.5	10.8	63.5	46	29	EX285225
EX290413	47	29	EX290413	63.5	10.8	63.5	47	29	EX290413
AL952068	49	29	AL952068	63.5	10.8	63.5	49	29	AL952068
EX291286	50	9	EX291286	63.5	10.8	63.5	50	9	EX291286
AU103576	50	9	AU103576	63.5	10.8	63.5	50	9	AU103576
AU106261	52	9	AU106261	63.5	10.8	63.5	52	9	AU106261
AA795116	52	9	AA795116	63.5	10.8	63.5	52	9	AA795116
AV852627	53	9	AV852627	63.5	10.8	63.5	53	9	AV852627
AL944840	53	29	AL944840	63.5	10.8	63.5	53	29	AL944840
BH853866	54	28	BH853866	63.5	10.8	63.5	54	28	BH853866
AL940566	54	29	AL940566	63.5	10.8	63.5	54	29	AL940566
BM022920	55	12	BM022920	63.5	10.8	63.5	55	12	BM022920
AZ854808	55	28	AZ854808	63.5	10.8	63.5	55	28	AZ854808
AL944839	55	29	AL944839	63.5	10.8	63.5	55	29	AL944839
AZ821330	57	28	AZ821330	63.5	10.8	63.5	57	28	AZ821330
AA500076	58	9	AA500076	63.5	10.8	63.5	58	9	AA500076
AZ597097	58	28	AZ597097	63.5	10.8	63.5	58	28	AZ597097
AL753395	58	29	AL753395	63.5	10.8	63.5	58	29	AL753395
AZ487436	59	28	AZ487436	63.5	10.8	63.5	59	28	AZ487436
AI187871	46	9	AI187871	62.4	10.6	62.4	46	9	AI187871
CNS03V15	51	29	CNS03V15	62.4	10.6	62.4	51	29	CNS03V15
AA737190	52	9	AA737190	62.4	10.6	62.4	52	9	AA737190
AZ435804	54	28	AZ435804	62.4	10.6	62.4	54	28	AZ435804
AV833997	55	9	AV833997	62.4	10.6	62.4	55	9	AV833997
AV956623	55	9	AV956623	62.4	10.6	62.4	55	9	AV956623
BJ032890	56	12	BJ032890	62.4	10.6	62.4	56	12	BJ032890
AA896471	57	9	AA896471	62.4	10.6	62.4	57	9	AA896471
AY125858	57	10	AY125858	62.4	10.6	62.4	57	10	AY125858
AZ77527	57	28	AZ77527	62.4	10.6	62.4	57	28	AZ77527
BH218589	58	28	BH218589	62.4	10.6	62.4	58	28	BH218589
CF340173	19	14	CF340173	61.2	10.4	61.2	19	14	CF340173
AU253942	37	9	AU253942	61.2	10.4	61.2	37	9	AU253942
AZ429862	37	28	AZ429862	61.2	10.4	61.2	37	28	AZ429862
EX532099	39	29	EX532099	61.2	10.4	61.2	39	29	EX532099
AU252932	41	9	AU252932	61.2	10.4	61.2	41	9	AU252932
AI205721	43	9	AI205721	61.2	10.4	61.2	43	9	AI205721
AA429927	43	9	AA429927	61.2	10.4	61.2	43	9	AA429927
AI200861	46	9	AI200861	61.2	10.4	61.2	46	9	AI200861
N44633	47	14	N44633	61.2	10.4	61.2	47	14	N44633
AU254592	49	9	AU254592	61.2	10.4	61.2	49	9	AU254592
AA712026	52	9	AA712026	61.2	10.4	61.2	52	9	AA712026
BH629223	52	28	BH629223	61.2	10.4	61.2	52	28	BH629223
AZ810048	53	28	AZ810048	61.2	10.4	61.2	53	28	AZ810048

61.2	53	29	AL760562	AL760562 Arabidops	151	10	58.8	25	29	TA124C09P	AL465272
61.2	55	9	Al142674	Al142674 ok33g12.s	c 152	10	58.8	26	10	AW247005	AW247005
61.2	55	13	BQ622506	BQ622506 fch1c.pk0	c 153	10	58.8	26	10	AZ483929	AZ483929
61.2	56	14	CA796802	CA796802 Cac BL 38	c 154	10	58.8	31	28	BH906234	BH906234
61.2	56	28	BH864054	BH864054 SALK_0952	c 155	10	58.8	32	28	BH910754	BH910754
61.2	57	10	AW638114	AW638114 B166C09.w	c 156	10	58.8	37	9	AU255147	AU255147
61.2	57	28	BH911536	BH911536 SALK_0691	c 157	10	58.8	42	29	CG715948	CG715948
61.2	58	9	Al098692	Al098692 uh38g06.r	c 158	10	58.8	44	14	CF302318	CF302318
61.2	59	29	BK660118	BK660118 Arabidops	c 159	10	58.8	45	9	AV673231	AV673231
61.2	60	14	CD903182	CD903182 NISC gf05	c 160	10	58.8	49	12	BI906353	BI906353
61.2	60	14	CD903182	CD903182 G356_109G	c 161	10	58.8	49	29	CC889114	CC889114
61.2	60	28	BH631316	BH631316 1007081A0	c 162	10	58.8	50	9	AU102456	AU102456
60.0	23	28	BZ789371	BZ789371 2M0037L01	c 163	10	58.8	54	29	BX893743	BX893743
60.0	31	14	CF293938	CF293938 3ODGS--03	c 164	10	58.8	55	9	Al481901	Al481901
60.0	33	28	AZ304828	AZ304828 1M005018	c 165	10	58.8	55	28	CC019918	CC019918
60.0	33	29	TA82C04P	Al462237 T. brucei	c 166	10	58.8	57	9	AU259142	AU259142
60.0	34	28	BZ291017	BZ291017 SALK_1123	c 167	10	58.8	58	28	BZ593156	BZ593156
60.0	36	9	AV404101	AV404101 AV404101	c 168	9.8	57.6	22	14	L81203	L81203
60.0	36	12	BQ666024	BQ666024 BQ666024	c 169	9.8	57.6	22	28	AZ583839	AZ583839
60.0	36	28	BH910980	BH910980 SALK_0640	c 170	9.8	57.6	25	13	BQ589704	BQ589704
60.0	38	12	BQ79017	BQ79017 BQ79017	c 171	9.8	57.6	25	28	AZ810739	AZ810739
60.0	39	9	Al558069	Al558069 vw63e08.x	c 172	9.8	57.6	27	28	AZ406142	AZ406142
60.0	39	28	BZ767312	BZ767312 SALK_1386	c 173	9.8	57.6	28	29	TA38C12Q	TA38C12Q
60.0	40	14	D19983	D19983 HUMGS00949	c 174	9.8	57.6	29	28	BZ384399	BZ384399
60.0	42	29	BX535105	BX535105 Arabidops	c 175	9.8	57.6	31	29	BX534828	BX534828
60.0	43	14	T77974	T77974 yc97c11.r1	c 176	9.8	57.6	32	9	AV855414	AV855414
60.0	43	28	AZ833640	AZ833640 2M0115B23	c 177	9.8	57.6	34	14	CF542952	CF542952
60.0	43	29	BK656288	BK656288 Arabidops	c 178	9.8	57.6	34	14	BF971438	BF971438
60.0	44	28	BH910633	BH910633 SALK_0607	c 179	9.8	57.6	36	28	BZ762036	BZ762036
60.0	44	28	BZ289327	BZ289327 SALK_0227	c 180	9.8	57.6	36	9	AV833687	AV833687
60.0	45	28	BZ593250	BZ593250 SALK_0682	c 181	9.8	57.6	37	13	BQ595099	BQ595099
60.0	46	9	Al105291	Al105291 mp36g11.r	c 182	9.8	57.6	37	28	AZ601975	AZ601975
60.0	46	9	Al806198	Al806198 wf26c01.x	c 183	9.8	57.6	40	9	AA790820	AA790820
60.0	46	28	AZ313975	AZ313975 1M0030X06	c 184	9.8	57.6	40	14	H85898	H85898
60.0	47	12	BQ46987	BQ46987 BQ46987	c 185	9.8	57.6	40	14	N27080	N27080
60.0	47	28	BH910648	BH910648 SALK_0608	c 186	9.8	57.6	42	28	AZ977990	AZ977990
60.0	47	28	BH910666	BH910666 SALK_0609	c 187	9.8	57.6	43	28	BH644282	BH644282
60.0	47	28	BH910817	BH910817 SALK_0627	c 188	9.8	57.6	43	28	BZ766776	BZ766776
60.0	48	28	AZ777915	AZ777915 2M0012113	c 189	9.8	57.6	44	14	N47451	N47451
60.0	48	28	BH910669	BH910669 SALK_0610	c 190	9.8	57.6	44	28	AZ625682	AZ625682
60.0	49	14	H46153	H46153 ycl3e12.r1	c 191	9.8	57.6	45	29	AL758813	AL758813
60.0	50	9	Al104072	Al104072 AU104072	c 192	9.8	57.6	45	28	BH619838	BH619838
60.0	50	9	Al104439	Al104439 AU104439	c 193	9.8	57.6	46	9	Al787001	Al787001
60.0	51	12	BQ50851	BQ50851 BQ50851	c 194	9.8	57.6	46	9	AV833659	AV833659
60.0	51	28	AZ917636	AZ917636 1006001F1	c 195	9.8	57.6	46	28	AZ310504	AZ310504
60.0	51	29	Al941962	Al941962 Arabidops	c 196	9.8	57.6	47	28	AZ649857	AZ649857
60.0	52	10	BF634021	BF634021 NFO65G09D	c 197	9.8	57.6	47	29	DM545250	DM545250
60.0	52	14	CA850000	CA850000 k118b10.y	c 198	9.8	57.6	49	9	AA826426	AA826426
60.0	53	9	Al861663	Al861663 AL861663	c 199	9.8	57.6	49	9	Al282035	Al282035
60.0	53	9	AV954041	AV954041 AV954041	c 200	9.8	57.6	50	9	Al282035	Al282035
60.0	53	14	H46692	H46692 ycl7e10.r1	c 201	9.8	57.6	50	9	Al03668	Al03668
60.0	53	28	AZ773134	AZ773134 1M0584D03	c 202	9.8	57.6	50	9	Al06029	Al06029
60.0	53	28	BH910699	BH910699 SALK_0613	c 203	9.8	57.6	50	9	Al07888	Al07888
60.0	53	29	Al753444	Al753444 Arabidops	c 204	9.8	57.6	50	13	BQ286117	BQ286117
60.0	53	29	Al765905	Al765905 Arabidops	c 205	9.8	57.6	50	13	BQ625758	BQ625758
60.0	54	28	AZ310557	AZ310557 1M0025N03	c 206	9.8	57.6	50	14	CA771979	CA771979
60.0	55	9	Al976674	Al976674 cq04f06.s	c 207	9.8	57.6	50	14	CF290829	CF290829
60.0	55	9	Al173634	Al173634 AU173634	c 208	9.8	57.6	50	28	AZ492887	AZ492887
60.0	55	28	AZ923049	AZ923049 OsAc4-42	c 209	9.8	57.6	50	29	AL946817	AL946817
60.0	55	28	BQ5394	BQ5394 CSRL-61e3-u	c 210	9.8	57.6	51	10	BE968894	BE968894
60.0	55	29	BX893938	BX893938 Arabidops	c 211	9.8	57.6	51	29	DM545141	DM545141
60.0	56	28	BH911434	BH911434 SALK_0686	c 212	9.8	57.6	52	10	BE253310	BE253310
60.0	56	29	Al769755	Al769755 Arabidops	c 213	9.8	57.6	52	29	CG716123	CG716123
60.0	57	12	BM068905	BM068905 id70d02.x	c 214	9.8	57.6	52	29	CG726870	CG726870
60.0	57	28	AZ803892	AZ803892 2M0064F05	c 215	9.8	57.6	52	29	CG727207	CG727207
60.0	58	9	AA272215	AA272215 vb06g07.r	c 216	9.8	57.6	53	9	Al966527	Al966527
60.0	58	14	CF776309	CF776309 jaa18d03	c 217	9.8	57.6	53	9	AV528308	AV528308
60.0	58	28	AZ798644	AZ798644 2M0055L04	c 218	9.8	57.6	53	28	AZ834008	AZ834008
60.0	60	9	AU255977	AU255977 AU255977	c 219	9.8	57.6	53	28	AZ931440	AZ931440
60.0	60	13	BX688329	BX688329 BX688329	c 220	9.8	57.6	54	9	AV528109	AV528109
60.0	60	28	B35099	B35099 HS-1027-Al-	c 221	9.8	57.6	54	9	AV528227	AV528227
60.0	60	28	BH854821	BH854821 SALK_0884	c 222	9.8	57.6	54	10	BE315582	BE315582
60.0	60	29	BX654025	BX654025 Arabidops	c 223	9.8	57.6	54	29	CG727436	CG727436



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57.6	55	9	AI708934	AI708934 as96hl2.x	297	9.6	56.5	52	9	AI828877	AI828877
57.6	55	13	BX783328	BX783328	C 298	9.6	56.5	52	9	AA157685	AA157685
57.6	56	29	CC548632	CC548632 CH240 432	C 299	9.6	56.5	52	9	AU012544	AU012544
57.6	56	9	AI565568	AI565568 to16b11.x	C 300	9.6	56.5	52	13	BQ519736	BQ519736
57.6	56	12	BM516179	BM516179 kj7ad09.y	C 301	9.6	56.5	52	28	AZ660384	AZ660384
57.6	56	28	AZ467443	AZ467443 IM0278016	C 302	9.6	56.5	52	29	AL760643	AL760643
57.6	56	28	AZ576175	AZ576175 AST-TD1.1	C 303	9.6	56.5	52	29	BX661038	BX661038
57.6	57	9	AI363771	AI363771 qv79d06.x	C 304	9.6	56.5	53	28	AZ537388	AZ537388
57.6	57	10	BF636979	BF636979 NF048B11L	C 305	9.6	56.5	53	28	AZ576724	AZ576724
57.6	57	28	AZ537462	AZ537462 AST-2P046	C 306	9.6	56.5	53	29	CG785595	CG785595
57.6	57	28	AZ648926	AZ648926 IM0518623	C 307	9.6	56.5	53	29	CG892104	CG892104
57.6	57	28	AZ521243	AZ521243 1006029A0	C 308	9.6	56.5	53	29	AL754529	AL754529
57.6	57	28	B46831	B46831 HS-1066-A1-	C 309	9.6	56.5	53	29	AL771068	AL771068
57.6	57	29	BX547649	BX547649 Arabidops	C 310	9.6	56.5	53	29	BX289093	BX289093
57.6	58	9	AA904196	AA904196 OG20e04.s	C 311	9.6	56.5	53	29	BX893295	BX893295
57.6	58	9	AI368552	AI368552 QV62f02.x	C 312	9.6	56.5	53	29	AL454571	AL454571
57.6	58	9	AL966510	AL966510 AL966510	C 313	9.6	56.5	54	14	CB210770	CB210770
57.6	58	28	BH846480	BH846480 SALK_0083	C 314	9.6	56.5	54	29	BX004244	BX004244
57.6	58	29	BX535392	BX535392 Arabidops	C 315	9.6	56.5	54	29	BX651485	BX651485
57.6	59	12	BI837573	BI837573 603086946	C 316	9.6	56.5	55	9	AI736052	AI736052
57.6	59	28	AZ397241	AZ397241 IM0162E12	C 317	9.6	56.5	55	28	AZ514470	AZ514470
57.6	59	28	AZ604999	AZ604999 IM0426C09	C 318	9.6	56.5	55	28	AZ789273	AZ789273
57.6	60	10	BZ318074	BZ318074 NF052F01L	C 319	9.6	56.5	56	28	AZ419420	AZ419420
57.6	60	28	AZ812565	AZ812565 2M0079M17	C 320	9.6	56.5	56	28	AZ818221	AZ818221
57.6	60	28	AZ920346	AZ920346 IM06019E0	C 321	9.6	56.5	56	28	HSMC43C10	HSMC43C10
57.6	60	29	CNS028B0	AL185733 Tetraodon	C 322	9.6	56.5	57	29	AZ442356	AZ442356
56.5	21	12	BX398924	BM398924 5009-0-50	C 323	9.6	56.5	57	29	CG1713052	CG1713052
56.5	24	28	AZ505483	AZ505483 IM0346M07	C 324	9.6	56.5	58	9	AI427915	AI427915
56.5	25	28	TA202D06Q	AL477040 T. brucei	C 325	9.6	56.5	58	9	AA500946	AA500946
56.5	25	28	AZ767918	AZ767918 IM0567B09	C 326	9.6	56.5	58	9	AA520032	AA520032
56.5	31	28	CO60438	AL484616 T. brucei	C 327	9.6	56.5	58	9	AA520032	AA520032
56.5	31	29	AL767149	CC060438 EY01840-5	C 328	9.6	56.5	58	28	AZ343886	AZ343886
56.5	32	13	BX567530	AL767149 Arabidops	C 329	9.6	56.5	58	28	AZ921746	AZ921746
56.5	32	14	L81205	BX567530 BX567530	C 330	9.6	56.5	58	29	CG1716924	CG1716924
56.5	34	9	AI354718	L81205 SCRAP0212	C 331	9.6	56.5	59	9	AI340686	AI340686
56.5	34	28	BH901339	AI354718 qc54h12.x	C 332	9.6	56.5	59	28	AZ769442	AZ769442
56.5	34	29	TA244E09Q	BH901339 SALK_0745	C 333	9.6	56.5	59	29	AL943603	AL943603
56.5	35	28	AZ19308	AL482376 T. brucei	C 334	9.6	56.5	59	29	CNS04CWT	CNS04CWT
56.5	38	28	BH906172	AZ19308 IM0038A21	C 335	9.6	56.5	60	10	BE323655	BE323655
56.5	38	29	BX658508	BH906172 SALK_1093	C 336	9.6	56.5	60	12	BP136318	BP136318
56.5	39	29	AL754526	BX658508 Arabidops	C 337	9.6	56.5	60	14	CA903323	CA903323
56.5	40	9	AA878693	AL754526 Arabidops	C 338	9.6	56.5	60	28	AZ335850	AZ335850
56.5	40	12	BJ152894	AA878693 OJ23b12.s	C 339	9.6	56.5	60	28	AZ424905	AZ424905
56.5	40	12	BJ047687	BJ152894 602918054	C 340	9.6	56.5	60	29	CG780197	CG780197
56.5	40	28	BZ597447	BJ047687 BJ047687	C 341	9.4	55.3	60	28	AZ482011	AZ482011
56.5	40	29	BX891603	BZ597447 SALK_1050	C 342	9.4	55.3	60	14	CF332861	CF332861
56.5	42	28	AQ073571	BX891603 Arabidops	C 343	9.4	55.3	60	28	AZ364143	AZ364143
56.5	42	29	CG776618	AQ073571 EP(2)2421	C 344	9.4	55.3	60	13	C53818	C53818
56.5	44	28	BZ768692	CG776618 1123002C0	C 345	9.4	55.3	60	28	BH811445	BH811445
56.5	45	29	AL754525	BZ768692 SALK_1405	C 346	9.4	55.3	61	13	BX564106	BX564106
56.5	46	14	H55376	AL754525 Arabidops	C 347	9.4	55.3	61	13	T77145	T77145
56.5	46	28	AZ330759	H55376 CHR220315 C	C 348	9.4	55.3	61	13	AU257374	AU257374
56.5	46	28	AZ330759	AZ330759 IM0056108	C 349	9.4	55.3	61	13	CG780197	CG780197
56.5	46	29	AL765547	AL765547 Arabidops	C 350	9.4	55.3	62	28	AZ659027	AZ659027
56.5	46	29	TA169H01P	AL765547 T. brucei	C 351	9.4	55.3	62	28	BZ380116	BZ380116
56.5	47	14	CB223045	AL769552 T. brucei	C 352	9.4	55.3	62	14	N73483	N73483
56.5	47	28	BH856951	CB223045 1JEJ18H8	C 353	9.4	55.3	62	28	BH908490	BH908490
56.5	47	29	AL760555	BH856951 SALK_0775	C 354	9.4	55.3	62	14	CF044574	CF044574
56.5	47	29	TA122802P	AL760555 Arabidops	C 355	9.4	55.3	62	28	AZ460813	AZ460813
56.5	48	14	CB210229	AL462628 T. brucei	C 356	9.4	55.3	62	14	CA899931	CA899931
56.5	49	9	AI829100	CB210229 OML00509	C 357	9.4	55.3	62	28	AZ810846	AZ810846
56.5	49	9	AV832597	AI829100 wj38f09.x	C 358	9.4	55.3	62	28	BH792213	BH792213
56.5	49	12	BM129399	AV832597 AV832597	C 359	9.4	55.3	62	28	AG222684	AG222684
56.5	49	12	BM129543	BM129399 if21g08.x	C 360	9.4	55.3	62	10	BE313345	BE313345
56.5	50	9	AU103642	BM129543 if23h12.x	C 361	9.4	55.3	62	10	AA237443	AA237443
56.5	50	9	AU108023	AU103642 AU103642	C 362	9.4	55.3	62	10	BE272089	BE272089
56.5	50	28	AZ427184	AU108023 AU108023	C 363	9.4	55.3	62	28	BH624185	BH624185
56.5	50	29	AL752296	AZ427184 IM0209D02	C 364	9.4	55.3	62	28	BZ767723	BZ767723
56.5	50	29	BX535832	AL752296 Arabidops	C 365	9.4	55.3	62	28	AZ771208	AZ771208
56.5	51	28	BH904891	BX535832 Arabidops	C 366	9.4	55.3	62	28	CG801983	CG801983
56.5	51	29	TA130809P	BH904891 SALK_1052	C 367	9.4	55.3	62	28	AZ810878	AZ810878
56.5	52	9	AA912652	AL464091 T. brucei	C 368	9.4	55.3	62	28	AZ822468	AZ822468
56.5	52	9	AA938048	AA912652 oii8G04.s	C 369	9.4	55.3	62	28	BH640418	BH640418
56.5	52	9	AA938048	AA938048 ny32d06.s	C 369	9.4	55.3	62	14	T63717	T63717

55.3	43	28	AZ443922	1M0238N08	443	9.4	55.3	56	12	BM318931	BM318931
55.3	43	28	AZ778245	AZ778245 2M0013O22	C 444	9.4	55.3	56	28	AZ445458	AZ445458
55.3	43	28	BV589387	BV589387 3590 1.69	445	9.4	55.3	56	29	LBFA031H02	LBFA031H02
55.3	44	9	AV834222	AV834222 AV834222	C 446	9.4	55.3	57	9	AA911978	AA911978
55.3	44	9	AV955705	AV955705 AV955705	447	9.4	55.3	57	12	BM283095	BM283095
55.3	44	28	AZ826118	AZ826118 2M0101009	448	9.4	55.3	57	28	BH223365	BH223365
55.3	44	28	BH791831	BH791831 SALK 0615	449	9.4	55.3	57	28	BH636414	BH636414
55.3	44	28	BH791833	BH791833 SALK 0615	450	9.4	55.3	57	28	BH866260	BH866260
55.3	45	13	C01390	C01390 HUMGS000837	C 451	9.4	55.3	57	29	AL937738	AL937738
55.3	45	28	BH17077	BH17077 SALK 0037	452	9.4	55.3	58	9	AI132163	AI132163
55.3	45	28	BZ383056	BZ383056 SALK 1193	453	9.4	55.3	58	9	AI159065	AI159065
55.3	45	28	BZ766643	BZ766643 SALK 11376	C 454	9.4	55.3	58	9	AI302327	AI302327
55.3	45	29	AL938540	AL938540 Arabidops	455	9.4	55.3	58	9	AA460339	AA460339
55.3	45	29	TA65A10Q	TA65A10Q Arabidops	C 456	9.4	55.3	58	12	BJ078599	BJ078599
55.3	46	9	AA826705	AA826705 nr5B10.s	457	9.4	55.3	58	12	BP137275	BP137275
55.3	46	28	BH897333	BH897333 3526 1.7	458	9.4	55.3	58	14	CA844500	CA844500
55.3	46	28	CC178445	CC178445 XD060 Bay	C 459	9.4	55.3	58	14	H25069	H25069
55.3	48	28	BH906776	BH906776 SALK 0358	460	9.4	55.3	58	28	AZ776004	AZ776004
55.3	49	9	AA986590	AA986590 uc81G03.y	461	9.4	55.3	58	28	BH910745	BH910745
55.3	49	9	AI126696	AI126696 qb94B03.x	462	9.4	55.3	58	29	CC889005	CC889005
55.3	49	28	AZ771132	AZ771132 1M0573002	C 463	9.4	55.3	59	28	AZ340350	AZ340350
55.3	49	28	AZ979579	AZ979579 2M0256M16	C 464	9.4	55.3	59	28	BH631194	BH631194
55.3	49	28	AL949701	AL949701 Arabidops	C 465	9.4	55.3	59	29	EX656791	EX656791
55.3	50	9	AU102912	AU102912 AU102912	466	9.4	55.3	60	12	BI495393	BI495393
55.3	50	9	AU103231	AU103231 AU103231	C 467	9.4	55.3	60	28	BH128663	BH128663
55.3	50	9	AU107117	AU107117 AU107117	C 468	9.4	55.3	60	28	BH643203	BH643203
55.3	50	9	AU107119	AU107119 AU107119	469	9.4	55.3	60	29	EX894127	EX894127
55.3	50	9	AU107120	AU107120 AU107120	470	9.2	54.1	21	12	BM398509	BM398509
55.3	50	9	AU107121	AU107121 AU107121	471	9.2	54.1	25	28	AZ937549	AZ937549
55.3	50	9	AU107123	AU107123 AU107123	C 472	9.2	54.1	25	29	CG727695	CG727695
55.3	50	9	AU107124	AU107124 AU107124	C 473	9.2	54.1	25	29	TA274G11Q	TA274G11Q
55.3	50	9	AU107125	AU107125 AU107125	474	9.2	54.1	26	28	AZ486575	AZ486575
55.3	50	9	AU107126	AU107126 AU107126	C 475	9.2	54.1	27	28	BH911668	BH911668
55.3	50	9	AU107128	AU107128 AU107128	476	9.2	54.1	28	14	CF297940	CF297940
55.3	50	9	AU107129	AU107129 AU107129	C 477	9.2	54.1	28	28	AZ451650	AZ451650
55.3	50	9	AU107131	AU107131 AU107131	C 478	9.2	54.1	30	28	AZ831042	AZ831042
55.3	50	9	AU107135	AU107135 AU107135	479	9.2	54.1	31	9	AA904383	AA904383
55.3	50	9	AU107180	AU107180 AU107180	480	9.2	54.1	31	9	AA500249	AA500249
55.3	50	9	AU107624	AU107624 AU107624	C 481	9.2	54.1	31	28	CC180142	CC180142
55.3	50	9	AU108097	AU108097 AU108097	C 482	9.2	54.1	32	28	BZ353865	BZ353865
55.3	50	29	CC516353	CC516353 CH240 362	C 483	9.2	54.1	33	28	BH847961	BH847961
55.3	51	9	AU109111	AU109111 AU109111	484	9.2	54.1	34	9	A1911947	A1911947
55.3	51	10	BF507243	BF507243 5923P-1 P	C 485	9.2	54.1	34	28	AZ832818	AZ832818
55.3	51	28	BZ660751	BZ660751 SALK 0242	C 486	9.2	54.1	35	28	AZ462615	AZ462615
55.3	51	29	DR7C38	DR7C38 Danio rer	487	9.2	54.1	35	28	AZ499700	AZ499700
55.3	52	9	AA834903	AA834903 oe02F09.s	488	9.2	54.1	35	28	AZ774639	AZ774639
55.3	52	10	BF647713	BF647713 NF011A06E	489	9.2	54.1	35	28	BH851743	BH851743
55.3	52	12	BG108905	BG108905 HRPE1560	490	9.2	54.1	35	28	BH910740	BH910740
55.3	52	13	EX705172	EX705172 EX705172	491	9.2	54.1	35	28	BZ353610	BZ353610
55.3	52	28	BH847749	BH847749 SALK 0564	493	9.2	54.1	36	28	AZ486331	AZ486331
55.3	52	29	CC795215	CC795215 SALK 0723	C 494	9.2	54.1	37	9	AA978054	AA978054
55.3	52	29	TA328D01Q	TA328D01Q ki54f07.y	C 495	9.2	54.1	37	9	AI118302	AI118302
55.3	53	12	BM283470	BM283470 ki54f07.y	C 496	9.2	54.1	37	9	AV832940	AV832940
55.3	53	12	BM534022	BM534022 fw95e12.x	C 497	9.2	54.1	37	29	AL764186	AL764186
55.3	53	14	CF775809	CF775809 jaa25d02	C 498	9.2	54.1	37	29	AL938007	AL938007
55.3	53	28	BZ287397	BZ287397 SALK 0207	499	9.2	54.1	38	29	TA24D09P	TA24D09P
55.3	54	10	CF310690	CF310690 ABF--05-H	C 500	9.2	54.1	38	29	EX893155	EX893155
55.3	54	14	CF775837	CF775837 jaa22a09	501	9.2	54.1	39	29	CG723167	CG723167
55.3	54	14	CF775780	CF775780 jaa24h04	502	9.2	54.1	40	9	AA681836	AA681836
55.3	54	28	AZ405076	AZ405076 1M0173005	C 504	9.2	54.1	40	9	AI757694	AI757694
55.3	54	28	B06735	B06735 CSRL-84h1-u	C 505	9.2	54.1	40	29	AL756146	AL756146
55.3	54	28	BZ354506	BZ354506 SALK 1252	C 506	9.2	54.1	40	29	AL758596	AL758596
55.3	54	29	CC795677	CC795677 SALK 0878	C 507	9.2	54.1	40	29	AL759372	AL759372
55.3	54	29	AL767877	AL767877 Arabidops	C 508	9.2	54.1	40	29	AL760347	AL760347
55.3	54	29	AL952340	AL952340 Arabidops	C 509	9.2	54.1	40	29	EX655203	EX655203
55.3	55	9	AU258698	AU258698 AU258698	C 510	9.2	54.1	41	28	AZ304505	AZ304505
55.3	55	12	BM283329	BM283329 ki48e07.y	511	9.2	54.1	41	28	BZ596544	BZ596544
55.3	55	13	BX780735	BX780735 BX780735	512	9.2	54.1	41	28	BZ593433	BZ593433
55.3	55	28	CC182874	CC182874 XG096 Bay	513	9.2	54.1	41	29	AL765139	AL765139
55.3	55	29	BX662491	BX662491 Arabidops	C 514	9.2	54.1	41	29	AL945523	AL945523

54.1	41	29	BX288982	BX288982 Arabidops	c 589	9.2	54.1	48	29	BX533275	BX533275
54.1	41	29	BX291553	BX291553 Arabidops	590	9.2	54.1	49	9	AI118170	AI118170
54.1	41	29	TA77D03Q	TA77D03Q T. brucei	c 591	9.2	54.1	49	9	AI152487	AI152487
54.1	42	14	CA797521	CA797521 Cac BL 46	592	9.2	54.1	49	9	AI264752	AI264752
54.1	42	28	AZ351396	AZ351396 IM0089M21	c 593	9.2	54.1	49	13	C21077	C21077
54.1	42	28	BH256477	BH256477 KG03309-3	c 594	9.2	54.1	49	28	BZ764534	BZ764534
54.1	42	28	BZ762011	BZ762011 SALK_0842	c 595	9.2	54.1	49	29	AL759656	AL759656
54.1	42	29	AL770919	AL770919 Arabidops	c 596	9.2	54.1	49	29	AL761341	AL761341
54.1	42	29	AL940280	AL940280 Arabidops	c 597	9.2	54.1	49	29	AL947669	AL947669
54.1	42	29	AL946068	AL946068 Arabidops	c 598	9.2	54.1	49	29	BX289548	BX289548
54.1	42	29	AL952663	AL952663 Arabidops	c 599	9.2	54.1	49	29	BX891921	BX891921
54.1	42	29	BX291769	BX291769 Arabidops	c 600	9.2	54.1	49	29	BX893214	BX893214
54.1	42	29	BX897261	BX897261 Arabidops	601	9.2	54.1	50	9	AU011291	AU011291
54.1	42	29	TA34F02Q	TA34F02Q T. brucei	c 602	9.2	54.1	50	9	AU102376	AU102376
54.1	42	29	TA95B10Q	TA95B10Q T. brucei	603	9.2	54.1	50	9	AU106387	AU106387
54.1	43	9	AA967042	AA967042 ua39e07.r	c 604	9.2	54.1	50	9	AU106406	AU106406
54.1	43	9	AI917027	AI917027 ts51a12.x	c 605	9.2	54.1	50	9	AU106468	AU106468
54.1	43	29	AL770788	AL770788 Arabidops	c 606	9.2	54.1	50	9	AU106529	AU106529
54.1	43	29	AL947531	AL947531 Arabidops	c 607	9.2	54.1	50	9	AU106541	AU106541
54.1	43	29	BX002308	BX002308 Arabidops	c 608	9.2	54.1	50	9	AU106544	AU106544
54.1	43	29	BX288411	BX288411 Arabidops	609	9.2	54.1	50	9	AU106881	AU106881
54.1	43	29	BX292237	BX292237 Arabidops	c 610	9.2	54.1	50	9	AU106891	AU106891
54.1	43	29	BX661875	BX661875 Arabidops	c 611	9.2	54.1	50	10	BF461263	BF461263
54.1	44	9	AV967136	AV967136 AV967136	612	9.2	54.1	50	28	AZ308799	AZ308799
54.1	44	28	AZ804533	AZ804533 2M0065L01	c 613	9.2	54.1	50	29	AL754688	AL754688
54.1	44	29	AL757660	AL757660 Arabidops	c 614	9.2	54.1	50	29	AL767249	AL767249
54.1	44	29	AL758953	AL758953 Arabidops	c 615	9.2	54.1	50	29	AL938385	AL938385
54.1	44	29	AL763755	AL763755 Arabidops	c 616	9.2	54.1	50	29	AL938433	AL938433
54.1	44	29	AL766239	AL766239 Arabidops	c 617	9.2	54.1	50	29	AL944393	AL944393
54.1	44	29	AL771654	AL771654 Arabidops	c 618	9.2	54.1	50	29	AL944953	AL944953
54.1	44	29	AL918680	AL918680 Arabidops	c 619	9.2	54.1	50	29	AL947641	AL947641
54.1	44	29	BX232587	BX232587 Arabidops	c 620	9.2	54.1	50	29	BX204795	BX204795
54.1	45	14	H64922	H64922 Yu65h09.r1	c 621	9.2	54.1	50	29	BX650252	BX650252
54.1	45	28	AZ575902	AZ575902 AST-T2280	c 622	9.2	54.1	51	14	H30101	H30101
54.1	45	28	BH809064	BH809064 1008083H0	623	9.2	54.1	51	28	AZ329549	AZ329549
54.1	45	29	AL760580	AL760580 Arabidops	c 624	9.2	54.1	51	28	AZ837490	AZ837490
54.1	45	29	AL764340	AL764340 Arabidops	625	9.2	54.1	51	28	B00387	B00387
54.1	45	29	BX002842	BX002842 Arabidops	626	9.2	54.1	51	29	AL758135	AL758135
54.1	45	29	BX286485	BX286485 Arabidops	c 627	9.2	54.1	51	29	AL762242	AL762242
54.1	45	29	BX287762	BX287762 Arabidops	c 628	9.2	54.1	51	29	AL952873	AL952873
54.1	45	29	BX897142	BX897142 Arabidops	c 629	9.2	54.1	51	29	AL953734	AL953734
54.1	46	9	AA953796	AA953796 oo38b09.s	c 630	9.2	54.1	51	29	BX291747	BX291747
54.1	46	9	AA616469	AA616469 vn66d10.r	c 631	9.2	54.1	51	29	BX292378	BX292378
54.1	46	28	AZ404113	AZ404113 IM0172A15	c 632	9.2	54.1	51	29	BX292425	BX292425
54.1	46	29	AL944055	AL944055 Arabidops	c 633	9.2	54.1	51	29	BX653622	BX653622
54.1	47	9	AV832665	AV832665 AV832665	c 634	9.2	54.1	51	29	BX662436	BX662436
54.1	47	12	BI685348	BI685348 603310374	635	9.2	54.1	51	29	TA162H07Q	TA162H07Q
54.1	47	28	AZ400633	AZ400633 IM0167F06	c 636	9.2	54.1	51	29	AL487732	AL487732
54.1	47	28	AZ624632	AZ624632 IM0463M21	c 637	9.2	54.1	52	9	AI554319	AI554319
54.1	47	28	BH791124	BH791124 SALK_0587	c 638	9.2	54.1	52	9	AI747503	AI747503
54.1	47	28	BH791157	BH791157 SALK_0588	639	9.2	54.1	52	9	AI799301	AI799301
54.1	47	28	BH891856	BH891856 3526_1.19	c 640	9.2	54.1	52	9	AU012497	AU012497
54.1	47	28	BZ662640	BZ662640 SALK_0261	c 641	9.2	54.1	52	9	AU012546	AU012546
54.1	47	29	AL758034	AL758034 Arabidops	c 642	9.2	54.1	52	9	AU012547	AU012547
54.1	47	29	AL759250	AL759250 Arabidops	643	9.2	54.1	52	28	BH614721	BH614721
54.1	47	29	AL946412	AL946412 Arabidops	644	9.2	54.1	52	28	BH622642	BH622642
54.1	47	29	BX201354	BX201354 Denio rer	645	9.2	54.1	52	28	BH904986	BH904986
54.1	47	29	BX292218	BX292218 Arabidops	646	9.2	54.1	52	29	CG782579	CG782579
54.1	48	9	AV833378	AV833378 AV833378	c 647	9.2	54.1	52	29	AL751664	AL751664
54.1	48	9	AV834599	AV834599 AV834599	c 648	9.2	54.1	52	29	AL757821	AL757821
54.1	48	12	BI730786	BI730786 603350475	c 649	9.2	54.1	52	29	AL759350	AL759350
54.1	48	28	AZ576812	AZ576812 Old05 Sho	c 650	9.2	54.1	52	29	AL936314	AL936314
54.1	48	28	AZ833039	AZ833039 2M0113P15	c 651	9.2	54.1	52	29	BX289135	BX289135
54.1	48	28	AZ942244	AZ942244 2M0202M14	c 652	9.2	54.1	52	29	BX291412	BX291412
54.1	48	28	BH911554	BH911554 SALK_0694	c 653	9.2	54.1	52	29	BX655031	BX655031
54.1	48	29	CG722350	CG722350 1119071F0	c 654	9.2	54.1	52	29	BX661610	BX661610
54.1	48	29	AL765906	AL765906 Arabidops	c 655	9.2	54.1	52	29	BX891532	BX891532
54.1	48	29	AL767661	AL767661 Arabidops	656	9.2	54.1	53	12	BG521345	BG521345
54.1	48	29	AL938919	AL938919 Arabidops	657	9.2	54.1	53	12	BI439906	BI439906
54.1	48	29	AL941984	AL941984 Arabidops	658	9.2	54.1	53	13	BX704759	BX704759
54.1	48	29	AL947540	AL947540 Arabidops	659	9.2	54.1	53	14	W07998	W07998
54.1	48	29	BX288820	BX288820 Arabidops	c 660	9.2	54.1	53	28	B06774	B06774
54.1	48	29	BX288861	BX288861 Arabidops	c 661	9.2	54.1	53	28	BH790547	BH790547

54.1	53	29	AL765150	AL765150 Arabidops	c 735	9.2	54.1	56	29	EX292089	EX292089
54.1	53	29	AL766638	AL766638 Arabidops	c 736	9.2	54.1	56	29	EX292375	EX292375
54.1	53	29	AL770675	AL770675 Arabidops	c 737	9.2	54.1	56	29	EX655581	EX655581
54.1	53	29	AL938469	AL938469 Arabidops	c 738	9.2	54.1	56	29	EX659639	EX659639
54.1	53	29	EX291332	EX291332 Arabidops	c 739	9.2	54.1	57	12	BJ031394	BJ031394
54.1	53	29	EX533126	EX533126 Arabidops	740	9.2	54.1	57	14	H28537	H28537
54.1	53	29	EX533575	EX533575 Arabidops	741	9.2	54.1	57	28	AZ921731	AZ921731
54.1	53	29	EX657916	EX657916 Arabidops	c 742	9.2	54.1	57	28	B02087	B02087
54.1	54	9	AU257493	AU257493 Arabidops	c 743	9.2	54.1	57	28	BH811906	BH811906
54.1	54	28	AZ346920	AZ346920 Arabidops	744	9.2	54.1	57	28	BH889487	BH889487
54.1	54	28	BH233691	BH233691 Arabidops	745	9.2	54.1	57	28	BH889495	BH889495
54.1	54	28	BH909216	BH909216 Arabidops	c 746	9.2	54.1	57	29	AL944349	AL944349
54.1	54	28	BZ380337	BZ380337 Arabidops	c 747	9.2	54.1	57	29	EX002702	EX002702
54.1	54	28	CC457855	CC457855 Arabidops	c 748	9.2	54.1	57	29	EX004487	EX004487
54.1	54	29	AL751431	AL751431 Arabidops	c 749	9.2	54.1	57	29	EX291765	EX291765
54.1	54	29	AL751983	AL751983 Arabidops	c 750	9.2	54.1	57	29	EX291770	EX291770
54.1	54	29	AL756050	AL756050 Arabidops	c 751	9.2	54.1	57	29	EX651229	EX651229
54.1	54	29	AL765764	AL765764 Arabidops	c 752	9.2	54.1	57	29	EX652026	EX652026
54.1	54	29	AL770564	AL770564 Arabidops	c 753	9.2	54.1	57	29	EX654520	EX654520
54.1	54	29	AL945423	AL945423 Arabidops	c 754	9.2	54.1	57	29	EX661212	EX661212
54.1	54	29	AL945582	AL945582 Arabidops	c 755	9.2	54.1	57	29	EX662190	EX662190
54.1	54	29	AL953799	AL953799 Arabidops	c 756	9.2	54.1	57	29	EX893754	EX893754
54.1	54	29	EX001192	EX001192 Arabidops	c 757	9.2	54.1	58	9	AL193125	AL193125
54.1	54	29	EX001254	EX001254 Arabidops	c 758	9.2	54.1	58	9	AL266959	AL266959
54.1	54	29	EX288739	EX288739 Arabidops	759	9.2	54.1	58	9	AI315720	AI315720
54.1	54	29	EX291744	EX291744 Arabidops	c 760	9.2	54.1	58	12	BI416933	BI416933
54.1	54	29	EX291866	EX291866 Arabidops	c 761	9.2	54.1	58	14	CF312550	CF312550
54.1	54	29	EX533244	EX533244 Arabidops	c 762	9.2	54.1	58	14	R34882	R34882
54.1	54	29	EX659227	EX659227 Arabidops	c 763	9.2	54.1	58	28	AZ346461	AZ346461
54.1	54	29	EX892126	EX892126 Arabidops	764	9.2	54.1	58	28	AZ921711	AZ921711
54.1	54	29	EX893146	EX893146 Arabidops	c 765	9.2	54.1	58	28	B02422	B02422
54.1	54	29	EX893664	EX893664 Arabidops	c 766	9.2	54.1	58	28	B46574	B46574
54.1	54	29	EX895924	EX895924 Arabidops	c 767	9.2	54.1	58	28	BH410854	BH410854
54.1	55	9	AI354331	AI354331 Arabidops	c 768	9.2	54.1	58	28	BH901568	BH901568
54.1	55	9	AZ327672	AZ327672 Arabidops	c 769	9.2	54.1	58	28	BZ762173	BZ762173
54.1	55	10	BG073100	BG073100 Arabidops	c 770	9.2	54.1	58	28	BZ767910	BZ767910
54.1	55	12	BG314660	BG314660 Arabidops	c 771	9.2	54.1	58	28	CC887783	CC887783
54.1	55	14	UL7539	UL7539 Arabidops	c 772	9.2	54.1	58	29	CG781019	CG781019
54.1	55	28	B02262	B02262 Arabidops	c 773	9.2	54.1	58	29	AL767671	AL767671
54.1	55	29	CG671812	CG671812 Arabidops	c 774	9.2	54.1	58	29	AL767748	AL767748
54.1	55	29	AL758499	AL758499 Arabidops	c 775	9.2	54.1	58	29	AL768047	AL768047
54.1	55	29	AL761941	AL761941 Arabidops	c 776	9.2	54.1	58	29	AL938875	AL938875
54.1	55	29	AL765568	AL765568 Arabidops	c 777	9.2	54.1	58	29	AL947689	AL947689
54.1	55	29	AL942454	AL942454 Arabidops	c 778	9.2	54.1	58	29	AL948740	AL948740
54.1	55	29	AL944123	AL944123 Arabidops	c 779	9.2	54.1	58	29	AL949035	AL949035
54.1	55	29	AL944727	AL944727 Arabidops	c 780	9.2	54.1	58	29	AL949322	AL949322
54.1	55	29	AL950225	AL950225 Arabidops	c 781	9.2	54.1	58	29	AL951825	AL951825
54.1	55	29	AL950485	AL950485 Arabidops	c 782	9.2	54.1	58	29	EX536333	EX536333
54.1	55	29	EX289789	EX289789 Arabidops	c 783	9.2	54.1	58	29	EX547884	EX547884
54.1	55	29	EX291339	EX291339 Arabidops	c 784	9.2	54.1	58	29	EX892137	EX892137
54.1	55	29	EX531700	EX531700 Arabidops	c 785	9.2	54.1	58	29	EX893348	EX893348
54.1	55	29	EX661592	EX661592 Arabidops	c 786	9.2	54.1	59	9	AU256445	AU256445
54.1	56	9	AL800543	AL800543 Arabidops	787	9.2	54.1	59	9	AW053615	AW053615
54.1	56	9	AA389121	AA389121 Arabidops	c 788	9.2	54.1	59	12	BI218087	BI218087
54.1	56	9	AA464776	AA464776 Arabidops	c 789	9.2	54.1	59	13	EX700090	EX700090
54.1	56	28	AZ657747	AZ657747 Arabidops	c 790	9.2	54.1	59	14	CF312549	CF312549
54.1	56	28	AZ676618	AZ676618 Arabidops	c 791	9.2	54.1	59	14	CF851726	CF851726
54.1	56	28	AZ938203	AZ938203 Arabidops	c 792	9.2	54.1	59	28	AZ458586	AZ458586
54.1	56	28	BH231699	BH231699 Arabidops	c 793	9.2	54.1	59	28	AZ458586	AZ458586
54.1	56	28	BH862524	BH862524 Arabidops	794	9.2	54.1	59	28	AZ475901	AZ475901
54.1	56	29	CG707530	CG707530 Arabidops	c 795	9.2	54.1	59	28	AZ537411	AZ537411
54.1	56	29	AL754220	AL754220 Arabidops	c 796	9.2	54.1	59	28	BH908548	BH908548
54.1	56	29	AL760112	AL760112 Arabidops	c 797	9.2	54.1	59	29	AL753933	AL753933
54.1	56	29	AL762719	AL762719 Arabidops	c 798	9.2	54.1	59	29	AL757646	AL757646
54.1	56	29	AL943659	AL943659 Arabidops	c 799	9.2	54.1	59	29	AL766809	AL766809
54.1	56	29	AL951045	AL951045 Arabidops	c 800	9.2	54.1	59	29	AL766957	AL766957
54.1	56	29	AL952124	AL952124 Arabidops	c 801	9.2	54.1	59	29	AL767458	AL767458
54.1	56	29	EX001808	EX001808 Arabidops	c 802	9.2	54.1	59	29	AL938432	AL938432
54.1	56	29	EX002727	EX002727 Arabidops	c 803	9.2	54.1	59	29	AL938434	AL938434
54.1	56	29	EX002873	EX002873 Arabidops	c 804	9.2	54.1	59	29	AL938456	AL938456
54.1	56	29	EX003041	EX003041 Arabidops	c 805	9.2	54.1	59	29	AL938554	AL938554
54.1	56	29	EX291501	EX291501 Arabidops	c 806	9.2	54.1	59	29	AL950618	AL950618
54.1	56	29	EX291890	EX291890 Arabidops	c 807	9.2	54.1	59	29	AL952471	AL952471

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54.1	59	29	AL953723 Arabidops	C 881	9	52.9	42	14	CF338219	CF338219
54.1	59	29	BM291316 Arabidops	C 882	9	52.9	42	14	CF339767	CF339767
54.1	59	29	BM547090 Arabidops	C 883	9	52.9	42	28	AZ514593	AZ514593
54.1	59	29	BM652724 Arabidops	C 884	9	52.9	42	28	AZ789082	AZ789082
54.1	59	29	BM656793 Arabidops	C 885	9	52.9	42	28	BZ383008	BZ383008
54.1	59	29	BM891291 Arabidops	C 886	9	52.9	42	28	BZ662280	BZ662280
54.1	60	9	AA834171 of14ell.s	C 887	9	52.9	42	29	TA14F10Q	TA14F10Q
54.1	60	9	AA174457 mc09f10.r	C 888	9	52.9	43	9	AA523903	AA523903
54.1	60	12	BG910408 602806048	C 889	9	52.9	43	12	BI283315	BI283315
54.1	60	28	AZ778764 2M0014C15	C 890	9	52.9	43	14	CF338563	CF338563
54.1	60	29	CC596088 2M040_398	C 891	9	52.9	43	14	CF338824	CF338824
54.1	60	29	AL758969 Arabidops	C 892	9	52.9	43	14	CF339433	CF339433
54.1	60	29	AL763865 Arabidops	C 893	9	52.9	43	14	CF339728	CF339728
54.1	60	29	AL766515 Arabidops	C 894	9	52.9	43	14	CF339743	CF339743
54.1	60	29	AL936419 Arabidops	C 895	9	52.9	43	14	CF340327	CF340327
54.1	60	29	AL940643 Arabidops	C 896	9	52.9	43	28	BZ382990	BZ382990
54.1	60	29	AL942427 Arabidops	C 897	9	52.9	43	29	BX546561	BX546561
54.1	60	29	AL947740 Arabidops	C 898	9	52.9	44	9	AV842450	AV842450
54.1	60	29	BM286093 Arabidops	C 899	9	52.9	44	29	CC888677	CC888677
54.1	60	29	BM290391 Arabidops	C 900	9	52.9	44	29	CG705740	CG705740
54.1	60	29	BM291566 Arabidops	C 901	9	52.9	45	28	AZ769215	AZ769215
54.1	60	29	BM292263 Arabidops	C 902	9	52.9	45	28	AZ815371	AZ815371
54.1	60	29	BM531561 Arabidops	C 903	9	52.9	45	28	AZ853600	AZ853600
54.1	60	29	BM534355 Arabidops	C 904	9	52.9	45	28	BH641805	BH641805
54.1	60	29	BM893293 Arabidops	C 905	9	52.9	46	9	AA052407	AA052407
54.1	60	29	BM893699 Arabidops	C 906	9	52.9	46	9	AI863959	AI863959
54.1	60	29	BM895086 Arabidops	C 907	9	52.9	46	14	CF315365	CF315365
54.1	60	29	BM897088 Arabidops	C 908	9	52.9	46	29	CG712534	CG712534
54.1	60	29	BM897414 Arabidops	C 909	9	52.9	47	12	BI916743	BI916743
54.1	60	29	BM939000 5009-0-51	C 910	9	52.9	47	28	CC199541	CC199541
52.9	21	28	AZ852233 2M0154D23	C 911	9	52.9	48	29	CG672207	CG672207
52.9	22	9	AL930371 AL930371	C 912	9	52.9	49	9	AA690317	AA690317
52.9	24	12	BM399134 5009-0-53	C 913	9	52.9	49	9	AA987399	AA987399
52.9	24	28	AZ848167 2M0149C11	C 914	9	52.9	49	9	AI521631	AI521631
52.9	26	12	BM398348 5009-0-44	C 915	9	52.9	49	9	AI528223	AI528223
52.9	26	28	BZ290508 SALK_0898	C 916	9	52.9	49	9	AI889232	AI889232
52.9	26	28	BZ763068 SALK_1118	C 917	9	52.9	49	9	AI900473	AI900473
52.9	26	29	CG712062 1119023H1	C 918	9	52.9	49	9	AA620370	AA620370
52.9	27	14	D19578 MUGS00985	C 919	9	52.9	49	14	W17887	W17887
52.9	27	29	TA249G06Q	C 920	9	52.9	49	28	AZ808932	AZ808932
52.9	28	28	AZ475208 1M0293E18	C 921	9	52.9	49	29	CC886568	CC886568
52.9	29	10	AW246945	C 922	9	52.9	49	29	CG723151	CG723151
52.9	29	28	BZ665244 SALK_1109	C 923	9	52.9	49	29	CG779221	CG779221
52.9	29	29	TA190B07P	C 924	9	52.9	49	29	TA108E04P	TA108E04P
52.9	30	12	BM395595 5009-0-1-	C 925	9	52.9	50	9	AA847284	AA847284
52.9	30	28	AZ317049 1M0035B14	C 926	9	52.9	50	9	AI750109	AI750109
52.9	30	28	AZ433900 1M0220F03	C 927	9	52.9	50	9	AU103184	AU103184
52.9	30	28	BH909588 SALK_0545	C 928	9	52.9	50	9	AU103635	AU103635
52.9	31	9	AA667984 v93B11.x	C 929	9	52.9	50	9	AU103636	AU103636
52.9	31	12	BI830964	C 930	9	52.9	50	9	AU105856	AU105856
52.9	31	28	BH791155 SALK_0588	C 931	9	52.9	50	9	AU105857	AU105857
52.9	31	29	TA209E04P	C 932	9	52.9	50	9	AU106307	AU106307
52.9	32	9	AU252838	C 933	9	52.9	50	9	AU106367	AU106367
52.9	32	10	BF568357 602184546	C 934	9	52.9	50	9	AU106372	AU106372
52.9	32	29	BM391555 Arabidops	C 935	9	52.9	50	9	AU106375	AU106375
52.9	33	29	AL945047 Arabidops	C 936	9	52.9	50	9	AU106379	AU106379
52.9	35	28	BZ356521 SALK_1292	C 937	9	52.9	50	9	AU106382	AU106382
52.9	37	9	AI539693 tp71h05.x	C 938	9	52.9	50	9	AU106434	AU106434
52.9	37	9	AI794982 sb74e12.y	C 939	9	52.9	50	9	AU106828	AU106828
52.9	37	10	BE307655 601096785	C 940	9	52.9	50	9	AU106834	AU106834
52.9	37	14	D38654 HUNC110242	C 941	9	52.9	50	9	AU106835	AU106835
52.9	37	29	BX288367 Arabidops	C 942	9	52.9	50	9	AU106837	AU106837
52.9	38	14	CF338710 RCL1--02-	C 943	9	52.9	50	9	AU107179	AU107179
52.9	38	28	AZ964176 2M0233F13	C 944	9	52.9	50	9	AU107180	AU107180
52.9	38	28	BH863233 SALK_0934	C 945	9	52.9	50	9	AU107181	AU107181
52.9	39	10	BE275929 601121563	C 946	9	52.9	50	9	AA594651	AA594651
52.9	40	9	AA912227 0193a08.8	C 947	9	52.9	50	11	CNS08XE7	CNS08XE7
52.9	40	28	BH801511 1008117C0	C 948	9	52.9	50	28	AZ480460	AZ480460
52.9	40	28	BH864142 SALK_0954	C 949	9	52.9	50	28	BH862793	BH862793
52.9	41	28	BH908025 SALK_0452	C 950	9	52.9	50	28	BZ663576	BZ663576
52.9	41	28	BZ357757 SALK_1312	C 951	9	52.9	50	29	AL756931	AL756931
52.9	41	28	CC028458 3591_1-10	C 952	9	52.9	51	12	BI175753	BI175753
52.9	41	29	CG720602 1119063A0	C 953	9	52.9	51	13	BQ626411	BQ626411

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51 28 AQ025577
52.9 51 28 AQ025577 fs(3).0708
52.9 51 28 BH218157 1006077D0
52.9 51 28 CC502382 CH240_341
52.9 51 29 BX2070707 Danio rer
52.9 52 9 AI022550 ow58d11.s
52.9 52 9 AI309536 qo5f01.x
52.9 52 9 AI524189 th10c09.x
52.9 52 9 AI571481 tr56g03.x
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52.9 52 14 CF338464 RCL1--01-
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52.9 52 28 BH637952 1008019F0
52.9 52 28 BZ764623 SALK_1259
52.9 52 29 AG217042 Drosophila
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52.9 53 10 BG037362 dg49b08.Y
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52.9 53 29 CG724037 1109079D0
52.9 53 29 AG215854 Drosophila
52.9 53 29 TA300B07P
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52.9 54 12 BJ046711 BJ046711
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52.9 54 14 CF927815 laf57h10.
52.9 54 28 AF149434 AF149434
52.9 54 28 BH638103 1008020D0
52.9 54 28 AL767122 Arabidops
52.9 54 29 AL944217 Arabidops
52.9 54 29 AL949602 Arabidops
52.9 55 9 AA983584 on41c07.s
52.9 55 14 W31056 Zb86c10.r1
52.9 55 28 AZ804709 2M0065D20
52.9 55 28 B03369 CSRL-177B9-
52.9 55 28 BH222077 1006105B0
52.9 55 28 BH409434 1007012C0
52.9 55 28 BZ763166 SALK_1140
52.9 55 29 CG722070 1109070C0
52.9 56 9 AU257475 AU257475
52.9 56 12 BJ063843 BJ063843
52.9 56 28 BH628418 1007079H0
52.9 56 28 BH852370 SALK_0745
52.9 57 13 BX740623 BX740623
52.9 57 28 BH864081 SALK_0952
52.9 57 28 BH889151 3526_1_32
52.9 57 28 BH889151

ALIGNMENTS

6273 60 bp mRNA linear EST 02-SEP-1998
g10.r1 Soares mammary_gland_NbMMG Mus musculus cDNA clone
R:1398306 5' similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8
AN1; mRNA sequence.
6273
6273.1 GI:3516597

musculus (house mouse)
myota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
bases 1 to 60)
a.M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
el,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,B.,
illenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,R.,
sing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
rston,R.
WashU-HHMI Mouse EST Project
blished (1996)

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousees@watson.wustl.edu
This clone is available royalty-free through LLNL; cont
IMAGE Consortium (info@image.llnl.gov) for further infor
MGI:910022
Trace considered overall poor quality
Seq primer: -28ml3 rev2 RT from Amersham
High quality sequence stop: 1.
Location/Qualifiers
source
1. 60
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1398306"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_mammary_gland_NbMMG"
/notes="Organ: mammary gland; Vector: pRT73D-Pac
(Pharmacia) with a modified polylinker; Site 1:
Site 2: Eco RI; 1st strand cDNA was primed with
oligo(dT) primer [5',
TGTTACCAATCTGAGTGGAGCGGCGCGAATGTTT
T 3']; double-stranded cDNA was ligated to Eco
adaptors (Pharmacia), digested with Not I and
the Not I and Eco RI sites of the modified pRT
RNA provided by Dr. Minoru Ko, Wayne State Univ
constructed and normalized by Bento Soares and
Bonaldo."

ORIGIN

Query Match 75.34; Score 12.8; DB 9; Length 60;
Best Local Similarity 87.5%; Pred.No.2.le+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0;

Qy 1 CGAGTGAAGATCCCT 16
|||
Db 29 CGAGTGAAGTCCCT 44

RESULT 2
BE321851
LOCUS BE321851 52 bp mRNA linear EST
DEFINITION NF009F111N1F1092 Insect herbivory Medicago truncatula cD
NF009F111N 5', mRNA sequence.
ACCESSION BE321851
VERSION BE321851.2 GI:11963009
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; T
Medicago.
REFERENCE 1 (bases 1 to 52)
AUTHORS Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C
Flores,H.R., Imman,J.T., Weiler,J.W. and May,G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Fo
Medicago truncatula insect herbivory library
JOURNAL Unpublished (2000)
COMMENT On Jul 14, 2000 this sequence version replaced gi:919562
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191

```

09:38:24 2004

us-10-090-326-17.max.rst

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501 575 7601
: kkortheomp.uark.edu
ago Genome Initiative accession: MGI:S:23216
t Length: 501 Std Error: 0.00
: 009 row: F column: 11
rimer: TCACACGAGAAACAGCTATGAC.
Location/Qualifiers
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/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="MF009F11N"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/clone_lib="Insect herbivory"
/note="Vector: Lambda Zap; Library was produced from fully
expanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
(undamaged leaves from injured plants) and wounded leaves
were harvested and pooled."
71.8%; Score 12.2; DB 10; Length 52;
larity 82.4%; Pred. No. 4.2e+04; Indels 0; Gaps 0;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;
GTGAGATCCCTT 17
|||||
CTGAGATCTCTCT 32
37 bp mRNA linear EST 04-MAY-1995
09.s1 Soares infant brain LNB Homo sapiens cDNA clone
:24408 3' similar to gb:X66114.mnal MITOCHONDRIAL
GLUTARATE/MALATE CARRIER PROTEIN (HUMAN); mRNA sequence.
7
7.1 GI:795033
sapiens (human)
sapiens
yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ases 1 to 37)
er.L., Clark.N., Dubucq.T., Elliston.K., Hawkins.M.,
n.M., Hultman.M., Kucaba.T., Le.M., Lennon.G., Marra.M.,
ns.J., Rifkin.L., Rohlfing.T., Soares.M., Tan.F.,
skis.E., Waterston.R., Williamson.A., Wohldmann.P. and
n.R.
ashU-Merck EST Project
lished (1995)
ct: Wilson RK
ngton University School of Medicine
Forest Park Parkway, Box 8501, St. Louis, MO 63108
314 286 1800
314 286 1810
: est@watson.wustl.edu
t Size: 1676
quality sequence starts: 1 High quality sequence stops: 1
e: IMAGE Consortium, LBNL This clone is available royalty-free
gh LBNL; contact the IMAGE Consortium (info@image.lbnl.gov)
urther information. Trace considered overall poor quality
t Length: 1676 Std Error: 0.00
rimer: -21ml3
quality sequence stop: 1.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:396755"
/db_xref="taxon:9606"
/clone="IMAGE:24408"
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/sex="female"
/dev stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain LNB"
/note="Organ: whole brain; Vector: Lfamid BA; Si
I; Site 2: Hind III; 1st strand cDNA was primed
I - oligo(GT) primer [5',
AACTGGAAGAATTCGGCGCGAGGAATTTTTTTTTTTT 3',
double-stranded cDNA was ligated to Hind III ad
(Pharmacia), digested with Not I and directional
into the Not I and Hind III sites of the Lfamid
Library went through one round of normalization.
constructed by Bento Soares and M.Fatima Bonaldc
Query Match 70.6%; Score 12; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.7e+04; Indels 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0;
QY 6 GAAGATCCCTT 17
|||||
DB 29 GAAGATCCCTT 18
BM862480
mgcm003xC08f.b Magnaporthe grisea CM Uni-Zap XR Library N
Grisea cDNA clone mgcm003xC08 5', mRNA sequence.
BM862480
BM862480.2 GI:30392312
EST.
Magnaporthe grisea (anamorph: Pyricularia grisea)
MAGNAPORTE GRISEA
MAGNAPORTE GRISEA
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomyc
Sordariomycetes; incertae sedis; Magnaporthaceae; Magnapo
1 (bases 1 to 49)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bhatterai,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magna
grisea
Unpublished (2002)
On Mar 7, 2002 this sequence version replaced gi:19230162
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, US
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see cont
person:
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm003 row: C column: 08
Seq primer: T3.
Location/Qualifiers
1..49
/organism="Magnaporthe grisea"
/mol_type="mRNA"
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/db_xref="taxon:148305"
/clone="mgcm003xC08"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Lib
XhoI; Vector: pBluescriptSK-; Site 1: EcoRI; Si
XhoI; Unidirectional cloning. EcoRI side has T3
predominantly 5' reads. T7 primer on XhoI side o
Strain inoculated into complete medium grown for
at room temperature, 150 rpm, harvested, blended
reinoculated into complete medium 24 h, room tem
```

150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

69.4%; Score 11.8; DB 12; Length 49;  
 ilarity 86.7%; Pred. No. 6.7e+04;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 AGTGAGATCCCC 15  
 |||||  
 AGAGAAGATCGCC 9

3440 59 bp DNA linear GSS 18-JUN-2002  
 idopsis thaliana T-DNA flanking sequence GK-037A01-015009,  
 mic survey sequence.  
 3440  
 3440.1 GI:21512904

idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

zhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.  
 Weisshaar,B.  
 peline for automated high-throughput generation of FSTs  
 nking sequence tags) from Arabidopsis thaliana T-DNA  
 sformed lines  
 blished

o.M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
 w Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 flanking sequence tag based reverse genetics  
 blished  
 bases 1 to 59)  
 ., Rosso,M., Strizhov,N. and Weisshaar,B.  
 ct Submission  
 itted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer  
 htungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 . sequence is recovered from the left border of the T-DNA. It  
 . caten an insertion close to or within gene At2g36300. The  
 . ences are generated at the MPI for Plant Breeding Research in  
 context of the GABI-Kat project. GABI-Kat is part of the German  
 t Genomics program designated 'GABI'. Information on line  
 liability can be found at:  
 .://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers  
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 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector PAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

Query Match 69.4%; Score 11.8; DB 29; Length 59;  
 Best Local Similarity 86.7%; Pred. No. 7.2e+04;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0;  
 QY 1 CGAGTGAAGATCCCC 15  
 |||||  
 Db 27 CGCTGAAGATCCCC 13

RESULT 6  
 CB353581/c  
 LOCUS  
 DEFINITION  
 CB353581 50 bp mRNA linear EST  
 ZF001-P00007-DPE-F-C E05 GISZF001 Danio rerio cDNA clone  
 IMAGE:6894154 5' similar to fx68c08.y1 Zebrafish SJD 5 d  
 Danio rerio cDNA clone IMAGE:5628303 5' similar to SW:AC  
 P53485 ACTIN, CYTOPLASMIC 2, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 CB353581.1 GI:28991343  
 EST.  
 Danio rerio (zebrafish)  
 Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 1 (bases 1 to 60)  
 Mathavan,S., Wei,C., Thoreau,H., Chia,J.M. and Ruan,Y.  
 Genome Institute of Singapore, Zebrafish EST Collection  
 Unpublished (2003)  
 Contact: Ruan Y  
 Laboratory of Molecular Biotechnology  
 Genome Institute of Singapore  
 1 Science Park Road, The Capricorn #05-01, Singapore 117  
 Tel: +65 6827 5200  
 Fax: +65 6827 5201  
 Email: gisry@nus.edu.sg  
 GIS Clone ID: ZF001-P00007-PP\_J09  
 PCR Primers  
 FORWARD: M13  
 BACKWARD: M13  
 Plate: ZF001-P00007-DPE-F-C  
 Seq primer: CCGCATAACTGTATAGCA  
 High quality sequence stop: 60.

FEATURES  
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 /lab\_host="DH10B"  
 /clone\_lib="GISZF001"  
 /note="Vector: pDNR-LIB; Site 1: Sfi A (GGCCATT  
 Site 2: Sfi B (GGCCGCTCGGC) Priming method:  
 Primed; Priming sequence: 5.ATTCTAGA GGCCGAGGC  
 GACAG(T)30VN; Directionally cloned, 5' cl  
 Sfi A site GGCCATTACGGC; 5' linker/adaptc  
 5.AAGCAGTGTATCAACGAGATGGCC; 3' cloning  
 site GGCCGCTCGGC; 3' linker/adaptor sequ  
 as the priming sequence; Average insert size:  
 PCR insert analysis: Use M13 Forward and revers  
 Library Amplified Recombinants (inserts): 98%  
 complexity: 5x106; Full-length construction (n  
 SMART, a Clontech method; Library constructed  
 Mathavan, Chia-Lin Wei, and Yijun Ruan Genome I  
 Singapore"

ORIGIN  
 Query Match 69.4%; Score 11.8; DB 14; Length 60;  
 Best Local Similarity 86.7%; Pred. No. 7.3e+04;  
 Matches 13; Conservative 0; Mismatches 2; Indels 0;



TGAAGATCCCT 16  
|||||  
TGAAGATCTCT 29

1452 47 bp DNA linear GSS 13-DEC-2000  
3108F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
UUGC1M0463108 F, genomic survey sequence.

1452.1 GI:11746642

musculus (house mouse)  
musculus  
Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
Mus musculus (house mouse)  
D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,  
SLC, UT  
801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0463 row: I column: 08  
Seq primer: CGGTGTAACGACGGCAGT  
3: plasmid ends  
quality sequence stop: 47.

Location/Qualifiers  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/)  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RL. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 67.1%; Score 11.4; DB 28; Length 47;  
Best Local Similarity 92.3%; Pred. No. 1.1e+05;  
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTGAAGATCCCC 15  
|||||  
DB 19 AGTGATGATCCCC 7

RESULT 8  
AZ769807/c

LOCUS  
DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ769807 57 bp DNA linear GSS  
1M0570A22R Mouse 10kb plasmid UUGC1M library Mus musculus  
clone UUGC1M0570A22 R, genomic survey sequence.

AZ769807

AZ769807.1 GI:12890335

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
Mus musculus (house mouse)  
1 (bases 1 to 57)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Whole genome scaffolding with paired end reads from  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,  
SLC, UT  
801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0570 row: A column: 22  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 57.

Location/Qualifiers

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0570A22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/)  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RL. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

FEATURES

source

1. .57  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0570A22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/)  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RL. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 67.1%; Score 11.4; DB 28; Length 57;  
Best Local Similarity 92.3%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 1; Indels 0;

JTGAAGATCCC 14  
|||||  
JTGAAGATCCC 12

2G04P 31 bp DNA linear GSS 13-DEC-2000  
brucei sheared genomic DNA clone 122g04, forward sequence,  
mic survey sequence.  
2661  
2661.1 GI:11833541

anosoma brucei  
anosoma brucei  
ryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
anosoma.  
bases 1 to 31)  
N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
lingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
ille, S.E., Rajandream, M.A. and Barrell, B.G.  
ct Submission  
ited (10-DEC-2000) Trypanosoma brucei genome sequencing  
ect, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
ridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
sanger.ac.uk  
tracted at the Institute for Genomic Research (TIGR),  
ville, MD. Genomic DNA isolated from a cloned population of  
anosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
ive a tight size distribution (  
). The v + i method used for the library construction is  
ribed in detail in Smith, H. and Venter, J.C. (Making small  
it libraries for whole genome shotgun sequencing projects. In  
me Sequencing: A Practical Approach, eds. M. Vaudin and B.  
ell, Oxford University Press, 1999).

l: nelsayed@tigr.org  
ils of T. brucei sequencing at the Sanger Centre are available  
http://www.sanger.ac.uk/Projects/T\_brucei/.

Location/Qualifiers  
1. 31  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="122g04"

65.9%; Score 11.2; DB 29; Length 31;  
ilarity 81.2%; Pred. No. 1.2e+05;  
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AGTGAAGATCCCTT 17  
|||||  
AGCAAGATCCCGT 9

20952 35 bp DNA linear GSS 20-OCT-2003  
3064F11.2EL\_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic  
vey sequence.

20952  
20952.1 GI:37754344

mays  
mays

aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
rmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
de; Panicoideae; Andropogoneae; Zea.  
(bases 1 to 35)

bot, v.

ze genomic sequences found using engineered RescueMu transposon  
ublished (2001)

## COMMENT

Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonu  
Reverse complemented post-ligation sequence from source  
Plate: 1119064 row: F column: 11  
Class: transposon-tagged.

## FEATURES

Location/Qualifiers  
1. 35  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73/K55"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1119 - RescueMu Grid AA"  
/note="Organ: leaf; Vector: RescueMu (engineere  
pBlueScript backbone); Site 1: BamHI; Site 2: P  
RescueMu is a 4.9 kb, modified maize Mu transpc  
designed to allow plasmid rescue from total gen  
Mu elements insert preferentially into transcri  
sites. For more information on RescueMu, go to  
site 'www.zmdb.iastate.edu' and follow the link  
'RescueMu.' Grid AA was grown at UC San Diego i  
was extracted from leaf strips, double digested  
BamHI and BglII, and ligated to form circular p  
DH10B cells were transformed and then screened  
plates with ampicillin."

## ORIGIN

Query Match 65.9%; Score 11.2; DB 29; Length 35;  
Best Local Similarity 81.2%; Pred. No. 1.3e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCTT 16

DB 14 CGAAAAAAGATCCCTT 29

## RESULT 11

AZ771147  
LOCUS  
DEFINITION  
1M0573B07F Mouse 10kb plasmid UUGC1M library Mus musculi  
clone UUGC1M0573B07 F, genomic survey sequence.

ACCESSION  
AZ771147  
VERSION  
AZ771147.1 GI:12893094

## KEYWORDS

GSS.

## SOURCE

ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu

## REFERENCE

AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Har  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads fr  
plasmid inserts

## JOURNAL

COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

```
/strain="CU428.1"  
/db xref=taxon:5911  
/clone lib="Chilcoat/Turkewitz cDNA (large frag  
/note=Vector: Bluescript2 SK4; Details on libr  
preparation can be found in Chilcoat and Turkew  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
```

## ORIGIN

```
DB 12; Length 45;  
4e+05;  
s 3; Indels 0;
```

2 GAGTGAAGATCCCCCTT 17  
| | | | | | | | | |  
22 GGGTAAAGATCCCCCCT 7

	49 bp	mRNA	linear	EST
AA288062				
va25f06.r1	GuayWoodford	Beier	mouse	kidney day 7
clone IMAGE:732419	5'	similar to SW:RPB6	HUMAN	P41584
DN				
RNA POLYMERASE II	14.4	KD POLYPEPTIDE	;	mRNA
sequence.				

AA288062  
AA288062.1 GI:1934314  
EST.

Mus musculus (house mouse)  
Mus musculus

1 (bases 1 to 49)  
Marria, M.; Hillier, L.; Allen, M.; Bowles, M.; Dietrich, N.,

Medicine  
St. Louis, MO 63108

gov) for further infor  
y on wrong strand

FEATURES

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:732419"

```

lays old) "  
n resistant) "  
Beier mouse kidney day

ttor: pBluescript SK-;  
ed unidirectionally.  
size: 1.0 kb; Uni-ZAP

GAATTCGGCAG 3' ~3' TTTT TTTT TTTT 3' Librar

\_\_\_\_\_

Quem

```
4e+05;
:s 3; Indels 0;
```

GTGAAGATCCCTT 17  
|||||  
GAGTGATCGCTT 8

5161 51 bp mRNA linear EST 20-SEP-2002  
7902.y1 McCarrey Eddy 18 day leptotene and zygotene  
matocytes Mus musculus cDNA clone IMAGE:6367659 5', mRNA  
ence.

5161  
5161.1 GI:23261331

musculus (house mouse)

musculus  
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
bases 1 to 51)

rey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,  
in, J., Wylie, T., Dente, M., Bowers, Y., Theising, B., Gibbons, M.,  
er, E., Tsagaris, R., Ronko, A., Maguire, L., Kennedy, S.,  
ett, J., Waterston, R. and Wilson, R.

S Mouse  
blished (2002)

act: McCarrey/Eddy NIEHS Mouse

S Mouse

ington University School of Medicine

Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

314 286 1800

314 286 1810

l: est@watson.wustl.edu

ary constructed and donated by J. McCarrey, Ph.D. (Southwest  
ation for Biomedical Research, Dept. of Genetics) - excision  
: by E.M. Eddy, Ph.D. (National Institutes of Health, National  
itute of Environmental Health Sciences).

2045091

primer: -40RP from Gibco.

Location/Qualifiers

1. .51

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:6367659"

/sex="male"

/tissue\_type="18-day leptotene and zygotene spermatocytes"

/lab\_host="PH10B (phage-resistant)"

/clone\_lib="McCarrey Eddy 18 day leptotene and zygotene  
spermatocytes"

/note="Organ: testis; Vector: pBluescript SK+

(Stratagene); Site 1: EcoRI; Site 2: XhoII; cDNA oligo

dt-primerd [5'-(GA)10-ACTAGTCGAGTTTCTTTT-3'] and

directionally cloned using 5' linkers 5'-AATTCGACAG-3'

and 5'-CTCGGCG-3'. Size selection of >400bp material

gives average insert size ranging from 1-2 kb. Library was

mass excised (from lambda-UnizAP-XR) and resulting

single-stranded phagemids were prepped and transformed into

PH10B. Library constructed and donated by J. McCarrey,

Ph.D. (Southwest Foundation for Biomedical Research, Dept.

of Genetics); excision done by E.M. Eddy, Ph.D. (National

Institutes of Health, National Institute of Environmental

Health Sciences)."

65.9%; Score 11.2; DB 13; Length 51;

ilarity 81.2%; Pred. No. 1.4e+05;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

ACTGAGATCCCTT 17

|||||

ACTGACGATCGCTT 23

RESULT 15  
CNS07HRH  
LOCUS  
DEFINITION

51 bp DNA linear GSS  
Anopheles gambiae GSS T7 end of clone 30D22 of library N  
from strain PEST of Anopheles gambiae (African malaria m  
genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS

AL611423  
AL611423.1 GI:15962846

GSS.

ANOPHELES GAMBIAE (African malaria mosquito)

ANOPHELES GAMBIAE

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Ptery

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea

Anopheles.

1 (bases 1 to 51)

Genoscope.

Direct Submission

Submitted (01-OCT-2001) Genoscope - Centre National de S

BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genosc

- Web : www.genoscope.cns.fr)

2 (bases 1 to 51)

Roth, C.W., Brey, P.T., Ke, Z. and Collins, F.H.

Direct Submission

Submitted (01-OCT-2001) BIMI, Institut Pasteur, 25, rue

Roux, Paris 75015, France

This clone is from an A. gambiae BAC library provided by

Collins and sequenced by Genoscope in collaboration with

Laboratory of Biochem. and Biol. Molec. of Insects, Inst

Pasteur.

Location/Qualifiers

1. .51

/organism="Anopheles gambiae"

/mol\_type="genomic DNA"

/strain="PEST"

/db\_xref="taxon:7165"

/clone="30D22"

/clone\_lib="NotreDamel"

/note="end : T7"

Query Match 65.9%; Score 11.2; DB 29; Length 51;

Best Local Similarity 81.2%; Pred. No. 1.4e+05;

Matches 13; Conservative 0; Mismatches 3; Indels 0;

QY 1 CGAGTGAAGATCCCT 16

|||||

Db 36 CGATGAGATCGCT 51

|||||

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|||||

sequence is from a Xenopus Gene Collection (XGC) library  
 ructed by Aaron M. Zorn.  
 was oligo dt primed from Sug of poly A+ RNA from egg.  
 -NotI cut cDNA was then ligated into pCS107 with EcoRI at the  
 d and NotI at the 3' end.  
 r: pCS107; Site 1: EcoRI; Site 2: NotI  
 Escherichia coli XLI-blue.

Location/Qualifiers

1. .56  
 /organism="Silurana tropicalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8364"  
 /clone="TEGG042j14"  
 /dev\_stage="egg"  
 /lab\_host="Escherichia coli XLI-blue"  
 /clone\_lib="XGC-egg"  
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA  
 was oligo dt primed from Sug of poly A+ RNA from egg.  
 EcoRI-NotI cut cDNA was then ligated into pCS107 with  
 EcoRI at the 5' end and NotI at the 3' end"

65.9%; Score 11.2; DB 13; Length 56;  
 Clarity 81.2%; Pred. No. 1.5e+05; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 3; Indels 0;

AGTGAAGATCCCT 16

|||||

XGGAGATCCGCT 56

9991 58 bp DNA linear GSS 04-SEP-2002  
 064381.30.15.x Arabidopsis thaliana TDNA insertion lines  
 idopsis thaliana genomic clone SALK\_064381.30.15.x, genomic  
 ay sequence.

9991

0991.1 GI:22723924

idopsis thaliana (thale cress)

idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 natophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsi

bases 1 to 58)  
 so,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 inab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 n.P., Zimmerman,J. and Ecker,J.R.

quence-indexed library of insertion mutations in the

idopsis Genome

blished (2001)

act: Joseph R. Ecker

Institute Genomic Analysis Laboratory (SIGNAL)

Salk Institute for Biological Studies

0 N. Torrey Pines Road, La Jolla, CA 92037, USA

858 453 4100 x1752

858 558 6379

1: eckersalk.edu

is single pass sequence recovered from the left border of  
 .. This sequence lies within 300 bases of the 3' end of  
 02400.

is: TDNA tagged.

Location/Qualifiers

1. .58

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_064381.30.15.x"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line  
 directly sequenced to determine the genomic seq  
 the site of insertion. Details of the protocol  
 be found at [http://signal.salk.edu/tdna\\_protocol](http://signal.salk.edu/tdna_protocol)

#### ORIGIN

Query Match 65.9%; Score 11.2; DB 28; Length 58;  
 Best Local Similarity 81.2%; Pred. No. 1.5e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0;

QY 2 GAGTGAAGATCCCTT 17

|||||

Db 34 GAATGAGATGCCCT 19

#### RESULT 18

AW511427

LOCUS

DEFINITION  
 XUS8h01.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:28

mRNA sequence.

ACCESSION  
 AW511427

VERSION  
 AW511427.1 GI:7149592

KEYWORDS  
 EST.

SOURCE  
 Homo sapiens (human)

ORGANISM  
 Homo sapiens

REFERENCE  
 1 (bases 1 to 59)

AUTHORS  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE  
 National Cancer Institute, Cancer Genome Anatomy Project

JOURNAL  
 Tumor Gene Index

COMMENT  
 Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., M

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequenc

Clone distribution: NCI-CGAP clone distribution informa

found through the I.M.A.G.E. Consortium/LLNL at:

[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)

Seq primer: -40UP from Gibco.

Location/Qualifiers

1. .59

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2805937"

/tissue\_type="well-differentiated endometrial

adenocarcinoma, 7 pooled tumors"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Ut1"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site

Site 2: NotI; Cloned unidirectionally. Primer:

Average insert size 1.75 kb. Life Technologies

11538-014"

#### ORIGIN

Query Match 65.9%; Score 11.2; DB 10; Length 59;  
 Best Local Similarity 81.2%; Pred. No. 1.5e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0;

QY 2 GAGTGAAGATCCCTT 17

|||||

Db 11 GAGTGACAATCCACTT 26

#### RESULT 19

AA466912

LOCUS

DEFINITION

AA466912 53 bp mRNA linear EST

vf10f03.x1 Knowles Solter mouse blastocyst B3 Mus muscul

clone IMAGE:835325 5' similar to gb:M36829 Mouse heat-st

4 mRNA (MOUSE); mRNA sequence.

6912

6912.1 GI:2193052

musculus (house mouse)

musculus

ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
bases 1 to 53)

a.M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
el, S., Kucaba, I., Lacy, M., Le, M., Martin, J., Morris, M.,  
llenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
sing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
rston, R.

MashU-HMMI Mouse EST Project

blished (1996)

act: Marra M/Mouse EST Project

U-HMMI Mouse EST Project

ington University School of MedicineP

Forest Park Parkway, Box 8501, St. Louis, MO 63108

314 286 1800

314 286 1810

l: mouseest@watson.wustl.edu

clone is available royalty-free through LNL; contact the  
E Consortium (info@image.lnl.gov) for further information.

495541

e considered overall poor quality

or to vector length read

or to vector length is 120

quality sequence stop: 1.

Location/Qualifiers

1. .53

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J x DBA/2J F1"

/db\_xref="taxon:10090"

/clone="IMAGE:835325"

/tissue\_type="blastocyst"

/dev\_stage="embryo (pre-implantation)"

/lab\_host="DH10B"

/clone\_lib="Knowles Solter mouse blastocyst B3"

/note="Organ: embryo; Vector: pSPORT; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally from mRNA prepared

from 800 blastocysts. Primer: SalI(dn):

5'-CGGTCGACCGTCGACCGTTTTTTT-3'. cDNAs were

cloned into the NotI/SalI sites of a pSPORT vector (Life

Technologies). Two different size selections: B1 (larger

inserts) and B3."

64.7%; Score 11; DB 9; Length 53;

similarity 100.0%; Pred. No. 1.9e+05;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGATCCCT 16

|||||

AGATCCCT 16

30373 8124D09.2EL x1 1008 - RescueMu Grid I Zea mays genomic, genomic  
vey sequence.

00373

00373.1 GI:20312363

mays

mays

aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

matophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

de; Panicoideae; Andropogoneae; Zea.

(bases 1 to 57)

AUTHORS  
TITLE  
JOURNAL  
COMMENT

Walbot, V.  
Maize genomic sequences found using engineered RescueMu  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221

Email: walbot@stanford.edu  
Possible ligation site of ends cut by 2 different endonu  
Reverse complemented post-ligation sequence from source  
Plate: 1008124 row: 32  
Class: transposon-tagged.

FEATURES  
source

1. .57  
Location/Qualifiers  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1008 - RescueMu Grid I"  
/note="Organ: leaf; Vector: RescueMu (engineere  
pBlueScript backbone); Site\_1: BamHI; Site\_2: B  
RescueMu is a 4.9 Kb, modified maize Mu transpc  
designed to allow plasmid rescue from total gen  
Mu elements insert preferentially into transcri  
units. For more information on RescueMu, go to  
site www.zmdb.iastate.edu and follow the links  
'RescueMu.' Grid I was grown at Berkeley in 200  
extracted from leaf punches, double digested u  
and BglII, and ligated to form circular plasmid  
cells were transformed and then screened on LB  
ampicillin."

ORIGIN

Query Match 64.7%; Score 11; DB 28; Length 57;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 2 GAGTCGAGATC 12

|||||

DB 47 GAGTCGAGATC 57

RESULT 21

AL767128/c

LOCUS AL767128 59 bp DNA linear GSS  
Arabidopsis thaliana T-DNA flanking sequence GK-216G01-(  
genomic survey sequence.

ACCESSION AL767128

VERSION AL767128.1 GI:21520247

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidoj

REFERENCE 1

Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., S  
and Weissnaar, B.

A pipeline for automated high-throughput generation of l  
(flanking sequence tags) from Arabidopsis thaliana T-DN  
transformed lines

Unpublished

REFERENCE 2

Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and W  
A new Arabidopsis thaliana T-DNA mutagenised population  
for flanking sequence tag based reverse genetics

Unpublished

JOURNAL

REFERENCE 3 (bases 1 to 59)

hov,N., Li,Y., Rosso,M. and Weisshaar,B.  
 at Submission  
 tted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer  
 tungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 ates an insertion within the locus defined by clone R6F9. The  
 nces are generated at the MPI for Plant Breeding Research in  
 :ontext of the GABI-Kat project. GABI-Kat is part of the German  
 : Genomics program designated 'GABI'. Information on line  
 ability can be found at:  
 //www.mpi-z-koeln.mpg.de/GABI-Kat/.  
 Location/Qualifiers

1. .59  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-216G01-014145"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /notes="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

64.7%; Score 11; DB 29; Length 59;  
 ilarity 100.0%; Pred. No. 2e+05;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FTGAAGATC 12

|||||

FTGAAGATC 24

2034  
 IG04EL1F1034 Phosphate starved leaf Medicago truncatula cDNA  
 3 NF064G04PL 5', mRNA sequence.  
 3034  
 3034.1 GI:11903192

ago truncatula (barrel medic)  
 ago truncatula  
 cyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 natophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 is; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
 ago.

ases 1 to 60)  
 J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
 ss,H.R., Iman,J.T., Wellner,J.W., May,G.D. and Harrison,M.J.  
 ssed Sequence Tags from the Samuel Roberts Noble Foundation  
 ago truncatula phosphate-starved leaf library  
 ublished (2000)

act: Harrison MJ  
 t Biology Division  
 Samuel Roberts Noble Foundation  
 Sam Noble Parkway, Ardmore, OK 73402, USA  
 580 221 7325  
 580 221 7380

l: mjharrison@noble.org  
 rt Length: 60 Std Error: 0.00  
 e: 064 row: G column: 04  
 primer: TCACACAGGAACAGCTATGAC.  
 Location/Qualifiers

1. .60  
 /organism="Medicago truncatula"  
 /mol\_type="mRNA"

/db\_xref="taxon:3880"  
 /clone="NF064G04PL"  
 /tissue\_type="leaf"  
 /dev\_stage="trifoliolate"  
 /clone\_lib="Phosphate starved leaf"  
 /note="Vector: Lambda Zap; At the trifoliolate st;  
 truncatula plants were transplanted to phosphat;  
 and grown for a further 30 days. During this 3;  
 period, the plants were fertilized twice weekly  
 Hoaglands solution containing only 20uM potassi;  
 phosphate. RNA was prepared from above ground

# ORIGIN

Query Match 64.7%; Score 11; DB 10; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 2e+05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 1 CGAGTGAAGAT 11

|||||

Db 5 CGAGTGAAGAT 15

# RESULT 23

AZ423553

LOCUS

DEFINITION

clone UUGCLM0202N09 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Genome Center

RM. 308, Biomedical

Polymers Research Bldg., 20 S. 2030

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: adunn@genetics.utah.edu

Insert Length: 10000

Plate: 0202

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGCLM0202N09"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, TI-resista"

/clone\_lib="Mouse 10kb plasmid UUGCLM library"

/note="Vector: PWD42nv; Purified genomic DNA fr"

musculus C57BL/6J (male) was obtained from the

laboratory Jax DNA Resource

(http://www.jax.org/resources/documents/dnares/

was hydrodynamically sheared by repeated passag

0.005 inch orifice at constant velocity. The sh

was blunt end-repaired with T4 DNA polymerase a

polynucleotide kinase. Adaptor oligonucleotides

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 63.5%; Score 10.8; DB 28; Length 22;  
Best Local Similarity 85.7%; Pred. No. 1.8e+05;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GAAGATCCCGCTT 17  
|||||  
GAACATCCCACTT 16

4980 29 bp DNA linear GSS 27-APR-2001  
80607R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
e UUGC2M0280G07 R, genomic survey sequence.

4980.1 GI:13866207

musculus (house mouse)

LOCUS  
DEFINITION  
Eukaryote; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Rodentia; Sciurognathi; Muridae; Musinae; Mus.  
bases 1 to 29)

Authors: Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
M.H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Ly, M., Rose, R., Stokes, R., Tingey, A., von  
erhausen, A. and Wright, D., Weiss, R.

The whole genome scaffolding with paired end reads from 10kb  
mid inserts

blished (2000)

act: Robert B. Weiss  
ersity of Utah Genome Center

ersity of Utah  
308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
2, USA

801 585 5606

801 585 7177

l: ddunn@genetics.utah.edu

rt Length: 10000. Std Error: 0.00

e: 0280 row: G column: 07

primer: CACACAGGAACAGCTATGACC

s: plasmid ends

quality sequence stop: 29.

Location/Qualifiers

1..29

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="CS7BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0280G07"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus CS7BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess adapted DNA was purified and size-selected for 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 63.5%; Score 10.8; DB 28; Length 29;  
Best Local Similarity 85.7%; Pred. No. 1.9e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0;

Qy 2 GAGTGAAGATCCCC 15  
|||||  
Db 18 GAGTGAAGATTCAC 5

# RESULT 25

BJ064687

LOCUS

DEFINITION  
BJ064687 NIBB Mochii normalized Xenopus tailbud library  
laevis cDNA clone XL080g16 5', mRNA sequence.

ACCESSION

BJ064687

VERSION

BJ064687.1 GI:17471662

KEYWORDS

EST.

SOURCE

ORGANISM

Xenopus laevis (African clawed frog)

Xenopus laevis

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pip

Xenopodinae; Xenopus.

1 (bases 1 to 36)

Kitayama, A., Terakawa, C., Mochii, M., Ueno, N., Shin-i, T.

Kohara, Y.

Expressed genes in X. laevis embryo

Unpublished (2001)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp

The information of this clone is available through the f

URL: <http://xenopus.nibb.ac.jp>.

Location/Qualifiers

1..36

/organism="Xenopus laevis"

/mol\_type="mRNA"

/db\_xref="taxon:8355"

/clone="XL080g16"

/tissue\_type="whole embryo"

/dev\_stage="stage 25"

/clone\_lib="NIBB Mochii normalized Xenopus tail

library"

# ORIGIN

Query Match 63.5%; Score 10.8; DB 12; Length 36;  
Best Local Similarity 85.7%; Pred. No. 2.1e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0;

Qy 4 GTGAAGATCCCGCTT 17  
|||||  
Db 2 GTGAACACCCCGCTT 15

# RESULT 26

HSMC39C10



9C10  
 iens DNA for trapped exon (ID HMC39C10), genomic survey  
 nce.  
 10  
 0.1 GI:1437968  
 sapiens (human)  
 sapiens  
 yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 lia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 ases 1 to 38)  
 H..Chrast,R., Rossier,C., Morris,M.A., Lalioti,M.D. and  
 arakis,S.E.  
 ng of 559 potential exons of genes of human chromosome 21 by  
 trapping  
 ie Res. 6 (8), 747-760 (1996)  
 340  
 50  
 ases 1 to 38)  
 H.M., Rossier,C., Chrast,R. and Antonarakis,S.E.  
 ng of trapped exons from human chromosome 21  
 lished  
 ases 1 to 38)  
 arakis,S.E.  
 t Submission  
 ted (17-MAR-1995) Stylianos E. Antonarakis, Division of  
 al Genetics, University and Cantonal Hospital of Geneva, CMU,  
 : Michel-Servet, 1211 Geneva, SWITZERLAND  
 Location/Qualifiers  
 1  
 38  
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 /db\_xref="taxon:9606"  
 /chromosome="21"  
 1  
 38  
 /note="trapped exon"  
 63.5%; Score 10.8; DB 29; Length 38;  
 larity 85.7%; Pred.No.2.1e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 TGAAGATCCCC 15'  
 |||||  
 AGAAGCTCCCC 26'  
 310  
 dopsis thaliana T-DNA flanking sequence GK-303C11-015560,  
 ic survey sequence.  
 310  
 310.1 GI:24403932  
 dopsis thaliana (thale cress)  
 dopsis thaliana  
 yota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 atophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ls; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 :hov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.  
 eisshaar,B.  
 eline for automated high-throughput generation of FSTs  
 iking sequence tags) from Arabidopsis thaliana T-DNA  
 :formed lines  
 lished  
 ,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
 ; Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 :lanking sequence tag based reverse genetics  
 lished  
 ases 1 to 40)

AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 FEATURES  
 source  
 1. 40  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strains="Columbia 0"  
 /db\_xref="taxon:3702"  
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 /clone\_lib="Arabidopsis thaliana T-DNA insertior  
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 plants (T1) which were transformed with the T-DNA  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the  
 were directly sequenced to determine the genomic  
 flanking the insertion. Sequences displaying sig  
 similarity to the A. thaliana nuclear genome se  
 processed for submission. T-DNA derived sequence  
 removed"  
 ORIGIN  
 Query Match 63.5%; Score 10.8; DB 29; Length 40;  
 Best Local Similarity 85.7%; Pred.No.2.2e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0;  
 QY 1 CGAGTGAAGATCCCC 14  
 |||||  
 Db 28 CGAGTGAATGATGCC 15  
 RESULT 28  
 AZ598104  
 LOCUS  
 IM0412M.2R Mouse 10kb plasmid UUGC1M library Mus musculus  
 clone UUGC1M0412M12 R, genomic survey sequence.  
 AZ598104  
 AZ598104.1 GI:11720294  
 GSS.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur  
 1 (bases 1 to 41)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hami  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingley,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0412 row: M column: 12  
 Seq primer: CACACAGGAACACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 41.  
 Location/Qualifiers  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 FEATURES

1. .41  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0412M12"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

63.5%; Score 10.8; DB 28; Length 41;  
 ilarity 85.7%; Pred. No. 2.2e+05; Mismatches 2; Indels 0; Gaps 0;  
 Conservative 0;

AGTGAAGATCCC 14  
 |||||  
 TTGTGATATCCC 34

1610 43 bp DNA linear GSS 04-DEC-2002  
 idopsis thaliana T-DNA flanking sequence GK-357D05-016834,  
 mic survey sequence.

1610.1 GI:26186570  
 idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 zhov.N., Li.Y., Rosso.M., Viehoveer.P., Dekker,K., Saedler,H.  
 Weishaar,B.  
 peline for automated high-throughput generation of ESTs  
 nking sequence tags) from Arabidopsis thaliana T-DNA  
 formed lines  
 blished

O.M., Strizhov.N., Li.Y., Reiss.B., Dekker,K. and Weishaar,B.  
 w Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 flanking sequence tag based reverse genetics  
 blished  
 bases 1 to 43)  
 zhov.N., Rosso.M., Li.Y. and Weishaar,B.  
 ct Submission  
 itted (04-DEC-2002) Weishaar B., Max-Planck-Institut fuer  
 htungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 cates an insertion within the locus defined by clone K22F20.  
 sequences are generated at the MPI for Plant Breeding Research  
 he context of the GABI-Kat project. GABI-Kat is part of the

German Plant Genomics program designated 'GABI'. Informa  
 line availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

#### FEATURES source

1. .43  
 Location/Qualifiers  
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 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
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 /clone\_lib="Arabidopsis thaliana T-DNA insertio  
 /note="PCR was performed on DNA from Arabidopsi  
 plants (T1) which were transformed with the T-D  
 vector pAC161. The lines contain one or more T-  
 insertions. The DNA fragment(s) resulting from  
 were directly sequenced to determine the genom  
 flanking the insertion. Sequences displaying si  
 milarity to the A. thaliana nuclear genome se  
 processed for submission. T-DNA derived sequenc  
 removed"

#### ORIGIN

Query Match 63.5%; Score 10.8; DB 29; Length 43;  
 Best Local Similarity 85.7%; Pred. No. 2.2e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0;

Qy 3 AGTGAAGATCCCCT 16  
 |||||  
 AGGGAAGATCCCAT 23

Db 36 AGGGAAGATCCCAT 23

#### RESULT 30

EX625656  
 LOCUS BX625656 NAPI Anopheles gambiae cDNA clone ANGNP1153F02T  
 DEFINITION sequence.  
 BX625656  
 BX625656.1 GI:33551353

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Anopheles gambiae (African malaria mosquito)  
 Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Insecta; Ptery  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea  
 Anopheles.

REFERENCE  
 AUTHORS Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.  
 TITLE Anopheles gambiae EST, Center for Tropical Disease Resea  
 JOURNAL Training  
 COMMENT Unpublished (2003)  
 Contact: Frank H. Collins  
 Center for Tropical Disease Research and Training  
 University of Notre Dame  
 Notre Dame, IN 46556, USA  
 Tel: 574-631-9245  
 Fax: 574-631-3996  
 Email: frank.h.collins.75@nd.edu.

1 (bases 1 to 44)  
 Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.  
 Anopheles gambiae EST, Center for Tropical Disease Resea  
 Training  
 Unpublished (2003)  
 Contact: Frank H. Collins  
 Center for Tropical Disease Research and Training  
 University of Notre Dame  
 Notre Dame, IN 46556, USA  
 Tel: 574-631-9245  
 Fax: 574-631-3996  
 Email: frank.h.collins.75@nd.edu.

Location/Qualifiers  
 1. .44  
 /organism="Anopheles gambiae"  
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 /lab\_host="E. coli DH10B"  
 /clone\_lib="NAPI"  
 /note="Vector: pT73D-Pac (Pharmacia); Site 1:  
 Site 2: EcoRI; ESTs sequenced from the T7 primi  
 that reads from the 5' end of cDNA. The NAPI is  
 directionally cloned and normalized. Oligo-T pr  
 library constructed from a mixture of Anopheles  
 developmental stages according to: Bonaldo, Len  
 Soares (1996): Normalization and Subtraction: T  
 Approaches To Facilitate Gene Discovery, Genome  
 6, 791-806."

FEATURES  
 source  
 1. .44  
 Location/Qualifiers  
 /organism="Anopheles gambiae"  
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 /lab\_host="E. coli DH10B"  
 /clone\_lib="NAPI"  
 /note="Vector: pT73D-Pac (Pharmacia); Site 1:  
 Site 2: EcoRI; ESTs sequenced from the T7 primi  
 that reads from the 5' end of cDNA. The NAPI is  
 directionally cloned and normalized. Oligo-T pr  
 library constructed from a mixture of Anopheles  
 developmental stages according to: Bonaldo, Len  
 Soares (1996): Normalization and Subtraction: T  
 Approaches To Facilitate Gene Discovery, Genome  
 6, 791-806."

63.5%; Score 10.8; DB 13; Length 44;  
 larity 85.7%; Pred. No. 2.3e+05; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 GTGAAGATCCCC 15  
 ||||| |||||  
 TGAATTTCGCC 18

311 44 bp DNA linear GSS 24-OCT-2002  
 dopsis thaliana T-DNA flanking sequence GK-303C11-015563,  
 dic survey sequence.

311.1 GI:24403933  
 dopsis thaliana (thale cress)  
 dopsis thaliana  
 yoka; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 atophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 is; eucosids II; Brassicales; Brassicaceae; Arabidopsiis;

hov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.  
 Feisshaar,B.  
 eline for automated high-throughput generation of FSTs  
 eking sequence tags) from Arabidopsis thaliana T-DNA  
 ished lines

,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
 Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 lanking sequence tag based reverse genetics  
 ished

ases 1 to 44)  
 hov,N., Li,Y., Rosso,M. and Weisshaar,B.  
 t Submission  
 tted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer  
 tungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 ates an insertion within the locus defined by clone T25K17.  
 sequences are generated at the MPI for Plant Breeding Research  
 e context of the GABI-Kat project. GABI-Kat is part of the  
 n Plant Genomics program designated 'GABI'. Information on  
 availability can be found at:  
 //www.mpiz-koeln.mpg.de/GABI-Kat/  
 Location/Qualifiers

1..44  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
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 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

63.5%; Score 10.8; DB 29; Length 44;  
 larity 85.7%; Pred. No. 2.3e+05; Indels 0; Gaps 0;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 GTGAAGATCCCC 14  
 ||||| |||||

Db 31 CGAGTGATGATGCC 18

RESULT 32  
 AA410197 46 bp mRNA linear EST J  
 LOCUS zV32d06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clc  
 DEFINITION IMAGE:755339 5', similar to TR:G307153 G307153 MAC-2 BIND:  
 PRECURSOR. ;, mRNA sequence.

ACCESSION AA410197  
 VERSION AA410197.1 GI:2069220  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo  
 1 (bases 1 to 46)  
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G.,  
 Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,  
 Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,I,  
 White,Y., Wylie,T., Waterston,R. and Wilson,R.  
 TITLE WashU-Werck EST Project 1997  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estewatson.wustl.edu  
 This clone is available royalty-free through LNL; conta  
 IMAGE Consortium (info@image.llnl.gov) for further inform  
 Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28m3 rev2 ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

FEATURES  
 source  
 1..46  
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 /clone="IMAGE:755339"  
 /sex="Female"  
 /tissue\_type="ovarian tumor"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares ovary tumor NbHOT"  
 /note="Organ: ovary; Vector: pT73D (Pharmacia)  
 modified polylinker; Site 1: Not I; Site 2: Eco  
 strand cDNA was primed with a Not I oligo (dT)  
 TGTACCAATCTGAAGTGGAGCGCGGCTTTTCTTTTCTTTT  
 double-stranded cDNA was size selected, ligated  
 adapters (Pharmacia), digested with Not I and c  
 the Not I and Eco RI sites of a modified pT73 (v  
 (Pharmacia). Library constructed by Bento Soares  
 M.Fatima Bonaldo."

ORIGIN  
 Query Match 63.5%; Score 10.8; DB 9; Length 46;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0;  
 QY 4 GTGAAGATCCCCTT 17  
 ||||| |||||  
 Db 23 GAGAAGATCCGCTT 36

RESULT 33  
 BH759458/c  
 LOCUS BH759458  
 DEFINITION KG04418-3prime Drosophila melanogaster P(SUPor-P) p elem  
 insertion lines Drosophila melanogaster genomic Sequence  
 from 3', end of P element, genomic survey sequence.

ACCESSION BH759458  
 VERSION BH759458.1 GI:19352697



ences are generated at the MPI for Plant Breeding Research in context of the GABI-Kat project. GABI-Kat is part of the German t Genomics program designated 'GABI'. Information on line labiliy can be found at:  
 ://www.mpiz-koeln.mpg.de/GABI-Kat/.  
 Location/Qualifiers

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1. .46
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"
```

ilarity 63.5%; Score 10.8; DB 29; Length 46;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
TGAAGATCCCT 16
|||||||
GGAGATCCAT 24
```

2068 idopsis thaliana T-DNA flanking sequence GK-340G01-016161,  
 mac survey sequence.

2068.1 GI:24408690

idopsis thaliana (thale cress)  
 idopsis thaliana  
 ryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 ds; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

zhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.  
 Weisshaar,B.  
 peline for automated high-throughput generation of FSTs  
 nking sequence tags) from Arabidopsis thaliana T-DNA  
 stformed lines  
 blished

O.M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
 w Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 flanking sequence tag based reverse genetics

bases 1 to 47)  
 .. Rosso,M., Strizhov,N. and Weisshaar,B.  
 ct Submission

itted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer  
 hungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 sequence is recovered from the left border of the T-DNA. It  
 cates an insertion within the locus defined by clone F16N3. The  
 ences are generated at the MPI for Plant Breeding Research in  
 context of the GABI-Kat project. GABI-Kat is part of the German  
 t Genomics program designated 'GABI'. Information on line  
 labiliy can be found at:  
 ://www.mpiz-koeln.mpg.de/GABI-Kat/.  
 Location/Qualifiers

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1. .47
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/note="PCR was performed on DNA from Arabidopsis plants (T1) which were transformed with the T-DNA vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"
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Query Match 63.5%; Score 10.8; DB 29; Length 47;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0;

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Oy 3 AGTGAAGATCCCT 16
|||||||
Db 46 AGTGAAGATGCCAT 33
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RESULT 37  
 BX291286/c  
 LOCUS BX291286 49 bp DNA linear GSS  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-461D01-0  
 Genomic survey sequence.

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ACCESSION BX291286
VERSION BX291286.1 GI:28890282
KEYWORDS GSS.
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SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudic  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidof

1 Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., S  
 and Weisshaar,B.  
 A pipeline for automated high-throughput generation of F  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines  
 Unpublished

2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and We  
 A new Arabidopsis thaliana T-DNA mutagenised population  
 for flanking sequence tag based reverse genetics

Unpublished  
 3 (bases 1 to 49)  
 Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.

Direct Submission  
 Submitted (07-MAR-2003) Weisshaar B., Max-Planck-Institu  
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829  
 This sequence is recovered from the left border of the T  
 indicates an insertion close to or within gene At1g07530  
 sequences are generated at the MPI for Plant Breeding Re  
 the context of the GABI-Kat project. GABI-Kat is part of  
 Plant Genomics program designated 'GABI'. Information on  
 availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1. .49

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/note="PCR was performed on DNA from Arabidopsis plants (T1) which were transformed with the T-DNA vector pAC161. The lines contain one or more T-
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insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

63.5%; Score 10.8; DB 29; Length 49;  
 ilarity 85.7%; Pred. No. 2.3e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAAGATCCCT 16  
 |||||  
 XGAGGATCCCT 35

13576 50 bp mRNA linear EST 30-AUG-2001  
 13576 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 1416, mRNA sequence.

13576.1 GI:13553097

rganism (human)  
 sapiens  
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 (bases 1 to 50)  
 ki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese.J.,  
 i.H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Okubo.K.,  
 ki.Y., Nakamura.Y., Suyama.A. and Sugano.S.  
 rse transcriptional initiation revealed by fine, large-scale  
 ing of mRNA start sites  
 ) Rep. 2 (5), 388-393 (2001)  
 0072  
 5929

act: Yutaka Suzuki  
 ument of Virology  
 itute of Medical Science, University of Tokyo  
 1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 l: ysuzuki@ims.u-tokyo.ac.jp  
 ki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and  
 no.S. Construction and characterization of a full  
 th-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 156 (1997).

Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /clone\_lib="Sugano Homo sapiens cDNA library"

63.5%; Score 10.8; DB 9; Length 50;  
 ilarity 85.7%; Pred. No. 2.4e+05;  
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GTGAAGATCCCC 15  
 |||||  
 XGTGAAGTCCCC 21

16261 50 bp mRNA linear EST 30-AUG-2001  
 16261 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 14205, mRNA sequence.  
 16261  
 16261.1 GI:13555782

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo  
 REFERENCE 1 (bases 1 to 50)  
 AUTHORS Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese.J., Hata.H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Okubo.K., Nakamura.Y., Suyama.A. and Sugano.S.  
 TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 MEDLINE 21270072  
 PUBMED 11375929  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A.  
 Sugano.S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene  
 149-156 (1997).

FEATURES  
 source  
 Location/Qualifiers  
 1..50  
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 /clone="KA1A4205"  
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## ORIGIN

Query Match 63.5%; Score 10.8; DB 9; Length 50;  
 Best Local Similarity 85.7%; Pred. No. 2.4e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0;

QY 4 GTGAAGATCCCTT 17  
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DB 29 GTGGAGATCCCAT 16  
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## RESULT 40

AA795116/c

LOCUS  
 vs10d10.r1 Barstead mouse irradiated colon MPLRB7 Mus mus  
 clone IMAGE:1137811 5' similar to gb:U15647 cds1 Mus mus  
 (MOUSE);, mRNA sequence.

ACCESSION  
 AA795116  
 VERSION  
 AA795116.1 GI:2858071

KEYWORDS  
 EST.  
 SOURCE  
 Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus  
 1 (bases 1 to 52)  
 Marra.M., Hillier.L., Allen.M., Bowles.M., Dietrich.N.,  
 Geisler.S., Kucaba.T., Lacy.M., Le.M., Martin.J., Morris,  
 Schellenberg.K., Steptoe.M., Tan.F., Underwood.K., Moore,  
 Theising.B., Wylie.T., Lennon.G., Soares.B., Wilson.R. &  
 Waterston.R.

## REFERENCE

AUTHORS

TITLE  
 The WashU-HMI Mouse EST Project  
 JOURNAL  
 Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact  
 IMAGE Consortium (info@image.llnl.gov) for further information  
 MGI:619083  
 Trace considered overall poor quality  
 Seq primer: -28ml3 rev2 ET from Amersham



53866  
53866.1 GI:21424737

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
(bases 1 to 54)

SO, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
tinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
in, P., Zimmerman, J., and Ecker, J.R.  
sequence-indexed library of insertion mutations in the  
Arabidopsis Genome  
ublished (2001)

act: Joseph R. Ecker  
Institute Genomic Analysis Laboratory (IGNAL)  
Salk Institute for Biological Studies  
10 N. Torrey Pines Road, La Jolla, CA 92037, USA  
: 858 453 4100 x1752  
: 858 558 6379  
il: ecker@salk.edu  
s is single pass sequence recovered from the left border of  
A.

ss: TDNA tagged.  
Location/Qualifiers.  
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each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

ilarity 63.5%; Score 10.8; DB 28; Length 54;  
Conservative 85.7%; Pred. No. 2.4e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AGTGAAGATCCGC 15  
|||||  
AGTGAATACC 19

10566  
Arabidopsis thaliana T-DNA flanking sequence GK-249D07-01444,  
omic survey sequence.

10566.1 GI:24397015

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliophyta; eudicotyledons; core eudicots;  
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

zhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.  
Weishaar, B.  
ipeline for automated high-throughput generation of FSTs  
anking sequence tags) from Arabidopsis thaliana T-DNA  
nsformed lines  
ublished

so, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.  
Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Unpublished  
3 (bases 1 to 54)  
Rosso, M., Strizhov, N., Li, Y. and Weishaar, B.  
Direct Submission  
Submitted (21-OCT-2002) Weishaar B., Max-Planck-Institut  
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 5082  
This sequence is recovered from the left border of the  
indicates an insertion close to or within gene Atg3440  
sequences are generated at the MPI for Plant Breeding R  
the context of the GABI-Kat project. GABI-Kat is part o  
Plant Genomics program designated 'GABI'. Information o  
availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES  
source  
Location/Qualifiers  
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/note="PCR was performed on DNA from Arabidops  
plants (T1) which were transformed with the T-  
vector PAC161. The lines contain one or more T  
insertions. The DNA fragment(s) resulting from  
were directly sequenced to determine the genom  
flanking the insertion. Sequences displaying s  
similarity to the A. thaliana nuclear genome s  
processed for submission. T-DNA derived sequen  
removed"

ORIGIN  
Query Match 63.5%; Score 10.8; DB 29; Length 54;  
Best Local Similarity 85.7%; Pred. No. 2.4e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0;

QY 3 AGTGAAGATCCGC 16  
|||||  
Db 47 AGTGAATCCAT 34

RESULT 45  
BM022920  
LOCUS  
DEFINITION  
id63f10.y1 Melton Normalized Mixed Mouse Pancreas 1 NI-1  
musculus cDNA clone IMAGE:5667979 5', mRNA sequence.

ACCESSION  
BM022920  
VERSION  
BM022920.1 GI:16537276  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu

REFERENCE  
AUTHORS  
1 (bases 1 to 55)  
Melton, D., Brown, J., Kent, G., Permutt, A., Lee, C., Kaest  
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clif  
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blis  
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.  
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, Y.  
Williams, T., Jackson, Y. and Bowers, Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Ii  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu  
Library was constructed by Dr. Douglas Melton DNA sequer  
Washington University Genome Sequencing Center For info:



09:38:24 2004

us-10-090-326-17.max.rst

ining a clone please contact: Juliana Brown  
wh@fas.harvard.edu  
1954305 This sequence now available from the IMAGE consortium,  
clone orders contact: info@image.llnl.gov.

Location/Qualifiers  
1. 55  
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/mol\_type="mRNA"  
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adult islet"  
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adult, mixed"  
/lab\_host="DH10B"  
/clone\_lib="Melton Normalized Mixed Mouse Pancreas 1  
N1-MMS1"  
/note="vector: pSPORT1; Site 1: Not I; Site 2: Sal I; Five  
libraries representing E10.5/12.5 pancreatic bud, E16.5  
pancreas, newborn pancreas, adult pancreas, and adult  
islets of Langerhans were separately constructed using  
SuperScript Plasmid Library kit (Life Technologies). cDNA  
was made by oligo-dT priming and size-selected by column  
fractionation. Libraries were amplified once on solid  
support and plasmid DNA from each library was prepared  
and mixed in equal amounts. The mixed library DNA was  
normalized by method #4 from Bonaldo, Lennon, and Soares  
1996 Genome Research 6:791-806; 0.5 microgram  
single-stranded mixed library plasmid DNA was mixed with  
5 micrograms PCR product representing mixed library  
inserts and hybridized to an EcoT of 6. Single-stranded  
(unhybridized) plasmids were isolated by hydroxyapatite  
chromatography and used to make this library."

63.5%; Score 10.8; DB 12; Length 55;  
ilarity 85.7%; Pred.No. 2.4e+05;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TGAAGATCCCT 16  
|||||  
TGAATATCCCT 55

: February 29, 2004, 11:21:57  
1 secs